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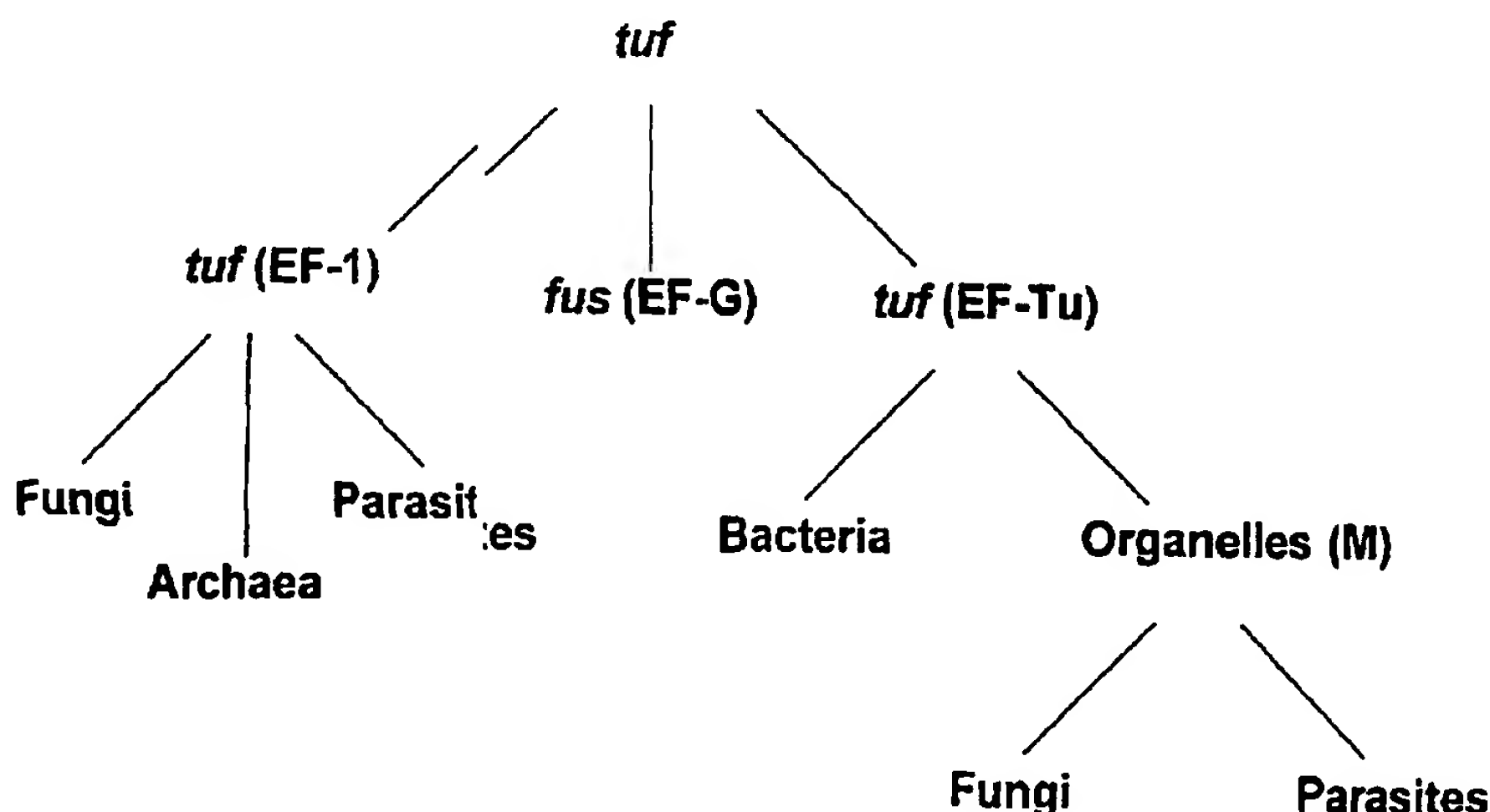
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(54) Title: HIGHLY CONSERVED GENES AND THEIR USE TO GENERATE PROBES AND PRIMERS FOR DETECTION OF MICROORGANISMS



(57) Abstract: Four highly conserved genes, encoding translation elongation factor Tu, translation elongation factor G, the catalytic subunit of proton-translocating ATPase and the RecA recombinase, are used to generate a sequence repertory or bank and species-specific, genus-specific, family-specific, group-specific and universal nucleic acid probes and amplification primers to rapidly detect and identify algal, archaeal, bacterial, fungal and parasitological microorganisms from specimens for diagnosis. The detection of associated antimicrobial agents resistance and toxin genes are also under the scope of the present invention.



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TITLE OF THE INVENTION

HIGHLY CONSERVED GENES AND THEIR USE TO GENERATE SPECIES-SPECIFIC, GENUS-SPECIFIC, FAMILY-SPECIFIC, GROUP-SPECIFIC AND UNIVERSAL NUCLEIC ACID PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY ALGAL, ARCHAEAL, BACTERIAL, FUNGAL AND PARASITICAL MICROORGANISMS FROM CLINICAL SPECIMENS FOR DIAGNOSIS

BACKGROUND OF THE INVENTION***Classical methods for the identification of microorganisms***

Microorganisms are classically identified by their ability to utilize different substrates as a source of carbon and nitrogen through the use of biochemical tests such as the API20E™ system (bioMérieux). For susceptibility testing, clinical microbiology laboratories use methods including disk diffusion, agar dilution and broth microdilution. Although identifications based on biochemical tests and antibacterial susceptibility tests are cost-effective, generally two days are required to obtain preliminary results due to the necessity of two successive overnight incubations to identify the bacteria from clinical specimens as well as to determine their susceptibility to antimicrobial agents. There are some commercially available automated systems (i.e. the MicroScan™ system from Dade Behring and the Vitek™ system from bioMérieux) which use sophisticated and expensive apparatus for faster microbial identification and susceptibility testing (Stager and Davis, 1992, Clin. Microbiol. Rev. 5:302-327). These systems require shorter incubation periods, thereby allowing most bacterial identifications and susceptibility testing to be performed in less than 6 hours. Nevertheless, these

faster systems always require the primary isolation of the bacteria or fungi as a pure culture, a process which takes at least 18 hours for a pure culture or 2 days for a mixed culture. So, the shortest time from sample reception to identification of the pathogen is around 24 hours. Moreover, fungi other than yeasts are often difficult or very slow to grow from clinical specimens. Identification must rely on labor-intensive techniques such as direct microscopic examination of the specimens and by direct and/or indirect immunological assays. Cultivation of most parasites is impractical in the clinical laboratory. Hence, microscopic examination of the specimen, a few immunological tests and clinical symptoms are often the only methods used for an identification that frequently remains presumptive.

The fastest bacterial identification system, the autoSCAN-Walk-Away™ system (Dade Behring) identifies both gram-negative and gram-positive bacterial species from standardized inoculum in as little as 2 hours and gives susceptibility patterns to most antibiotics in 5 to 6 hours. However, this system has a particularly high percentage (i.e. 3.3 to 40.5%) of non-conclusive identifications with bacterial species other than *Enterobacteriaceae* (Croizé J., 1995, Lett. Infectiol. 10:109-113; York *et al.*, 1992, J. Clin. Microbiol. 30:2903-2910). For *Enterobacteriaceae*, the percentage of non-conclusive identifications was 2.7 to 11.4%. The list of microorganisms identified by commercial systems based on classical identification methods is given in Table 15.

A wide variety of bacteria and fungi are routinely isolated and identified from clinical specimens in microbiology laboratories. Tables 1 and 2 give the incidence for the most commonly isolated bacterial and fungal pathogens from various types of clinical specimens. These pathogens are the main organisms associated with nosocomial and community-acquired human infections and are therefore considered the most clinically important.

Clinical specimens tested in clinical microbiology laboratories

Most clinical specimens received in clinical microbiology laboratories are urine and blood samples. At the microbiology laboratory of the Centre Hospitalier de l'Université Laval (CHUL), urine and blood account for approximately 55% and 30% of the specimens received, respectively (Table 3). The remaining 15% of clinical specimens comprise various biological fluids including sputum, pus, cerebrospinal fluid, synovial fluid, and others (Table 3). Infections of the urinary tract, the respiratory tract and the bloodstream are usually of bacterial etiology and require antimicrobial therapy. In fact, all clinical samples received in the clinical microbiology laboratory are tested routinely for the identification of bacteria and antibiotic susceptibility.

Conventional pathogen identification from clinical specimens

Urine specimens

The search for pathogens in urine specimens is so preponderant in the routine microbiology laboratory that a myriad of tests have been developed. However, the gold standard remains the classical semi-quantitative plate culture method in which 1 μ L of urine is streaked on agar plates and incubated for 18-24 hours. Colonies are then counted to determine the total number of colony forming units (CFU) per liter of urine. A bacterial urinary tract infection (UTI) is normally associated with a bacterial count of 10^7 CFU/L or more in urine. However, infections with less than 10^7 CFU/L in urine are possible, particularly in patients with a high incidence of diseases or those catheterized (Stark and Maki, 1984, N. Engl. J. Med. **311**:560-564). Importantly, approximately 80% of urine specimens tested in clinical microbiology laboratories are considered negative (i.e. bacterial count of less than 10^7 CFU/L; Table 3). Urine specimens found positive by culture are further characterized using standard biochemical tests to identify the bacterial pathogen and are also tested for susceptibility to antibiotics. The biochemical and susceptibility testing normally require 18-24 hours of incubation.

Accurate and rapid urine screening methods for bacterial pathogens would allow a faster identification of negative specimens and a more efficient treatment and care management of patients. Several rapid identification methods (Uriscreen™, UTIscreen™, Flash Track™ DNA probes and others) have been compared to slower standard biochemical methods, which are based on culture of the bacterial pathogens. Although much faster, these rapid tests showed low sensitivities and poor specificities as well as a high number of false negative and false positive results (Koenig *et al.*, 1992, J. Clin. Microbiol. 30:342-345; Pezzlo *et al.*, 1992, J. Clin. Microbiol. 30:640-684).

Blood specimens

The blood specimens received in the microbiology laboratory are always submitted for culture. Blood culture systems may be manual, semi-automated or completely automated. The BACTEC™ system (from Becton Dickinson) and the BacTAlert™ system (from Organon Teknika Corporation) are the two most widely used automated blood culture systems. These systems incubate blood culture bottles under optimal conditions for growth of most bacteria. Bacterial growth is monitored continuously to detect early positives by using highly sensitive bacterial growth detectors. Once growth is detected, a Gram stain is performed directly from the blood culture and then used to inoculate nutrient agar plates. Subsequently, bacterial identification and susceptibility testing are carried out from isolated bacterial colonies with automated systems as described previously. Blood culture bottles are normally reported as negative if no growth is detected after an incubation of 6 to 7 days. Normally, the vast majority of blood cultures are reported negative. For example, the percentage of negative blood cultures at the microbiology laboratory of the CHUL for the period February 1994-January 1995 was 93.1% (Table 3).

Other clinical samples

Upon receipt by the clinical microbiology laboratory, all body fluids other than blood and urine that are from normally sterile sites (i.e. cerebrospinal, synovial, pleural, pericardial and others) are processed for direct microscopic examination and subsequent culture. Again, most clinical samples are negative for culture (Table 3). In all these normally sterile sites, tests for the universal detection of algae, archaea, bacteria, fungi and parasites would be very useful .

Regarding clinical specimens which are not from sterile sites such as sputum or stool specimens, the laboratory diagnosis by culture is more problematic because of the contamination by the normal flora. The bacterial or fungal pathogens potentially associated with the infection are grown and separated from the colonizing microbes using selective methods and then identified as described previously. Of course, the DNA-based universal detection of bacteria would not be useful for the diagnosis of bacterial infections at these non-sterile sites. On the other hand, DNA-based assays for species or genus or family or group detection and identification as well as for the detection of antimicrobial agents resistance genes from these specimens would be very useful and would offer several advantages over classical identification and susceptibility testing methods.

DNA-based assays with any specimen

There is an obvious need for rapid and accurate diagnostic tests for the detection and identification of algae, archaea, bacteria, fungi and parasites directly from clinical specimens. DNA-based technologies are rapid and accurate and offer a great potential to improve the diagnosis of infectious diseases (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.; Bergeron and Ouellette, 1995, Infection 23:69-72; Bergeron and Ouellette, 1998, J Clin Microbiol. 36:2169-72). The DNA probes and amplification primers which are objects of the present invention are applicable for the detection and identification of algae, archaea, bacteria, fungi, and parasites directly from any clinical specimen such as blood,

urine, sputum, cerebrospinal fluid, pus, genital and gastro-intestinal tracts, skin or any other type of specimens (Table 3). These assays are also applicable to detection from microbial cultures (e.g. blood cultures, bacterial or fungal colonies on nutrient agar, or liquid cell cultures in nutrient broth). The DNA-based tests proposed in this invention are superior in terms of both rapidity and accuracy to standard biochemical methods currently used for routine diagnosis from any clinical specimens in microbiology laboratories. Since these tests can be performed in one hour or less, they provide the clinician with new diagnostic tools which should contribute to a better management of patients with infectious diseases. Specimens from sources other than humans (e.g. other primates, birds, plants, mammals, farm animals, livestock, food products, environment such as water or soil, and others) may also be tested with these assays.

A high percentage of culture-negative specimens

Among all the clinical specimens received for routine diagnosis, approximately 80% of urine specimens and even more (around 95%) for other types of normally sterile clinical specimens are negative for the presence of bacterial pathogens (Table 3). It would also be desirable, in addition to identify bacteria at the species or genus or family or group level in a given specimen, to screen out the high proportion of negative clinical specimens with a DNA-based test detecting the presence of any bacterium (i.e. universal bacterial detection). As disclosed in the present invention, such a screening test may be based on DNA amplification by PCR of a highly conserved genetic target found in all bacteria. Specimens negative for bacteria would not be amplified by this assay. On the other hand, those that are positive for any bacterium would give a positive amplification signal. Similarly, highly conserved genes of fungi and parasites could serve not only to identify particular species or genus or family or group but also to detect the presence of any fungi or parasite in the specimen.

Towards the development of rapid DNA-based diagnostic tests

A rapid diagnostic test should have a significant impact on the management of infections. DNA probe and DNA amplification technologies offer several advantages over conventional methods for the identification of pathogens and antimicrobial agents resistance genes from clinical samples (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.; Ehrlich and Greenberg, 1994, PCR-based Diagnostics in Infectious Disease, Blackwell Scientific Publications, Boston, MA). There is no need for culture of the pathogens, hence the organisms can be detected directly from clinical samples, thereby reducing the time associated with the isolation and identification of pathogens. Furthermore, DNA-based assays are more accurate for microbial identification than currently used phenotypic identification systems which are based on biochemical tests and/or microscopic examination. Commercially available DNA-based technologies are currently used in clinical microbiology laboratories, mainly for the detection and identification of fastidious bacterial pathogens such as *Mycobacterium tuberculosis*, *Chlamydia trachomatis*, *Neisseria gonorrhoeae* as well as for the detection of a variety of viruses (Tang Y. and Persing D. H., Molecular detection and identification of microorganisms, In: P. Murray *et al.*, 1999, Manual of Clinical Microbiology, ASM press, 7th edition, Washington D.C.). There are also other commercially available DNA-based assays which are used for culture confirmation assays.

Others have developed DNA-based tests for the detection and identification of bacterial pathogens which are objects of the present invention, for example: *Staphylococcus* sp. (US patent serial no. 5,437,978), *Neisseria* sp. (US patent serial no. 5,162,199 and European patent serial no. 0,337,896,131) and *Listeria monocytogenes* (US patent serial nos. 5,389,513 and 5,089,386). However, the diagnostic tests described in these patents are based either on rRNA genes or on genetic targets different from those described in the present invention. To our knowledge there are only four patents published by others mentioning the use of

any of the four highly conserved gene targets described in the present invention for diagnostic purposes (PCT international publication number WO92/03455 and WO00/14274, European patent publication number 0 133 671 B1, and European patent publication number 0 133 288 A2). WO92/03455 is focused on the inhibition of *Candida* species for therapeutic purposes. It describes antisense oligonucleotide probes hybridizing to *Candida* messenger RNA. Two of the numerous mRNA proposed as targets are coding for translation elongation factor 1 (tef1) and the beta subunit of ATPase. DNA amplification or hybridization are not under the scope of their invention and although diagnostic use is briefly mentioned in the body of the application, no specific claim is made regarding diagnostics. WO00/14274 describes the use of bacterial *recA* gene for identification and speciation of bacteria of the *Burkholderia cepacia* complex. Specific claims are made on a method for obtaining nucleotide sequence information for the *recA* gene from the target bacteria and a following comparison with a standard library of nucleotide sequence information (claim 1), and on the use of PCR for amplification of the *recA* gene in a sample of interest (claims 4 to 7, and 13). However, the use of a discriminatory restriction enzyme in a RFLP procedure is essential to fulfill the speciation and WO00/14274 did not mention that multiple *recA* probes could be used simultaneously. Patent EP 0 133 288 A2 describes and claims the use of bacterial *tuf* (and *fus*) sequence for diagnostics based on hybridization of a *tuf* (or *fus*) probe with bacterial DNA. DNA amplification is not under the scope of EP 0 133 288 A2. Nowhere it is mentioned that multiple *tuf* (or *fus*) probes could be used simultaneously. No mention is made regarding speciation using *tuf* (or *fus*) DNA nucleic acids and/or sequences. The sensitivities of the *tuf* hybridizations reported are 1×10^6 bacteria or 1-100 ng of DNA. This is much less sensitive than what is achieved by our assays using nucleic acid amplification technologies.

Although there are phenotypic identification methods which have been used for more than 125 years in clinical microbiology laboratories, these methods do not provide information fast enough to be useful in the initial management of patients.

There is a need to increase the speed of the diagnosis of commonly encountered bacterial, fungal and parasitical infections. Besides being much faster, DNA-based diagnostic tests are more accurate than standard biochemical tests presently used for diagnosis because the microbial genotype (e.g. DNA level) is more stable than the phenotype (e.g. physiologic level).

Bacteria, fungi and parasites encompass numerous well-known microbial pathogens. Other microorganisms could also be pathogens or associated with human diseases. For example, achlorophyllous algae of the *Prototheca* genus can infect humans. Archae, especially methanogens, are present in the gut flora of humans (Reeve, J.H., 1999, J. Bacteriol. **181**:3613-3617). However, methanogens have been associated to pathologic manifestations in the colon, vagina, and mouth (Belay *et al.*, 1988, Appl. Enviro. Microbiol. **54**:600-603; Belay *et al.*, 1990, J. Clin. Microbiol. **28**:1666-1668; Weaver *et al.*, 1986, Gut **27**:698-704).

In addition to the identification of the infectious agent, it is often desirable to identify harmful toxins and/or to monitor the sensitivity of the microorganism to antimicrobial agents. As revealed in this invention, genetic identification of the microorganism could be performed simultaneously with toxin and antimicrobial agents resistance genes.

Knowledge of the genomic sequences of algal, archaeal, bacterial, fungal and parasitical species continuously increases as testified by the number of sequences available from public databases such as GenBank. From the sequences readily available from those public databases, there is no indication therefrom as to their potential for diagnostic purposes. For determining good candidates for diagnostic purposes, one could select sequences for DNA-based assays for (i) the species-specific detection and identification of commonly encountered bacterial, fungal and parasitical pathogens, (ii) the genus-specific detection and identification of commonly encountered bacterial, fungal or parasitical pathogens, (iii) the family-specific detection and identification of commonly encountered bacterial, fungal or parasitical pathogens, (iv) the group-specific detection and identification of commonly encountered bacterial, fungal or parasitical pathogens, (v) the

universal detection of algal, archaeal, bacterial, fungal or parasitical pathogens, and/or (vi) the specific detection and identification of antimicrobial agents resistance genes, and/or (vii) the specific detection and identification of bacterial toxin genes. All of the above types of DNA-based assays may be performed directly from any type of clinical specimens or from a microbial culture.

In our assigned U.S. patent 6,001,564 and our WO98/20157 patent publication, we described DNA sequences suitable for (i) the species-specific detection and identification of clinically important bacterial pathogens, (ii) the universal detection of bacteria, and (iii) the detection of antimicrobial agents resistance genes.

The WO98/20157 patent publication describes proprietary *tuf* DNA sequences as well as *tuf* sequences selected from public databases (in both cases, fragments of at least 100 base pairs), as well as oligonucleotide probes and amplification primers derived from these sequences. All the nucleic acid sequences described in that patent publication can enter in the composition of diagnostic kits or products and methods capable of a) detecting the presence of bacteria and fungi b) detecting specifically at the species, genus, family or group levels, the presence of bacteria and fungi and antimicrobial agents resistance genes associated with these pathogens. However, these methods and kits need to be improved, since the ideal kit and method should be capable of diagnosing close to 100% of microbial pathogens and associated antimicrobial agents resistance genes and toxins genes. For example, infections caused by *Enterococcus faecium* have become a clinical problem because of its resistance to many antibiotics. Both the detection of these bacteria and the evaluation of their resistance profiles are desirable. Besides that, novel DNA sequences (probes and primers) capable of recognizing the same and other microbial pathogens or the same and additional antimicrobial agents resistance genes are also desirable to aim at detecting more target genes and complement our earlier patent applications.

The present invention improves the assigned application by disclosing new proprietary *tuf* nucleic acids and/or sequences as well as describing new ways to

obtain *tuf* nucleic acids and/or sequences. In addition we disclose new proprietary *atpD* and *recA* nucleic acids and/or sequences. In addition, new uses of *tuf*, *atpD* and *recA* DNA nucleic acids and/or sequences selected from public databases (Table 11) are disclosed.

Highly conserved genes for identification and diagnostics

Highly conserved genes are useful for identification of microorganisms. For bacteria, the most studied genes for identification of microorganisms are the universally conserved ribosomal RNA genes (rRNA). Among those, the principal targets used for identification purposes are the small subunit (SSU) ribosomal 16S rRNA genes (in prokaryotes) and 18S rRNA genes (in eukaryotes) (Relman and Persing, Genotyping Methods for Microbial Identification, *In*: D.H. Persing, 1996, PCR Protocols for Emerging Infectious Diseases, ASM Press, Washington D.C.). The rRNA genes are also the most commonly used targets for universal detection of bacteria (Chen *et al.*, 1988, FEMS Microbiol. Lett. **57**:19-24; McCabe *et al.*, 1999, Mol. Genet. Metabol. **66**:205-211) and fungi (Van Burik *et al.*, 1998, J. Clin. Microbiol. **36**:1169-1175).

However, it may be difficult to discriminate between closely related species when using primers derived from the 16S rRNA. In some instances, 16S rRNA sequence identity may not be sufficient to guarantee species identity (Fox *et al.*, 1992, Int. J. Syst. Bacteriol. **42**:166-170) and it has been shown that inter-operon sequence variation as well as strain to strain variation could undermine the application of 16S rRNA for identification purposes (Clayton *et al.*, 1995, Int. J. Syst. Bacteriol. **45**:595-599). The heat shock proteins (HSP) are another family of very conserved proteins. These ubiquitous proteins in bacteria and eukaryotes are expressed in answer to external stress agents. One of the most described of these HSP is HSP 60. This protein is very conserved at the amino acid level, hence it has been useful for phylogenetic studies. Similar to 16S rRNA, it would be difficult to

discriminate between species using the HSP 60 nucleotide sequences as a diagnostic tool. However, Goh *et al.* identified a highly conserved region flanking a variable region in HSP 60, which led to the design of universal primers amplifying this variable region (Goh *et al.*, US patent serial no. 5,708,160). The sequence variations in the resulting amplicons were found useful for the design of species-specific assays.

SUMMARY OF THE INVENTION

It is an object of the present invention to provide a specific, ubiquitous and sensitive method using probes and/or amplification primers for determining the presence and/or amount of nucleic acids:

- from any algal, archaeal, bacterial, fungal or parasitical species in any sample suspected of containing said nucleic acids, and optionally,
- from specific microbial species or genera selected from the group consisting of the species or genera listed in Table 4, and optionally,
- from an antimicrobial agents resistance gene selected from the group consisting of the genes listed in Table 5, and optionally,
- from a toxin gene selected from the group consisting of the genes listed in Table 6,

wherein each of said nucleic acids or a variant or part thereof comprises a selected target region hybridizable with said probes or primers;

said method comprising the steps of contacting said sample with said probes or primers and detecting the presence and/or amount of hybridized probes or amplified products as an indication of the presence and/or amount of said any

microbial species, specific microbial species or genus or family or group and antimicrobial agents resistance gene and/or toxin gene.

In a specific embodiment, a similar method directed to each specific microbial species or genus or family or group detection and identification, antimicrobial agents resistance genes detection, toxin genes detection, and universal bacterial detection, separately, is provided.

In a more specific embodiment, the method makes use of DNA fragments from conserved genes (proprietary sequences and sequences obtained from public databases), selected for their capacity to sensitively, specifically and ubiquitously detect the targeted algal, archaeal, bacterial, fungal or parasitical nucleic acids.

In a particularly preferred embodiment, oligonucleotides of at least 12 nucleotides in length have been derived from the longer DNA fragments, and are used in the present method as probes or amplification primers. To be a good diagnostic candidate, an oligonucleotide of at least 12 nucleotides should be capable of hybridizing with nucleic acids from given microorganism(s), and with substantially all strains and representatives of said microorganism(s); said oligonucleotide being species-, or genus-, or family-, or group-specific or universal.

In another particularly preferred embodiment, oligonucleotides primers and probes of at least 12 nucleotides in length are designed for their specificity and ubiquity based upon analysis of our databases of *tuf*, *atpD* and *recA* sequences. These databases are generated using both proprietary and public sequence information. Altogether, these databases form a sequence repertory useful for the design of primers and probes for the detection and identification of algal, archaeal, bacterial, fungal and parasitical microorganisms. The repertory can also be subdivided into subrepertories for sequence analysis leading to the design of various primers and probes.

The *tuf*, *atpD* and *recA* sequences databases as a product to assist the design of oligonucleotides primers and probes for the detection and identification of algal, archaeal, bacterial, fungal and parasitical microorganisms are also covered.

The proprietary oligonucleotides (probes and primers) are also another object of this invention.

Diagnostic kits comprising probes or amplification primers such as those for the detection of a microbial species or genus or family or phylum or group selected from the following list consisting of *Abiotrophia adiacens*, *Acinetobacter baumannii*, *Actinomycetae*, *Bacteroides*, *Cytophaga* and *Flexibacter* phylum, *Bacteroides fragilis*, *Bordetella pertussis*, *Bordetella* sp., *Campylobacter jejuni* and *C. coli*, *Candida albicans*, *Candida dubliniensis*, *Candida glabrata*, *Candida guilliermondii*, *Candida krusei*, *Candida lusitaniae*, *Candida parapsilosis*, *Candida tropicalis*, *Candida zeylanoides*, *Candida* sp., *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium* sp., *Corynebacterium* sp., *Cryptococcus neoformans*, *Cryptococcus* sp., *Cryptosporidium parvum*, *Entamoeba* sp., *Enterobacteriaceae* group, *Enterococcus casseliflavus-flavescens-gallinarum* group, *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus gallinarum*, *Enterococcus* sp., *Escherichia coli* and *Shigella* sp. group, *Gemella* sp., *Giardia* sp., *Haemophilus influenzae*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Legionella* sp., *Leishmania* sp., *Mycobacteriaceae* family, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, platelets contaminants group (see Table 14), *Pseudomonas aeruginosa*, *Pseudomonads* group, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus saprophyticus*, *Staphylococcus* sp., *Streptococcus agalactiae*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Streptococcus* sp., *Trypanosoma brucei*, *Trypanosoma cruzi*, *Trypanosoma* sp., *Trypanosomatidae* family, are also objects of the present invention.

Diagnostic kits further comprising probes or amplification primers for the detection of an antimicrobial agents resistance gene selected from the group listed in Table 5 are also objects of this invention.

Diagnostic kits further comprising probes or amplification primers for the detection of a toxin gene selected from the group listed in Table 6 are also objects of this invention.

Diagnostic kits further comprising probes or amplification primers for the detection of any other algal, archaeal, bacterial, fungal or parasitical species than those specifically listed herein, comprising or not comprising those for the detection of the specific microbial species or genus or family or group listed above, and further comprising or not comprising probes and primers for the antimicrobial agents resistance genes listed in Table 5, and further comprising or not comprising probes and primers for the toxin genes listed in Table 6 are also objects of this invention.

In a preferred embodiment, such a kit allows for the separate or the simultaneous detection and identification of the above-listed microbial species or genus or family or group; or universal detection of algae, archaea, bacteria, fungi or parasites; or antimicrobial agents resistance genes; or toxin genes; or for the detection of any microorganism (algae, archaea, bacteria, fungi or parasites).

In the above methods and kits, probes and primers are not limited to nucleic acids and may include, but are not restricted to analogs of nucleotides such as: inosine, 3-nitropyrrole nucleosides (Nichols *et al.*, 1994, Nature **369**:492-493), Linked Nucleic Acids (LNA) (Koskin *et al.*, 1998, Tetrahedron **54**:3607-3630), and Peptide Nucleic Acids (PNA) (Egholm *et al.*, 1993, Nature **365**:566-568).

In the above methods and kits, amplification reactions may include but are not restricted to: a) polymerase chain reaction (PCR), b) ligase chain reaction (LCR), c) nucleic acid sequence-based amplification (NASBA), d) self-sustained sequence replication (3SR), e) strand displacement amplification (SDA), f) branched DNA signal amplification (bDNA), g) transcription-mediated amplification (TMA), h) cycling probe technology (CPT), i) nested PCR, j) multiplex PCR, k) solid phase amplification (SPA), l) nuclease dependent signal amplification (NDSA), m) rolling circle amplification technology (RCA), n) Anchored strand displacement amplification, o) Solid-phase (immobilized) rolling circle amplification.

In the above methods and kits, detection of the nucleic acids of target genes may include real-time or post-amplification technologies. These detection

technologies can include, but are not limited to, fluorescence resonance energy transfer (FRET)-based methods such as adjacent hybridization to FRET probes (including probe-probe and probe-primer methods), TaqMan, Molecular Beacons, scorpions, nanoparticle probes and Sunrise (Amplifluor). Other detection methods include target genes nucleic acids detection via immunological methods, solid phase hybridization methods on filters, chips or any other solid support, whether the hybridization is monitored by fluorescence, chemiluminescence, potentiometry, mass spectrometry, plasmon resonance, polarimetry, colorimetry, or scanometry. Sequencing, including sequencing by dideoxy termination or sequencing by hybridization, e.g. sequencing using a DNA chip, is another possible method to detect and identify the nucleic acids of target genes.

In a preferred embodiment, a PCR protocol is used for nucleic acid amplification, in diagnostic method as well as in method of construction of a repertory of nucleic acids and deduced sequences.

In a particularly preferred embodiment, a PCR protocol is provided, comprising, an initial denaturation step of 1-3 minutes at 95 °C, followed by an amplification cycle including a denaturation step of one second at 95 °C and an annealing step of 30 seconds at 45-65°C, without any time allowed specifically for the elongation step. This PCR protocol has been standardized to be suitable for PCR reactions with most selected primer pairs, which greatly facilitates the testing because each clinical sample can be tested with universal, species-specific, genus-specific, antimicrobial agents resistance gene and toxin gene PCR primers under uniform cycling conditions. Furthermore, various combinations of primer pairs may be used in multiplex PCR assays.

It is also an object of the present invention that *tuf*, *atpD* and *recA* sequences could serve as drug targets and these sequences and means to obtain them revealed in the present invention can assist the screening, design and modeling of these drugs.

It is also an object of the present invention that *tuf*, *atpD* and *recA* sequences could serve for vaccine purposes and these sequences and means to obtain them

revealed in the present invention can assist the screening, design and modeling of these vaccines.

We aim at developing a universal DNA-based test or kit to screen out rapidly samples which are free of algal, archaeal, bacterial, fungal or parasitical cells. This test could be used alone or combined with more specific identification tests to detect and identify the above algal and/or archaeal and/or bacterial and/or fungal and/or parasitical species and/or genera and/or family and/or group and to determine rapidly the bacterial resistance to antibiotics and/or presence of bacterial toxins. Although the sequences from the selected antimicrobial agents resistance genes are available from public databases and have been used to develop DNA-based tests for their detection, our approach is unique because it represents a major improvement over current diagnostic methods based on bacterial cultures. Using an amplification method for the simultaneous or independent or sequential microbial detection-identification and antimicrobial resistance genes detection, there is no need for culturing the clinical sample prior to testing. Moreover, a modified PCR protocol has been developed to detect all target DNA sequences in approximately one hour under uniform amplification conditions. This procedure should save lives by optimizing treatment, should diminish antimicrobial agents resistance because less antibiotics will be prescribed, should reduce the use of broad spectrum antibiotics which are expensive, decrease overall health care costs by preventing or shortening hospitalizations, and side effects of drugs, and decrease the time and costs associated with clinical laboratory testing.

In another embodiment, sequence repertories and ways to obtain them for other gene targets are also an object of this invention, such is the case for the *hexA* nucleic acids and/or sequences of Streptococci.

In yet another embodiment, for the detection of mutations associated with antibiotic resistance genes, we built repertories to distinguish between point mutations reflecting only gene diversity and point mutations involved in resistance. Such repertories and ways to obtain them for *pbp1a*, *pbp2b* and *pbp2x* genes of sensitive and penicillin-resistant *Streptococcus pneumoniae* and also for *gyrA* and

parC gene fragments from various bacterial species are also an object of the present invention.

The diagnostic kits, primers and probes mentioned above can be used to identify algae, archaea, bacteria, fungi, parasites, antimicrobial agents resistance genes and toxin genes on any type of sample, whether said diagnostic kits, primers and probes are used for *in vitro* or *in situ* applications. The said samples may include but are not limited to: any clinical sample, any environment sample, any microbial culture, any microbial colony, any tissue, and any cell line.

It is also an object of the present invention that said diagnostic kits, primers and probes can be used alone or in conjunction with any other assay suitable to identify microorganisms, including but not limited to: any immunoassay, any enzymatic assay, any biochemical assay, any lysotypic assay, any serological assay, any differential culture medium, any enrichment culture medium, any selective culture medium, any specific assay medium, any identification culture medium, any enumeration culture medium, any cellular stain, any culture on specific cell lines, and any infectivity assay on animals.

In the methods and kits described herein below, the oligonucleotide probes and amplification primers have been derived from larger sequences (i.e. DNA fragments of at least 100 base pairs). All DNA fragments have been obtained either from proprietary fragments or from public databases. DNA fragments selected from public databases are newly used in a method of detection according to the present invention, since they have been selected for their diagnostic potential.

In another embodiment, the amino acid sequences translated from the repertory of *tuf*, *atpD* and *recA* nucleic acids and/or sequences are also an object of the present invention.

It is clear to the individual skilled in the art that other oligonucleotide sequences appropriate for (i) the universal detection of algae, archaea, bacteria, fungi or parasites, (ii) the detection and identification of the above microbial species or genus or family or group, and (iii) the detection of antimicrobial agents resistance genes, and (iv) the detection of toxin genes, other than those listed in

Annexes I to III, XXI to XXII, XXXII to XXXVII, XXXIX to XLI, and XLIII to LIV may also be derived from the proprietary fragments or selected public database sequences. For example, the oligonucleotide primers or probes may be shorter or longer than the ones chosen; they may also be selected anywhere else in the proprietary DNA fragments or in the sequences selected from public databases; they may be also variants of the same oligonucleotide. If the target DNA or a variant thereof hybridizes to a given oligonucleotide, or if the target DNA or a variant thereof can be amplified by a given oligonucleotide PCR primer pair, the converse is also true; a given target DNA may hybridize to a variant oligonucleotide probe or be amplified by a variant oligonucleotide PCR primer. Alternatively, the oligonucleotides may be designed from any DNA fragment sequences for use in amplification methods other than PCR. Consequently, the core of this invention is the identification of universal, species-specific, genus-specific, family-specific, group-specific, resistance gene-specific, toxin gene-specific genomic or non-genomic DNA fragments which are used as a source of specific and ubiquitous oligonucleotide probes and/or amplification primers. Although the selection and evaluation of oligonucleotides suitable for diagnostic purposes requires much effort, it is quite possible for the individual skilled in the art to derive, from the selected DNA fragments, oligonucleotides other than the ones listed in Annexes I to III, XXI to XXII, XXXII to XXXVII, XXXIX to XLI, and XLIII to LIV which are suitable for diagnostic purposes. When a proprietary fragment or a public databases sequence is selected for its specificity and ubiquity, it increases the probability that subsets thereof will also be specific and ubiquitous.

Since a high percentage of clinical specimens are negative for bacteria (Table 3), DNA fragments having a high potential for the selection of universal oligonucleotide probes or primers were selected from proprietary and public database sequences. The amplification primers were selected from genes highly conserved in algae, archaea, bacteria, fungi and parasites, and are used to detect the presence of any algal, archaeal, bacterial, fungal or parasitical pathogen in clinical specimens in order to determine rapidly whether it is positive or negative for algae,

archaea, bacteria, fungi or parasites. The selected genes, designated *tuf*, *fus*, *atpD* and *recA*, encode respectively 2 proteins (elongation factors Tu and G) involved in the translational process during protein synthesis, a protein (beta subunit) responsible for the catalytic activity of proton pump ATPase and a protein responsible for the homologous recombination of genetic material. The alignments of *tuf*, *atpD* and *recA* sequences used to derive the universal primers include both proprietary and public database sequences. The universal primer strategy allows the rapid screening of the numerous negative clinical specimens (around 80% of the specimens received, see Table 3) submitted for microbiological testing.

Table 4 provides a list of the archaeal, bacterial, fungal and parasitical species for which *tuf* and/or *atpD* and/or *recA* nucleic acids and/or sequences are revealed in the present invention. Tables 5 and 6 provide a list of antimicrobial agents resistance genes and toxin genes selected for diagnostic purposes. Table 7 provides the origin of *tuf*, *atpD* and *recA* nucleic acids and/or sequences listed in the sequence listing. Tables 8-10 and 12-14 provide lists of species used to test the specificity, ubiquity and sensitivity of some assays described in the examples. Table 11 provides a list of microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases. Table 15 lists the microorganisms identified by commercial systems. Tables 16-18 are part of Example 42, whereas Tables 19-20 are part of Example 43. Tables 21-22 illustrate Example 44, whereas Tables 23-25 illustrate Example 45.

In accordance with the present invention is provided a method for generating a repertory of nucleic acids of *tuf*, *fus*, *atpD* and/or *recA* genes from which are derived probes or primers, or both, useful for the detection of one, more than one related microorganisms, or substantially all microorganisms of a group selected from algae, archaea, bacteria, fungi and parasites, which comprises the step of:

- amplifying the nucleic acids of a plurality of determined algal, archaeal, bacterial, fungal and parasitical species with any combination of the primer pairs defined in SEQ ID NOs.: 558-561, 562-574, 636-655, 664, 681-683, 696-697, 699-700, 708, 812-815, 911-917, 919-922, 935-938, 1203-1207, 1212-1213, 1221-1229, 1605-1606, 1974-1984, 1999- 2003, 2282-2285.

The terms "related microorganisms" are intended to cover microorganisms that share a common evolutive profile up to the speciation e.g. those that belong to a species, a genus, a family or a phylum. The same terms are also intended to cover a group of different species that are grouped for a specific reason, for example, because they all have a common host tissue or cell. In one specific example, a group of microorganisms potentially found in platelet preparations are grouped together and are considered "related" organisms for the purpose of their simultaneous detection in that particular type of sample.

The repertories *per se* of nucleic acids and of sequences derived therefrom are also provided, as well as "gene banks" comprising these repertories.

For generating sequences of probes or primers, the above method is reproduced or one may start from the sequence repertory or gene bank itself, and the following steps are added:

- aligning a subset of nucleic acid sequences of said repertory,
- locating nucleic acid stretches that are present in the nucleic acids of strains or representatives of said one, more than one related microorganisms, or substantially all microorganisms of said group, and not present in the nucleic acid sequences of other microorganisms, and

deriving consensus nucleic acid sequences useful as probes or primers from said stretches.

Once the sequences of probes or primers are designed, they are converted into real molecules by nucleic acid synthesis.

From the above methods and resulting repertories, probes and primers for the universal detection of any one of alga, archaeon, bacterium, fungus and parasite are obtainable.

More specifically, the following probes or primers having the sequence defined in SEQ ID NOs.: 543, 556-574, 636-655, 658-661, 664, 681-683, 694, 696, 697, 699, 700, 708, 812-815, 911-917, 919-922, 935-938, 1203-1207, 1212-1213, 1221-1229, 1605-1606, 1974-1984, 1999-2000, 2282-2285 or any variant of at least 12 nucleotides capable of hybridizing with the targeted microorganism(s) and these sequences and a diagnostic method using the same are provided.

Further, probes or primers having specific and ubiquitous properties for the detection and identification of any one of an algal, archaeal, bacterial, fungal and parasitital species, genus, family and group are also designed and derived from the same methods and repertories.

More specifically, are provided definite probes or primers having specific and ubiquitous properties for the detection and identification of microorganisms.

Indeed, a general method is provided for detecting the presence in a test sample of any microorganism that is an alga, archaeum, bacterium, fungus or parasite, which comprises:

a) putting in contact any test sample *tuf* or *atpD* or *recA* sequences and nucleic acid primers and/or probes, said primers and/or probes having been selected to be sufficiently complementary to hybridize to

one or more *tuf* or *atpD* or *recA* sequences that are specific to said microorganism:

b) allowing the primers and/or probes and any test sample *tuf* or *atpD* or *recA* sequences to hybridize under specified conditions such as said primers and/or probes hybridize to the *tuf* or *atpD* or *recA* sequences of said microorganism and does not delectably hybridize to *tuf* or *atpD* or *recA* sequences from other microorganisms; and,

c) testing for hybridization of said primers and/or probes to any test sample *tuf* or *atpD* or *recA* sequences.

In the latter, step c) is based on a nucleic acid target amplification method, or on a signal amplification method.

The terms "sufficiently complementary" cover perfect and imperfect complementarity.

In addition to the universal or the specific detection and/or identification of microorganisms, the simultaneous detection of antimicrobial agent resistance gene or of a toxin gene is provided in compositions of matter as well as in diagnostic methods. Such detection is brought by using probes or primers having at least 12 nucleotides in length capable of hybridizing with an antimicrobial agent resistance gene and/or toxin gene, a definite set thereof being particularly provided.

Of course, any propriatory nucleic acid and nucleotide sequence derived therefrom, and any variant of at least 12 nucleotides capable of a selective hybridization with the following nucleic acids are within the scope of this invention as well as derived recombinant vectors and hosts:

SEQ ID NOs.: 1-73, 75-241, 399-457, 498-529, 612-618, 621-624, 675, 677, 717-736, 779-792, 840-855, 865, 868-888, 897-910, 932, 967-989, 992, 1266-1297, 1518-1526, 1561-1575, 1578-1580, 1662-1664, 1666-1667, 1669-1670, 1673-1683, 1685-1689, 1786-1843, 1874-1881, 1956-1960, 2183-2185, 2187-2188, 2193-2201, 2214-2249, 2255-2272, which are all *tuf* sequences;

SEO ID NOs.: 242-270, 272-398, 458-497, 530-538, 663, 667, 673-676, 678-680, 737-778, 827-832, 834-839, 856-862, 866-867, 889-896, 929-931, 941-966, 1245-1254, 1256-1265, 1527, 1576-1577, 1600-1604, 1638-1647, 1649-1660, 1671, 1684, 1844-1848, 1849-1865, 2189-2192, which are all *atpD* sequences;

SEQ ID NOs.: 990-991, 1003, 1288-1289, 1714, 1756-1763, 1866-1873 and 2202-2212, which are all *recA* sequences; and

SEQ ID NOs.: 1004-1075, 1255, 1607-1608, 1648, 1764-1785, 2013-2014, 2056-2064, 2273-2280, which are antimicrobial agent resistance or toxin gene sequences found to be suitable for the detection and identification of microbial species.

To complement the following repertories, another one comprising *hexA* nucleic acids and derived sequences have been construed through amplification of nucleic acids of any streptococcal species with any combination of primers SEO ID NOs.: 1179, 1181, 1182 and 1184 to 1191. From this particular repertory, primers and/or probes for detecting *Streptococcus pneumoniae* have been designed and obtained. Particularly, a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with *Streptococcus pneumoniae* and with any one of SEQ ID NOs.: 1184 to 1187 or with SEQ ID NOs.: 1179, 1180, 1181 or 1182 are provided.

The remarkable sequence diversity of nucleic acids that encode proteins also provides diversity of peptide sequences which constitute another repertory that is also within the scope of this invention. From the protein and nucleic acid sequence repertories is derived a use therefrom for the design of a therapeutic agent effective against a target microorganism, for example, an antibiotic, a vaccine or a genic therapeutic agent.

Due to the constant evolution in the diagnostic methods, here is finally provided a method for the identification of a microorganism in a test sample, comprising the steps of:

a) obtaining a nucleic acid sequence from a *tuf*, *fus*, *atpD*, and/or *recA* genes of said microorganisms, and

b) comparing said nucleic acid sequence with the nucleic acid sequences of a bank as defined in claim 5, said repertory comprising a nucleic acid sequence obtained from the nucleic acids of said microorganism, whereby said microorganism is identify when there is a match between the sequences.

In this method, any way by which the specified given sequence is obtained is contemplated, and this sequence is simply compared to the sequences of a bank or a repertory. If the comparison results in a match, e.g. if bank comprises the nucleic acid sequence of interest, the identification of the microorganism is provided.

DETAILED DESCRIPTION OF THE INVENTION**HIGHLY CONSERVED GENES AND THEIR USE TO GENERATE SPECIES-SPECIFIC, GENUS-SPECIFIC, FAMILY-SPECIFIC, GROUP-SPECIFIC AND UNIVERSAL NUCLEIC ACID PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY ALGAL, ARCHAEAL, BACTERIAL, FUNGAL AND PARASITICAL MICROORGANISMS FROM CLINICAL SPECIMENS FOR DIAGNOSIS**

The present inventors reasoned that comparing the published *Haemophilus influenzae* and *Mycoplasma genitalium* genomes and searching for conserved genes could provide targets to develop useful diagnostic primers and probes. This sequence comparison is highly informative as these two bacteria are distantly related and most genes present in the minimal genome of *M. genitalium* are likely to be present in every bacterium. Therefore genes conserved between these two bacteria are likely to be conserved in all other bacteria.

Following the genomic comparison, it was found that several protein-coding genes were conserved in evolution. Highly conserved proteins included the translation elongation factors G (EF-G) and Tu (EF-Tu) and the β subunit of F₀F₁ type ATP-synthase, and to a lesser extent, the RecA recombinase. These four proteins coding genes were selected amongst the 20 most conserved genes on the basis that they all possess at least two highly conserved regions suitable for the design of universal amplification and sequencing primers. Moreover, within the fragment amplified by these primers, highly conserved and more variable regions are also present hence suggesting it might be possible to rapidly obtain sequence information from various microbial species to design universal as well as species-, genus-, family-, or group-specific primers and probes of potential use for the detection and identification and/or quantification of microorganisms.

Translation elongation factors are members of a family of GTP-binding proteins which intervene in the interactions of tRNA molecules with the ribosome machinery during essential steps of protein synthesis. The role of elongation factor Tu is to facilitate the binding of aminoacylated tRNA molecules to the A site of the ribosome. The eukaryotic, archaeal (archaeobacterial) and algal homolog of EF-Tu is called elongation factor 1 alpha (EF-1 α). All protein synthesis factors originated from a common ancestor via gene duplications and fusions (Cousineau *et al.*, 1997, J. Mol. Evol. **45**:661-670). In particular, elongation factor G (EF-G), although having a functional role in promoting the translocation of aminoacyl-tRNA molecules from the A site to the P site of the ribosome, shares sequence homologies with EF-Tu and is thought to have arisen from the duplication and fusion of an ancestor of the EF-Tu gene.

In addition, EF-Tu is known to be the target for antibiotics belonging to the elfamycin's group as well as to other structural classes (Anborgh and Parmeggiani, 1991, EMBO J. **10**:779-784; Luiten *et al.*, 1992, European patent application serial No. EP 0 466 251 A1). EF-G for its part, is the target of the antibiotic fusidic acid. In addition to its crucial activities in translation, EF-Tu has chaperone-like functions in protein folding, protection against heat denaturation of proteins and interactions with unfolded proteins (Caldas *et al.*, 1998, J. Biol. Chem **273**:11478-11482). Interestingly, a form of the EF-Tu protein has been identified as a dominant component of the periplasm of *Neisseria gonorrhoeae* (Porcella *et al.*, 1996, Microbiology **142**:2481-2489), hence suggesting that at least in some bacterial species, EF-Tu might be an antigen with vaccine potential.

F₀F₁ type ATP-synthase belongs to a superfamily of proton-translocating ATPases divided in three major families: P, V and F (Nelson and Taiz, 1989, TIBS **14**:113-116). P-ATPases (or E₁-E₂ type) operate via a phosphorylated intermediate and are not evolutionarily related to the other two families. V-ATPases (or V₀V₁ type) are present on the vacuolar and other endomembranes of eukaryotes, on the plasma membrane of archaea (archaeobacteria) and algae, and also on the plasma membrane of some eubacteria especially species belonging to the order

Spirochaetales as well as to the *Chlamydiaceae* and *Deinococcaceae* families. F-ATPases (or F₀F₁ type) are found on the plasma membrane of most eubacteria, on the inner membrane of mitochondria and on the thylakoid membrane of chloroplasts. They function mainly in ATP synthesis. They are large multimeric enzymes sharing numerous structural and functional features with the V-ATPases. F and V-type ATPases have diverged from a common ancestor in an event preceding the appearance of eukaryotes. The β subunit of the F-ATPases is the catalytic subunit and it possesses low but significant sequence homologies with the catalytic A subunit of V-ATPases.

The translation elongation factors EF-Tu, EF-G and EF-1 α , and the catalytic subunit of F or V-types ATP-synthase, are highly conserved proteins sometimes used for phylogenetic analysis and their genes are also known to be highly conserved (Iwabe *et al.*, 1989, Proc. Natl. Acad. Sci. USA **86**:9355-9359, Gogarten *et al.*, 1989, Proc. Natl. Acad. Sci. USA **86**:6661-6665, Ludwig *et al.*, 1993, Antonie van Leeuwenhoek **64**:285-305). A recent BLAST (Altschul *et al.*, 1997, J. Mol. Biol. **215**:403-410) search performed by the present inventors on the GenBank, European Molecular Biology Laboratory (EMBL), DNA Database of Japan (DDBJ) and specific genome project databases indicated that throughout bacteria, the EF-Tu and the β subunit of F₀F₁ type ATP-synthase genes may be more conserved than other genes that are well conserved between *H. influenzae* and *M. genitalium*.

The RecA recombinase is a multifunctional protein encoded by the *recA* gene. It plays a central role in homologous recombination, it is critical for the repair of DNA damage and it is involved in the regulation of the SOS system by promoting the proteolytic digestion of the LexA repressor. It is highly conserved in bacteria and could serve as a useful genetic marker to reconstruct bacterial phylogeny (Miller and Kokjohn, 1990, Annu. Rev. Microbiol. **44**:365-394). Although RecA possesses some highly conserved sequence segments that we used to design universal primers aimed at sequencing the *recA* fragments, it is clearly not as well conserved EF-G, EF-Tu and β subunit of F₀F₁ type ATP-synthase.

Hence, RecA may not be optimal for universal detection of bacteria with high sensitivity but it was chosen because preliminary data indicated that EF-G, EF-Tu and β subunit of F₀F₁ type ATP-synthase may sometimes be too closely related to find specific primer pairs that could discriminate between certain very closely related species and genera. While RecA, EF-G, EF-Tu and β subunit of F₀F₁ type ATP-synthase genes, possesses highly conserved regions suitable for the design of universal sequencing primers, the less conserved region between primers should be divergent enough to allow species-specific and genus-specific primers in those cases.

Thus, as targets to design primers and probes for the genetic detection of microorganisms, the present inventors have focused on the genes encoding these four proteins: *tuf*, the gene for elongation factor Tu (EF-Tu); *fus*, the gene for the elongation factor G (EF-G); *atpD*, the gene for β subunit of F₀F₁ type ATP-synthase; and *recA*, the gene encoding the RecA recombinase. In several bacterial genomes *tuf* is often found in two highly similar duplicated copies named *tufA* and *tufB* (Filer and Furano, 1981, J. Bacteriol. 148:1006-1011, Sela *et al.*, 1989, J. Bacteriol. 171:581-584). In some particular cases, more divergent copies of the *tuf* genes can exist in some bacterial species such as some actinomycetes (Luiten *et al.* European patent application publication No. EP 0 446 251 A1; Vijgenboom *et al.*, 1994, Microbiology 140:983-998) and, as revealed as part of this invention, in several enterococcal species. In several bacterial species, *tuf* is organized in an operon with its homolog gene for the elongation factor G (EF-G) encoded by the *fusA* gene (Figure 3). This operon is often named the *str* operon. The *tuf*, *fus*, *atpD* and *recA* genes were chosen as they are well conserved in evolution and have highly conserved stretches as well as more variable segments. Moreover, these four genes have eukaryotic orthologs which are described in the present invention as targets to identify fungi and parasites. The eukaryotic homolog of elongation factor Tu is called elongation factor 1-alpha (EF-1 α) (gene name: *tef*, *tefl*, *efl*, *ef-1* or *EF-1*). In fungi, the gene for EF-1 α occurs sometimes in two or more highly

similar duplicated copies (often named *tef1*, *tef2*, *tef3*...). In addition, eukaryotes have a copy of elongation factor Tu which is originating from their organelle genome ancestry (gene name: *tuf1*, *tufM* or *tufA*). For the purpose of the current invention, the genes for these four functionally and evolutionarily linked elongation factors (bacterial EF-Tu and EF-G, eukaryotic EF-1 α , and organellar EF-Tu) will hereafter be designated as «*tuf* nucleic acids and/or sequences». The eukaryotic (mitochondrial) F₀F₁ type ATP-synthase beta subunit gene is named *atp2* in yeast. For the purpose of the current invention, the genes of catalytic subunit of either F or V-type ATP-synthase will hereafter be designated as «*atpD* nucleic acids and/or sequences». The eukaryotic homologs of RecA are distributed in two families, typified by the Rad51 and Dmc1 proteins. Archaeal homologs of RecA are called RadA. For the purpose of the current invention, the genes corresponding to the latter proteins will hereafter be designated as «*recA* nucleic acids and/or sequences».

In the description of this invention, the terms «nucleic acids» and «sequences» might be used interchangeably. However, «nucleic acids» are chemical entities while «sequences» are the pieces of information derived from (inherent to) these «nucleic acids». Both nucleic acids and sequences are equivalently valuable sources of information for the matter pertaining to this invention.

Analysis of multiple sequence alignments of *tuf* and *atpD* sequences permitted the design of oligonucleotide primers (and probes) capable of amplifying (or hybridizing to) segments of *tuf* (and/or *fus*) and *atpD* genes from a wide variety of bacterial species (see Examples 1 to 4, 24 and 26, and Table 7). Sequencing and amplification primer pairs for *tuf* nucleic acids and/or sequences are listed in Annex I and hybridization probes are listed in Annexes III and XLVII. Sequencing and amplification primer pairs for *atpD* nucleic acids and/or sequences are listed in Annex II. Analysis of the main subdivisions of *tuf* and *atpD* sequences (see Figures 1 and 2) permitted to design sequencing primers amplifying specifically each of these subdivisions. It should be noted that these sequencing primers could also be used as universal primers. However, since some of these sequencing primers

include several variable sequence (degenerated) positions, their sensitivity could be lower than that of universal primers developed for diagnostic purposes. Further subdivisions could be done on the basis of the various phyla where these genes are encountered.

Similarly, analysis of multiple sequence alignments of *recA* sequences present in the public databases permitted the design of oligonucleotide primers capable of amplifying segments of *recA* genes from a wide variety of bacterial species. Sequencing and amplification primer pairs for *recA* sequences are listed in Annex XXI. The main subdivisions of *recA* nucleic acids and/or sequences comprise *recA*, *radA*, *rad51* and *dmc1*. Further subdivisions could be done on the basis of the various phyla where these genes are encountered.

The present inventor's strategy is to get as much sequence data information from the four conserved genes (*tuf*, *fus*, *atpD* and *recA*). This ensemble of sequence data forming a repertory (with subrepertories corresponding to each target gene and their main sequence subdivisions) and then using the sequence information of the sequence repertory (or subrepertories) to design primer pairs that could permit either universal detection of algae or archaea or bacteria or fungi or parasites, detection of a family or group of microorganism (e.g. *Enterobacteriaceae*), detection of a genus (e.g. *Streptococcus*) or finally a specific species (e.g. *Staphylococcus aureus*). It should be noted that for the purpose of the present invention a group of microorganisms is defined depending on the needs of the particular diagnostic test. It does not need to respect a particular taxonomical grouping or phylum. See Example 12 where primers were designed to amplify a group a bacteria consisting of the 17 major bacterial species encountered as contaminants of platelet concentrates. Also remark that in that Example, the primers are not only able to sensitively and rapidly detect at least the 17 important bacterial species, but could also detect other species as well, as shown in Table 14. In these circumstances the primers shown in Example 12 are considered universal for platelet-contaminating bacteria. To develop an assay specific for the latter, one or more primers or probes specific to each species could be designed. Another

example of primers and/or probes for group detection is given by the *Pseudomonad* group primers. These primers were designed based upon alignment of *tuf* sequences from real *Pseudomonas* species as well as from former *Pseudomonas* species such as *Stenotrophomonas maltophilia*. The resulting primers are able to amplify all *Pseudomonas* species tested as well as several species belonging to different genera, hence as being specific for a group including *Pseudomonas* and other species, we defined that group as Pseudomonads, as several members were former *Pseudomonas*.

For certain applications, it may be possible to develop a universal, group, family or genus-specific reaction and to proceed to species identification using sequence information within the amplicon to design species-specific internal probes or primers, or alternatively, to proceed directly by sequencing the amplicon. The various strategies will be discussed further below.

The ensembles formed by public and proprietary *tuf*, *atpD* and *recA* nucleic acids and/or sequences are used in a novel fashion so they constitute three databases containing useful information for the identification of microorganisms.

Sequence repertoires of other gene targets were also built to solve some specific identification problems especially for microbial species genetically very similar to each other such as *E. coli* and *Shigella* (see Example 23). Based on *tuf*, *atpD* and *recA* sequences, *Streptococcus pneumoniae* is very difficult to differentiate from the closely related species *S. oralis* and *S. mitis*. Therefore, we elected to build a sequence repertoire from *hexA* sequences (Example 19), a gene much more variable than our highly conserved *tuf*, *atpD* and *recA* nucleic acids and/or sequences.

For the detection of mutations associated with antibiotic resistance genes, we also built repertoires to distinguish between point mutations reflecting only gene diversity and point mutations involved in resistance. This was done for *pbp1a*, *pbp2b* and *pbp2x* genes of penicillin-resistant and sensitive *Streptococcus pneumoniae* (Example 18) and also for *gyrA* and *parC* gene fragments of various bacterial species for which quinolone resistance is important to monitor.

Oligonucleotide primers and probes design and synthesis

The *tuf*, *fus*, *atpD* and *recA* DNA fragments sequenced by us and/or selected from public databases (GenBank and EMBL) were used to design oligonucleotides primers and probes for diagnostic purposes. Multiple sequence alignments were made using subsets of the *tuf* or *atpD* or *recA* sequences repertory. Subsets were chosen to encompass as much as possible of the targetted microorganism(s) DNA sequence data and also include sequence data from phylogenetically related microorganisms from which the targetted microorganism(s) should be distinguished. Regions suitable for primers and probes should be conserved for the targetted microorganism(s) and divergent for the microorganisms from which the targetted microorganism(s) should be distinguished. The large amount of *tuf* or *atpD* or *recA* sequences data in our repertory permits to reduce trial and errors in obtaining specific and ubiquitous primers and probes. We also relied on the corresponding peptide sequences of *tuf*, *fus*, *atpD* and *recA* nucleic acids and/or sequences to facilitate the identification of regions suitable for primers and probes design. As part of the design rules, all oligonucleotides (probes for hybridization and primers for DNA amplification by PCR) were evaluated for their suitability for hybridization or PCR amplification by computer analysis using standard programs (i.e. the Genetics Computer Group (GCG) programs and the primer analysis software Oligo™ 5.0). The potential suitability of the PCR primer pairs was also evaluated prior to the synthesis by verifying the absence of unwanted features such as long stretches of one nucleotide and a high proportion of G or C residues at the 3' end (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). Oligonucleotide probes and amplification primers were synthesized using an automated DNA synthesizer (Perkin-Elmer Corp., Applied Biosystems Division).

The oligonucleotide sequence of primers or probes may be derived from either strand of the duplex DNA. The primers or probes may consist of the bases

A, G, C, or T or analogs and they may be degenerated at one or more chosen nucleotide position(s). The primers or probes may be of any suitable length and may be selected anywhere within the DNA sequences from proprietary fragments or from selected database sequences which are suitable for (i) the universal detection of algae or archaea or bacteria or fungi or parasites, (ii) the species-specific detection and identification of any microorganism, including but not limited to: *Abiotrophia adiacens*, *Bacteroides fragilis*, *Bordetella pertussis*, *Candida albicans*, *Candida dubliniensis*, *Candida glabrata*, *Candida guilliermondii*, *Candida krusei*, *Candida lusitanae*, *Candida parapsilosis*, *Candida tropicalis*, *Candida zeylanoides*, *Campylobacter jejuni* and *C. coli*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Cryptococcus neoformans*, *Cryptosporidium parvum*, *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus gallinarum*, *Escherichia coli*, *Haemophilus influenzae*, *Legionella pneumophila*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus saprophyticus*, *Streptococcus agalactiae*, *Streptococcus pneumoniae*, *Trypanosoma brucei*, *Trypanosoma cruzi*, (iii) the genus-specific detection of *Bordetella* species, *Candida* species, *Clostridium* species, *Corynebacterium* species, *Cryptococcus* species, *Entamoeba* species, *Enterococcus* species, *Gemella* species, *Giardia* species, *Legionella* species, *Leishmania* species, *Staphylococcus* species, *Streptococcus* species, *Trypanosoma* species, (iv) the family-specific detection of *Enterobacteriaceae* family members, *Mycobacteriaceae* family members, *Trypanosomatidae* family members, (v) the detection of *Enterococcus casseliflavus-flavescens-gallinarum* group, *Enterococcus*, *Gemella* and *Abiotrophia adiacens* group, *Pseudomonads* extended group, Platelet-contaminating bacteria group, (vi) the detection of clinically important antimicrobial agents resistance genes listed in Table 5, (vii) the detection of clinically important toxin genes listed in Table 6.

Variants for a given target microbial gene are naturally occurring and are attributable to sequence variation within that gene during evolution (Watson *et al.*, 1987, Molecular Biology of the Gene, 4th ed., The Benjamin/Cummings Publishing Company, Menlo Park, CA; Lewin, 1989, Genes IV, John Wiley & Sons, New York, NY). For example, different strains of the same microbial species may have a single or more nucleotide variation(s) at the oligonucleotide hybridization site. The person skilled in the art is well aware of the existence of variant algal, archaeal, bacterial, fungal or parasitica DNA nucleic acids and/or sequences for a specific gene and that the frequency of sequence variations depends on the selective pressure during evolution on a given gene product. The detection of a variant sequence for a region between two PCR primers may be demonstrated by sequencing the amplification product. In order to show the presence of sequence variants at the primer hybridization site, one has to amplify a larger DNA target with PCR primers outside that hybridization site. Sequencing of this larger fragment will allow the detection of sequence variation at this site. A similar strategy may be applied to show variants at the hybridization site of a probe. Insofar as the divergence of the target nucleic acids and/or sequences or a part thereof does not affect the specificity and ubiquity of the amplification primers or probes, variant microbial DNA is under the scope of this invention. Variants of the selected primers or probes may also be used to amplify or hybridize to a variant DNA.

Sequencing of *tuf* nucleic acids and/or sequences from a variety of archaeal, bacterial, fungal and parasitica species

The nucleotide sequence of a portion of *tuf* nucleic acids and/or sequences was determined for a variety of archaeal, bacterial, fungal and parasitica species. The amplification primers (SEQ ID NOs. 664 and 697), which amplify a *tuf* gene portion of approximately 890 bp, were used along with newly designed sequencing primer pairs (See Annex I for the sequencing primers for *tuf* nucleic acids and/or

sequences). Most primer pairs can amplify different copies of *tuf* genes (*tufA* and *tufB*). This is not surprising since it is known that for several bacterial species these two genes are nearly identical. For example, the entire *tufA* and *tufB* genes from *E. coli* differ at only 13 nucleotide positions (Neidhardt *et al.*, 1996, *Escherichia coli* and *Salmonella*: Cellular and Molecular Biology, 2nd ed., American Society for Microbiology Press, Washington, D.C.). Similarly, some fungi are known to have two nearly identical copies of *tuf* nucleic acids and/or sequences (EF-1 α). These amplification primers are degenerated at several nucleotide positions and contain inosines in order to allow the amplification of a wide range of *tuf* nucleic acids and/or sequences. The strategy used to select these amplification primers is similar to that illustrated in Annex I for the selection of universal primers. The *tuf* sequencing primers even sometimes amplified highly divergent copies of *tuf* genes (*tufC*) as illustrated in the case of some enterococcal species (SEQ ID NOs.: 73, 75, 76, 614 to 618, 621 and 987 to 989). To prove this, we have determined the enterococcal *tuf* nucleic acids and/or sequences from PCR amplicons cloned into a plasmid vector. Using the sequence data from the cloned amplicons, we designed new sequencing primers specific to the divergent (*tufC*) copy of enterococci (SEQ ID NOs.: 658-659 and 661) and then sequenced directly the *tufC* amplicons. The amplification primers (SEQ ID NOs.: 543, 556, 557, 643-645, 660, 664, 694, 696 and 697) could be used to amplify the *tuf* nucleic acids and/or sequences from any bacterial species. The amplification primers (SEQ ID NOs.: 558, 559, 560, 653, 654, 655, 813, 815, 1974-1984, 1999-2003) could be used to amplify the *tuf* (EF-1 α) genes from any fungal and/or parasitical species. The amplification primers SEQ ID NOs. 1221-1228 could be used to amplify bacterial *tuf* nucleic acids and/or sequences of the EF-G subdivision (*fusA*) (Figure 3). The amplification primers SEQ ID NOs. 1224, and 1227-1229 could be used to amplify bacterial *tuf* nucleic acids and/or sequences comprising the end of EF-G (*fusA*) and the beginning of EF-Tu (*tuf*), including the intergenic region, as shown in Figure 3. Most *tuf* fragments to be sequenced were amplified using the following amplification protocol: One μ l of cell suspension (or of purified genomic DNA

0.1-100 ng/ μ l) was transferred directly to 19 μ l of a PCR reaction mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl₂, 1 μ M of each of the 2 primers, 200 μ M of each of the four dNTPs, 0.5 unit of *Taq* DNA polymerase (Promega Corp., Madison, WI). PCR reactions were subjected to cycling using a PTC-200 thermal cycler (MJ Research Inc., Watertown, Mass.) as follows: 3 min at 94-96 °C followed by 30-45 cycles of 1 min at 95 °C for the denaturation step, 1 min at 50-55 °C for the annealing step and 1 min at 72 °C for the extension step. Subsequently, twenty microliters of the PCR-amplified mixture were resolved by electrophoresis in a 1.5% agarose gel. The amplicons were then visualized by staining with methylene blue (Flores *et al.*, 1992, Biotechniques, 13:203-205). The size of the amplification products was estimated by comparison with a 100-bp molecular weight ladder. The band corresponding to the specific amplification product was excised from the agarose gel and purified using the QIAquick™ gel extraction kit (QIAGEN Inc., Chatsworth, CA). The gel-purified DNA fragment was then used directly in the sequencing protocol. Both strands of the *tuf* genes amplification product were sequenced by the dideoxynucleotide chain termination sequencing method by using an Applied Biosystems automated DNA sequencer (model 377) with their Big Dye™ Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystems, Foster City, CA). The sequencing reactions were performed by using the same amplification primers and 10 ng/100 bp of the gel-purified amplicon per reaction. For the sequencing of long amplicons such as those of eukaryotic *tuf* (EF-1 α) nucleic acids and/or sequences, we designed internal sequencing primers (SEQ ID NOs.: 654, 655 and 813) to be able to obtain sequence data on both strands for most of the fragment length. In order to ensure that the determined sequence did not contain errors attributable to the sequencing of PCR artefacts, we have sequenced two preparations of the gel-purified *tuf* amplification product originating from two independent PCR amplifications. For most target microbial species, the sequences determined for both amplicon preparations were identical. In case of discrepancies, amplicons from a third independent PCR amplification

were sequenced. Furthermore, the sequences of both strands were 100% complementary thereby confirming the high accuracy of the determined sequence. The *tuf* nucleic acids and/or sequences determined using the above strategy are described in the Sequence Listing. Table 7 gives the originating microbial species and the source for each *tuf* sequence in the Sequence Listing.

The alignment of the *tuf* sequences determined by us or selected from databases revealed clearly that the length of the sequenced portion of the *tuf* genes is variable. There may be insertions or deletions of several amino acids. In addition, in several fungi introns were observed. Intron nucleic acids and/or sequences are part of *tuf* nucleic acids and/or sequences and could be useful in the design of species-specific primers and probes. This explains why the size of the sequenced *tuf* amplification products was variable from one fungal species to another. Consequently, the nucleotide positions indicated on top of each of Annexes IV to XX, XXIII to XXXI, XXXVIII and XLII do not correspond for sequences having insertions or deletions.

It should also be noted that the various *tuf* nucleic acids and/or sequences determined by us occasionally contain base ambiguities. These degenerated nucleotides correspond to sequence variations between *tufA* and *tufB* genes (or copies of the EF-G subdivision of *tuf* nucleic acids and/or sequences, or copies of EF-1 α subdivision of *tuf* nucleic acids and/or sequences for fungi and parasites) because the amplification primers amplify both *tuf* genes. These nucleotide variations were not attributable to nucleotide misincorporations by the *Taq* DNA polymerase because the sequence of both strands was identical and also because the sequences determined with both preparations of the gel-purified *tuf* amplicons obtained from two independent PCR amplifications were identical.

The selection of amplification primers from *tuf* nucleic acids and/or sequences

The *tuf* sequences determined by us or selected from public databases were used to select PCR primers for universal detection of bacteria, as well as for genus-

specific, species-specific family-specific or group-specific detection and identification. The strategy used to select these PCR primers was based on the analysis of multiple sequence alignments of various *tuf* sequences. For more details about the selection of PCR primers from *tuf* sequences please refer to Examples 5, 7-14, 17, 22, 24, 28, 30-31, 33, 36, and 38-40, and to Annexes VI-IX, XI-XIX and XXV.

Sequencing of *atpD* and *recA* nucleic acids and/or sequences from a variety of archaeal, bacterial, fungal and parasitical species

The method used to obtain *atpD* and *recA* nucleic acids and/or sequences is similar to that described above for *tuf* nucleic acids and/or sequences.

The selection of amplification primers from *atpD* or *recA* nucleic acids and/or sequences

The comparison of the nucleotide sequence for the *atpD* or *recA* genes from various archaeal, bacterial, fungal and parasitical species allowed the selection of PCR primers (refer to Examples 6, 13, 29, 34 and 37, and to Annexes IV, V, X, and XX).

DNA amplification

For DNA amplification by the widely used PCR (polymerase chain reaction) method, primer pairs were derived from proprietary DNA fragments or from database sequences. Prior to synthesis, the potential primer pairs were analyzed by using the Oligo™ 5.0 software to verify that they were good candidates for PCR amplification.

During DNA amplification by PCR, two oligonucleotide primers binding respectively to each strand of the heat-denatured target DNA from the microbial

genome are used to amplify exponentially *in vitro* the target DNA by successive thermal cycles allowing denaturation of the DNA, annealing of the primers and synthesis of new targets at each cycle (Persing *et al*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.).

Briefly, the PCR protocols were as follows: Treated clinical specimens or standardized bacterial or fungal or parasitical suspensions (see below) or purified genomic DNA from bacteria, fungi or parasites were amplified in a 20 μ l PCR reaction mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 2.5 mM MgCl₂, 0.4 μ M of each primer, 200 μ M of each of the four dNTPs and 0.5 unit of *Taq* DNA polymerase (Promega) combined with the TaqStartTM antibody (Clontech Laboratories Inc., Palo Alto, CA). The TaqStartTM antibody, which is a neutralizing monoclonal antibody to *Taq* DNA polymerase, was added to all PCR reactions to enhance the specificity and the sensitivity of the amplifications (Kellogg *et al.*, 1994, Biotechniques 16:1134-1137). The treatment of the clinical specimens varies with the type of specimen tested, since the composition and the sensitivity level required are different for each specimen type. It consists in a rapid protocol to lyse the microbial cells and eliminate or neutralize PCR inhibitors. For amplification from bacterial or fungal or parasitical cultures or from purified genomic DNA, the samples were added directly to the PCR amplification mixture without any pre-treatment step. An internal control was derived from sequences not found in the target microorganisms or in the human genome. The internal control was integrated into all amplification reactions to verify the efficiency of the PCR assays and to ensure that significant PCR inhibition was absent. Alternatively, an internal control derived from rRNA was also useful to monitor the efficiency of microbial lysis protocols.

PCR reactions were then subjected to thermal cycling (3 min at 94-96°C followed by 30 cycles of 1 second at 95°C for the denaturation step and 30 seconds at 50-65°C for the annealing-extension step) using a PTC-200 thermal cycler (MJ Research Inc.). The number of cycles performed for the PCR assays varies

according to the sensitivity level required. For example, the sensitivity level required for microbial detection directly from clinical specimens is higher for blood specimens than for urine specimens because the concentration of microorganisms associated with a septicemia can be much lower than that associated with a urinary tract infection. Consequently, more sensitive PCR assays having more thermal cycles are probably required for direct detection from blood specimens. Similarly, PCR assays performed directly from bacterial or fungal or parasitical cultures may be less sensitive than PCR assays performed directly from clinical specimens because the number of target organisms is normally much lower in clinical specimens than in microbial cultures.

The person skilled in the art of DNA amplification knows the existence of other rapid amplification procedures such as ligase chain reaction (LCR), transcription-mediated amplification (TMA), self-sustained sequence replication (3SR), nucleic acid sequence-based amplification (NASBA), strand displacement amplification (SDA), branched DNA (bDNA), cycling probe technology (CPT), solid phase amplification (SPA), rolling circle amplification technology (RCA), solid phase RCA, anchored SDA and nuclease dependent signal amplification (NDSA) (Lee *et al.*, 1997, Nucleic Acid Amplification Technologies: Application to Disease Diagnosis, Eaton Publishing, Boston, MA; Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.; Westin *et al.*, 2000, Nat. Biotechnol. 18:199-204). The scope of this invention is not limited to the use of amplification by PCR, but rather includes the use of any rapid nucleic acid amplification method or any other procedure which may be used to increase the sensitivity and/or the rapidity of nucleic acid-based diagnostic tests. The scope of the present invention also covers the use of any nucleic acids amplification and detection technology including real-time or post-amplification detection technologies, any amplification technology combined with detection, any hybridization nucleic acid chips or arrays technologies, any amplification chips or combination of amplification and

hybridization chips technologies. Detection and identification by any sequencing method is also under the scope of the present invention.

Any oligonucleotide suitable for the amplification of nucleic acids by approaches other than PCR or for DNA hybridization which are derived from the species-specific, genus-specific and universal DNA fragments as well as from selected antimicrobial agents resistance or toxin gene sequences included in this document are also under the scope of this invention.

Detection of amplification products

Classically, detection of amplification is performed by standard ethidium bromide-stained agarose gel electrophoresis. It is clear that other methods for the detection of specific amplification products, which may be faster and more practical for routine diagnosis, may be used. Such methods may be based on the detection of fluorescence after or during amplification. One simple method for monitoring amplified DNA is to measure its rate of formation by measuring the increase in fluorescence of intercalating agents such as ethidium bromide or SYBR[®] Green I (Molecular Probes). If more specific detection is required, fluorescence-based technologies can monitor the appearance of a specific product during the reaction. The use of dual-labeled fluorogenic probes such as in the TaqMan[™] system (Applied Biosystems) which utilizes the 5'-3' exonuclease activity of the *Taq* polymerase is a good example (Livak K.J. *et al.* 1995, PCR Methods Appl. 4:357-362). TaqMan[™] can be performed during amplification and this "real-time" detection can be done in a single closed tube hence eliminating post-PCR sample handling and consequently preventing the risk of amplicon carryover. Several other fluorescence-based detection methods can be performed in real-time. Fluorescence resonance energy transfer (FRET) is the principle behind the use of adjacent hybridization probes (Wittwer, C.T. *et al.* 1997. BioTechniques 22:130-138), molecular beacons (Tyagi S. and Kramer F.R. 1996. Nature Biotechnology 14:303-308) and scorpions (Whitcomb *et al.* 1999. Nature

Biotechnology 17:804-807). Adjacent hybridization probes are designed to be internal to the amplification primers. The 3' end of one probe is labelled with a donor fluorophore while the 5' end of an adjacent probe is labelled with an acceptor fluorophore. When the two probes are specifically hybridized in closed proximity (spaced by 1 to 5 nucleotides) the donor fluorophore which has been excited by an external light source emits light that is absorbed by a second acceptor that emit more fluorescence and yields a FRET signal. Molecular beacons possess a stem-and-loop structure where the loop is the probe and at the bottom of the stem a fluorescent moiety is at one end while a quenching moiety is at the other end. The beacons undergo a fluorogenic conformational change when they hybridize to their targets hence separating the fluorochrome from its quencher. The FRET principle is also used in an air thermal cycler with a built-in fluorometer (Wittwer, C.T. *et al.* 1997. *BioTechniques* 22:130-138). The amplification and detection are extremely rapid as reactions are performed in capillaries: it takes only 18 min to complete 45 cycles. Those techniques are suitable especially in the case where few pathogens are searched for. Boehringer-Roche Inc. sells the LightCycler™, and Cepheid makes the SmartCycler. These two apparatus are capable of rapid cycle PCR combined with fluorescent SYBR® Green I or FRET detection. We recently demonstrated in our laboratory, real-time detection of 10 CFU in less than 40 minutes using adjacent hybridization probes on the LightCycler™. Methods based on the detection of fluorescence are particularly promising for utilization in routine diagnosis as they are very rapid, quantitative and can be automated.

Microbial pathogens detection and identification may also be performed by solid support or liquid hybridization using species-specific internal DNA probes hybridizing to an amplification product. Such probes may be generated from any sequence from our repertory and designed to specifically hybridize to DNA amplification products which are objects of the present invention. Alternatively, the internal probes for species or genus or family or group detection and identification may be derived from the amplicons produced by a universal, family-, group-, genus- or species-specific amplification assay(s). The oligonucleotide

probes may be labeled with biotin or with digoxigenin or with any other reporter molecule (for more details see below the section on hybrid capture). Hybridization on a solid support is amendable to miniaturization.

At present the oligonucleotide nucleic acid microarray technology is appealing. Currently, available low to medium density arrays (Heller *et al.*, An integrated microelectronics hybridization system for genomic research and diagnostic applications. *In*: Harrison, D.J., and van den Berg, A., 1998, Micro total analysis systems '98, Kluwer Academic Publisher, Dordrecht.) could specifically capture fluorescent-labelled amplicons. Detection methods for hybridization are not limited to fluorescence; potentiometry, colorimetry and plasmon resonance are some examples of alternative detection methods. In addition to detection by hybridization, nucleic acid microarrays could be used to perform rapid sequencing by hybridization. Mass spectrometry could also be applicable for rapid identification of the amplicon or even for sequencing of the amplification products (Chiu and Cantor, 1999, Clinical Chemistry 45:1578; Berkenkamp *et al.*, 1998, Science 281:260).

For the future of our assay format, we also consider the major challenge of molecular diagnostics tools, *i.e.*: integration of the major steps including sample preparation, genetic amplification, detection, data analysis and presentation (Anderson *et al.*, Advances in integrated genetic analysis. *In*: Harrison, D.J., and van den Berg, A., 1998, Micro total analysis systems '98, Kluwer Academic Publisher, Dordrecht.).

To ensure PCR efficiency, glycerol, dimethyl sulfoxide (DMSO) or other related solvents can be used to increase the sensitivity of the PCR and to overcome problems associated with the amplification of a target DNA having a high GC content or forming strong secondary structures (Dieffenbach and Dveksler, 1995, PCR Primer: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Plainview, New York). The concentration ranges for glycerol and DMSO are 5-15% (v/v) and 3-10% (v/v), respectively. For the PCR reaction mixture, the concentration ranges for the amplification primers and $MgCl_2$ are 0.1-1.5 μM and

1.0-10.0 mM, respectively. Modifications of the standard PCR protocol using external and nested primers (i.e. nested PCR) or using more than one primer pair (i.e. multiplex PCR) may also be used (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). For more details about the PCR protocols and amplicon detection methods, see Examples.

Hybrid capture and chemiluminescence detection of amplification products

Hybridization and detection of amplicons by chemiluminescence were adapted from Nikiforov *et al.* (1994, PCR Methods and Applications 3:285-291 and 1995, Anal. Biochem. 227:201-209) and from the DIGTM system protocol of Boehringer Mannheim. Briefly, 50 μ l of a 25 picomoles solution of capture probe diluted in EDC {1-ethyl-3-(3-dimethylaminopropyl) carbodiimide hydrochloride} are immobilized in each well of 96-wells plates (MicroliteTM 2, Dynex) by incubation overnight at room temperature. The next day, the plates are incubated with a solution of 1% BSA diluted into TNTw (10 mM Tris-HCl, pH 7.5; 150 mM NaCl; 0.05% TweenTM 20) for 1 hour at 37 °C. The plates are then washed on a Wellwash AscentTM (Labsystems) with TNTw followed by Washing Buffer (100 mM maleic acid pH7.5; 150 mM NaCl; 0.3% TweenTM 20).

The amplicons were labelled with DIG-11-dUTP during PCR using the PCR DIG Labelling Mix from Boehringer Mannheim according to the manufacturer's instructions. Hybridization of the amplicons to the capture probes is performed in triplicate at stringent temperature (generally, probes are designed to allow hybridization at 55 °C, the stringent temperature) for 30 minutes in 1.5 M NaCl; 10 mM EDTA. It is followed by two washes in 2 X SSC; 0.1% SDS, then by four washes in 0.1X SSC; 0.1% SDS at the stringent temperature (55 °C). Detection with 1,2 dioxetane chemiluminescent alkaline phosphatase substrates like CSPD[®] (Tropix Inc.) is performed according to the manufacturer's instructions but with shorter incubations times and a different antibody concentration. The plates are

agitated at each step, the blocking incubation is performed for only 5 minutes, the anti-DIG-AP1 is used at a 1:1000 dilution, the incubation with antibody lasts 15 minutes, the plates are washed twice for only 5 minutes. Finally, after a 2 minutes incubation into the detection buffer, the plates are incubated 5 minutes with CSPD® at room temperature followed by a 10 minutes incubation at 37 °C without agitation. Luminous signal detection is performed on a Dynex Microtiter Plate Luminometer using RLU (Relative Light Units).

Specificity, ubiquity and sensitivity tests for oligonucleotide primers and probes

The specificity of oligonucleotide primers and probes was tested by amplification of DNA or by hybridization with bacterial or fungal or parasitical species selected from a panel comprising closely related species and species sharing the same anatomo-pathological site (see Annexes and Examples). All of the bacterial, fungal and parasitical species tested were likely to be pathogens associated with infections or potential contaminants which can be isolated from clinical specimens. Each target DNA could be released from microbial cells using standard chemical and/or physical treatments to lyse the cells (Sambrook *et al.*, 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY) or alternatively, genomic DNA purified with the GNOME™ DNA kit (Bio101, Vista, CA) was used. Subsequently, the DNA was subjected to amplification with the primer pairs. Specific primers or probes amplified only the target microbial species, genus, family or group.

Oligonucleotides primers found to amplify specifically the target species, genus, family or group were subsequently tested for their ubiquity by amplification (i.e. ubiquitous primers amplified efficiently most or all isolates of the target species or genus or family or group). Finally, the sensitivity of the primers or probes was determined by using 10-fold or 2-fold dilutions of purified genomic DNA from the targeted microorganism. For most assays, sensitivity levels in the

range of 1-100 copies were obtained. The specificity, ubiquity and sensitivity of the PCR assays using the selected amplification primer pairs were tested either directly from cultures of microbial species or from purified microbial genomic DNA.

Probes were tested in hybrid capture assays as described above. An oligonucleotide probe was considered specific only when it hybridized solely to DNA from the species or genus or family or group from which it was selected. Oligonucleotide probes found to be specific were subsequently tested for their ubiquity (i.e. ubiquitous probes detected efficiently most or all isolates of the target species or genus or family or group) by hybridization to microbial DNAs from different clinical isolates of the species or genus or family or group of interest including ATCC reference strains. Similarly, oligonucleotide primers and probes could be derived from antimicrobial agents resistance or toxin genes which are objects of the present invention.

Reference strains

The reference strains used to build proprietary *tuf*, *atpD* and *recA* sequence data subrepertories, as well as to test the amplification and hybridization assays were obtained from (i) the American Type Culture Collection (ATCC), (ii) the Laboratoire de santé publique du Québec (LSPQ), (iii) the Centers for Disease Control and Prevention (CDC), (iv) the National Culture Type Collection (NCTC) and (v) several other reference laboratories throughout the world. The identity of our reference strains was confirmed by phenotypic testing and reconfirmed by analysis of *tuf*, *atpD* and *recA* sequences (see Example 13).

Antimicrobial agents resistance genes

Antimicrobial resistance complicates treatment and often leads to therapeutic failures. Furthermore, overuse of antibiotics inevitably leads to the emergence of

microbial resistance. Our goal is to provide clinicians, in approximately one hour, the needed information to prescribe optimal treatments. Besides the rapid identification of negative clinical specimens with DNA-based tests for universal algal, archaeal, bacterial, fungal or parasitical detection and the identification of the presence of a specific pathogen in the positive specimens with species- and/or genus- and/or family- and/or group-specific DNA-based tests, clinicians also need timely information about the ability of the microbial pathogen to resist antibiotic treatments. We feel that the most efficient strategy to evaluate rapidly microbial resistance to antimicrobials is to detect directly from the clinical specimens the most common and clinically important antimicrobial agents resistance genes (i.e. DNA-based tests for the specific detection of antimicrobial agents resistance genes). Since the sequence from the most important and common antimicrobial agents resistance genes are available from public databases, our strategy is to use the sequence from a portion or from the entire resistance gene to design specific oligonucleotide primers or probes which will be used as a basis for the development of sensitive and rapid DNA-based tests. The list of each of the antimicrobial agents resistance genes selected on the basis of their clinical relevance (i.e. high incidence and importance) is given in Table 5; descriptions of the designed amplification primers and internal probes are given in Annexes XXXIV-XXXVII, XXXIX, XLV, and L-LI. Our approach is unique because the antimicrobial agents resistance genes detection and the microbial detection and identification can be performed simultaneously, or independently, or sequentially in multiplex or parallel or sequential assays under uniform PCR amplification conditions. These amplifications can also be done separately.

Toxin genes

Toxin identification is often very important to prescribe optimal treatments. Besides the rapid identification of negative clinical specimens with DNA-based tests for universal bacterial detection and the identification of the presence of a

specific pathogen in the positive specimens with species- and/or genus- and/or family- and/or group-specific DNA-based tests, clinicians sometimes need timely information about the ability of certain bacterial pathogens to produce toxins. Since the sequence from the most important and common bacterial toxin genes are available from public databases, our strategy is to use the sequence from a portion or from the entire toxin gene to design specific oligonucleotide primers or probes which will be used as a basis for the development of sensitive and rapid DNA-based tests. The list of each of the bacterial toxin genes selected on the basis of their clinical relevance (i.e. high incidence and importance) is given in Table 6; descriptions of the designed amplification primers and internal probes are given in Annexes XXII, XXXII and XXXIII. Our approach is unique because the toxin genes detection and the bacterial detection and identification can be performed simultaneously, or independently, or sequentially, in multiplex or parallel or sequential assays under uniform PCR amplification conditions. These amplifications can also be done separately.

Universal bacterial detection

In the routine microbiology laboratory, a high percentage of clinical specimens sent for bacterial identification are negative by culture. Testing clinical samples with universal amplification primers or universal probes to detect the presence of bacteria prior to specific identification and screening out the numerous negative specimens is thus useful as it reduces costs and may rapidly orient the clinical management of the patients. Several amplification primers and probes were therefore synthesized from highly conserved portions of bacterial sequences from the *tuf*, *atpD* and *recA* nucleic acids and/or sequences. The universal primers selection was based on a multiple sequence alignment constructed with sequences from our repertoire.

All computer analysis of amino acid and nucleotide sequences were performed by using the GCG programs. Subsequently, optimal PCR primers for

the universal amplification of bacteria were selected with the help of the Oligo™ program. The selected primers are degenerated at several nucleotide positions and contain several inosines in order to allow the amplification of all clinically relevant bacterial species. Inosine is a nucleotide analog able to specifically bind to any of the four nucleotides A, C, G or T. Degenerated oligonucleotides consist of an oligonucleotide mix having two or more of the four nucleotides A, C, G or T at the site of mismatches. The inclusion of inosine and/or of base ambiguities in the amplification primers allow mismatch tolerance thereby permitting the amplification of a wider array of target nucleotide sequences (Dieffenbach and Dveksler, 1995 PCR Primer: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Plainview, NY).

The amplification conditions with the universal primers are very similar to those used for the species- and genus-specific amplification assays except that the annealing temperature is slightly lower. The original universal PCR assay described in our assigned WO98/20157 (SEQ ID NOs. 23-24 of the latter application) was specific and nearly ubiquitous for the detection of bacteria. The specificity for bacteria was verified by amplifying genomic DNA isolated from the 12 fungal species as well as genomic DNA from *Leishmania donovani*, *Saccharomyces cerevisiae* and human lymphocytes. None of the above eukaryotic DNA preparations could be amplified by the universal assay, thereby suggesting that this test is specific for bacteria. The ubiquity of the universal assay was verified by amplifying genomic DNAs from 116 reference strains which represent 95 of the most clinically relevant bacterial species. These species have been selected from the bacterial species listed in Table 4. We found that at least 104 of these strains could be amplified. However, the assay could be improved since bacterial species which could not be amplified with the original *tuf* nucleic acids and/or sequences-based assay included species belonging to the following genera: *Corynebacterium* (11 species) and *Stenotrophomonas* (1 species). Sequencing of the *tuf* genes from these bacterial species and others has been performed in the scope of the present invention in order to improve the universal assay. This

sequencing data has been used to select new universal primers which may be more ubiquitous and more sensitive. Also, we improved our primer and probes design strategy by taking into consideration the phylogeny observed in analysing our repertoire of *tuf*, *atpD* and *recA* sequences. Data from each of the 3 main subrepertoires (*tuf*, *atpD* and *recA*) was subjected to a basic phylogenetic analysis using the Pileup command from version 10 of the GCG package (Genetics Computer Group, inc.). This analysis indicated the main branches or phyla reflecting the relationships between sequences. Instead of trying to design primers or probes able to hybridize to all phyla, we designed primers or probes able to hybridize to the main phyla while trying to use the largest phylum possible. This strategy should allow less degenerated primers hence improving sensitivity and by combining primers in a multiplex assay, improve ubiquity. Universal primers SEQ ID NOs. 643-645 based on *tuf* sequences have been designed to amplify most pathogenic bacteria except *Actinomycetaceae*, *Clostridiaceae* and the *Cytophaga*, *Flexibacter* and *Bacteroides* phylum (pathogenic bacteria of this phylum include mostly *Bacteroides*, *Porphyromonas* and *Prevotella* species). Primers to fill these gaps have been designed for *Actinomycetaceae* (SEQ ID NOs. 646-648), *Clostridiaceae* (SEQ ID NOs. 796-797, 808-811), and the *Cytophaga*, *Flexibacter* and *Bacteroides* phylum (SEQ ID NOs. 649-651), also derived from *tuf* nucleic acids and/or sequences. These primers sets could be used alone or in conjunction to render the universal assay more ubiquitous.

Universal primers derived from *atpD* sequences include SEQ ID NOs. 562-565. Combination of these primers does not amplify human DNA but should amplify almost all pathogenic bacterial species except proteobacteria belonging to the epsilon subdivision (*Campylobacter* and *Helicobacter*), the bacteria from the *Cytophaga*, *Flexibacter* and *Bacteroides* group and some actinomycetes and corynebacteria. By analysing *atpD* sequences from the latter species, primers and probes to specifically fill these gaps could be designed and used in conjunction with primers SEQ ID NOs. 562-565, also derived from *atpD* nucleic acids and/or sequences.

In addition, universality of the assay could be expanded by mixing *atpD* sequences-derived primers with *tuf* sequences-derived primers. Ultimately, even *recA* sequences-derived primers could be added to fill some gaps in the universal assay.

It is important to note that the 95 bacterial species selected to test the ubiquity of the universal assay include all of the most clinically relevant bacterial species associated with a variety of human infections acquired in the community or in hospitals (nosocomial infections). The most clinically important bacterial and fungal pathogens are listed in Tables 1 and 2.

Amino acid sequences derived from *tuf*, *atpD* and *recA* nucleic acids and/or sequences

The amino acid sequences translated from the repertory of *tuf*, *atpD* and *recA* nucleic acids and/or sequences are also an object of the present invention. The amino acid sequence data will be particularly useful for homology modeling of three-dimensional (3D) structure of the elongation factor Tu, elongation factor G, elongation factor 1 α , ATPase subunit beta and RecA recombinase. For all these proteins, at least one structure model has been published using X-ray diffraction data from crystals. Based on those structural informations it is possible to use computer software to build 3D model structures for any other protein having peptide sequence homologies with the known structure (Greer, 1991, Methods in Enzymology, 202:239-252; Taylor, 1994, Trends Biotechnol., 12(5):154-158; Sali, 1995, Curr. Opin. Biotechnol. 6:437-451; Sanchez and Sali, 1997, Curr. Opin. Struct. Biol. 7:206-214; Fischer and Eisenberg, 1999, Curr. Opin. Struct. Biol. 9:208-211; Guex *et al.*, 1999, Trends Biochem. Sci. 24: 364-367). Model structures of target proteins are used for the design or to predict the behavior of ligands and inhibitors such as antibiotics. Since EF-Tu and EF-G are already known as antibiotic targets (see above) and since the beta subunit of ATPase and RecA recombinase are essential to the survival of the microbial cells in natural

conditions of infection, all four proteins could be considered antibiotic targets. Sequence data, especially the new data generated by us could be very useful to assist the creation of new antibiotic molecules with desired spectrum of activity. In addition, model structures could be used to improve protein function for commercial purposes such as improving antibiotic production by microbial strains or increasing biomass.

The following detailed embodiments and appended drawings are provided as illustrative examples of his invention, with no intention to limit the scope thereof.

DESCRIPTION OF THE DRAWINGS

Figures 1 and 2 illustrate the principal subdivisions of the *tuf* and *atpD* sequences repertoires, respectively. For the design of primers and probes, depending on the needs, one may want to use the complete data set illustrated on the top of the pyramid or use only a subset illustrated by the different branching points. Smaller subdivisions, representing groups, families, genus and species, could even be made to extend to the bottom of the pyramid. Because the *tuf* and *atpD* sequences are highly conserved and evolved with each species, the design of primers and probes does not need to include all the sequences within the database or its subdivisions. As illustrated in Annexes IV to XX, XXIII to XXXI, XXXVIII and XLII, depending on the use, sequences from a limited number of species can be carefully selected to represent: i) only the main phylogenetic branches from which the intended probes and primers need to be differentiating, and ii) only the species for which they need to be matching. However, for ubiquity purposes, and especially for primers and probes identifying large groups of species (genus, family, group or universal, or sequencing primers), the more data is included into the sequence analysis, the better the probes and primers will be suitable for each particular intended use. Similarly, for specificity purposes, a larger data set (or repertoire) ensures optimal primers and probes design by reducing the chance of employing nonspecific oligonucleotides.

Figure 3 illustrates the approach used to design specific amplification primers from *fusA* as well as from the region between the end of *fusA* and the beginning of *tuf* in the streptomycin (*str*) operon (referred to as the *fusA-tuf* intergenic spacer in Table 7).

Figures 4 to 6 are illustrations to Example 42, whereas Figures 7 to 10 illustrate Example 43. Figures 11 and 12 illustrate Example 44.

FIGURE LEGENDS

Figure 3. Schematic organization of universal amplification primers (SEQ ID NOs. 1221-1229) in the *str* operon. Amplicon sizes are given in bases pairs. Drawing not to scale, as the *fusA-tuf* intergenic spacer size varies depending on the bacterial species. Indicated amplicon lengths are for *E. coli*.

Figure 4. Abridged multiple amino acid sequence alignment of the partial *tuf* gene products from selected species illustrated using the program Alscript. Residues highly conserved in bacteria are boxed in grey and gaps are represented with dots. Residues in reverse print are unique to the enterococcal *tufB* as well as to streptococcal and lactococcal *tuf* gene products. Numbering is based on *E. coli* EF-Tu and secondary structure elements of *E. coli* EF-Tu are represented by cylinders (α -helices) and arrows (β -strands).

Figure 5. Distance matrix tree of bacterial EF-Tu based on amino acid sequence homology. The tree was constructed by the neighbor-joining method. The tree was rooted using archeal and eukaryotic EF-1 α genes as the outgroup. The scale bar represents 5% changes in amino acid sequence, as determined by taking the sum of all of the horizontal lines connecting two species.

Figure 6. Southern hybridization of *Bgl*III/*Xba*I digested genomic DNAs of some enterococci (except for *E. casseliflavus* and *E. gallinarum* whose genomic DNA was digested with *Bam*HI/*Pvu*II) using the *tufA* gene fragment of *E. faecium* as probes. The sizes of hybridizing fragments are shown in kilobases. Strains tested are listed in Table 16.

Figure 7. *Pantoea* and *Tatumella* species specific signature indel in *atpD* genes. The nucleotide positions given are for *E. coli atpD* sequence (GenBank accession no. V00267). Numbering starts from the first base of the initiation codon.

Figure 8: Trees based on sequence data from *tuf* (left side) and *atpD* (right side). The phylogenetic analysis was performed using the Neighbor-Joining method calculated using the Kimura two-parameter method. The value on each branch indicates the occurrence (%) of the branching order in 750 bootstrapped trees.

Figure 9: Phylogenetic tree of members of the family *Enterobacteriaceae* based on *tuf* (a), *atpD* (b), and 16S rDNA (c) genes. Trees were generated by neighbor-joining method calculated using the Kimura two-parameter method. The value on each branch is the percentage of bootstrap replications supporting the branch. 750 bootstrap replications were calculated.

Figure 10: Plot of *tuf* distances versus 16S rDNA distances (a), *atpD* distances versus 16S rDNA distances (b), and *atpD* distances versus *tuf* distances (c). Symbols: ○, distances between pairs of strains belonging to the same species; ●, distances between *E. coli* strains and *Shigella* strains; □, distances between pairs belonging to the same genus; ■, distances between pairs belonging to different genera; △, distances between pairs belonging to different families.

EXAMPLES AND ANNEXES

For sake of clarity, here is a list of Examples and Annexes:

Example 1: Sequencing of bacterial *atpD* (F-type and V-type) gene fragments.

Example 2: Sequencing of eukaryotic *atpD* (F-type and V-type) gene fragments.

Example 3: Sequencing of eukaryotic *tuf* (EF-1) gene fragments.

- Example 4: Sequencing of eukaryotic *tuf* (organelle origin, M) gene fragments.
- Example 5: Specific detection and identification of *Streptococcus agalactiae* using *tuf* sequences.
- Example 6: Specific detection and identification of *Streptococcus agalactiae* using *atpD* sequences.
- Example 7: Development of a PCR assay for detection and identification of staphylococci at genus and species levels.
- Example 8: Differentiating between the two closely related yeast species *Candida albicans* and *Candida dubliniensis*.
- Example 9: Specific detection and identification of *Entamoeba histolytica*.
- Example 10: Sensitive detection and identification of *Chlamydia trachomatis*.
- Example 11: Genus-specific detection and identification of enterococci.
- Example 12: Detection and identification of the major bacterial platelets contaminants using *tuf* sequences with a multiplex PCR test.
- Example 13: The resolving power of the *tuf* and *atpD* sequences databases is comparable to the biochemical methods for bacterial identification.
- Example 14: Detection of group B streptococci from clinical specimens.
- Example 15: Simultaneous detection and identification of *Streptococcus pyogenes* and its pyrogenic exotoxin A.
- Example 16: Real-time detection and identification of Shiga toxin-producing bacteria.
- Example 17: Development of a PCR assay for the detection and identification of staphylococci at genus and species levels and its associated *mecA* gene.
- Example 18: Sequencing of *pbp1a*, *pbp2b* and *pbp2x* genes of *Streptococcus pneumoniae*.
- Example 19: Sequencing of *hexA* genes of *Streptococcus* species.
- Example 20: Development of a multiplex PCR assay for the detection of *Streptococcus pneumoniae* and its penicillin resistance genes.

- Example 21: Sequencing of the vancomycin resistance *vanA*, *vanC1*, *vanC2* and *vanC3* genes.
- Example 22: Development of a PCR assay for the detection and identification of enterococci at genus and species levels and its associated resistance genes *vanA* and *vanB*.
- Example 23: Development of a multiplex PCR assay for detection and identification of vancomycin-resistant *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus gallinarum*, *Enterococcus casseliflavus*, and *Enterococcus flavescens*.
- Example 24: Universal amplification involving the EF-G (*fusA*) subdivision of *tuf* sequences.
- Example 25: DNA fragment isolation from *Staphylococcus saprophyticus* by arbitrarily primed PCR.
- Example 26: Sequencing of prokaryotic *tuf* gene fragments.
- Example 27: Sequencing of procaryotic *recA* gene fragments.
- Example 28: Specific detection and identification of *Escherichia coli/Shigella* sp. using *tuf* sequences.
- Example 29: Specific detection and identification of *Klebsiella pneumoniae* using *atpD* sequences.
- Example 30: Specific detection and identification of *Acinetobacter baumannii* using *tuf* sequences.
- Example 31: Specific detection and identification of *Neisseria gonorrhoeae* using *tuf* sequences.
- Example 32: Sequencing of bacterial *gyrA* and *parC* gene fragments.
- Example 33: Development of a PCR assay for the specific detection and identification of *Staphylococcus aureus* and its quinolone resistance genes *gyrA* and *parC*.
- Example 34: Development of a PCR assay for the detection and identification of *Klebsiella pneumoniae* and its quinolone resistance genes *gyrA* and *parC*.

- Example 35: Development of a PCR assay for the detection and identification of *Streptococcus pneumoniae* and its quinolone resistance genes *gyrA* and *parC*.
- Example 36: Detection of extended-spectrum TEM-type β -lactamases in *Escherichia coli*.
- Example 37: Detection of extended-spectrum SHV-type β -lactamases in *Klebsiella pneumoniae*.
- Example 38: Development of a PCR assay for the detection and identification of *Neisseria gonorrhoeae* and its associated tetracycline resistance gene *tetM*.
- Example 39: Development of a PCR assay for the detection and identification of *Shigella* sp. and their associated trimethoprim resistance gene *dhfr1a*.
- Example 40: Development of a PCR assay for the detection and identification of *Acinetobacter baumannii* and its associated aminoglycoside resistance gene *aph(3')-VIa*.
- Example 41: Specific detection and identification of *Bacteroides fragilis* using *atpD* (V-type) sequences.
- Example 42: Evidence for horizontal gene transfer in the evolution of the elongation factor Tu in Enterococci.
- Example 43: Elongation factor Tu (*tuf*) and the F-ATPase beta-subunit (*atpD*) as phylogenetic tools for species of the family *Enterobacteriaceae*.
- Example 44: Testing new pairs of PCR primers selected from two species-specific genomic DNA fragments which are objects of US patent 6,001,564.
- Example 45: Testing modified versions of PCR primers derived from the sequence of several primers which are objects of US patent 6,001,564.

The various Annexes show the strategies used for the selection of a variety of DNA amplification primers, nucleic acid hybridization probes and molecular beacon internal probes:

- (i) Annex I shows the amplification primers used for nucleic acid amplification from *tuf* sequences.
- (ii) Annex II shows the amplification primers used for nucleic acid amplification from *atpD* sequences.
- (iii) Annex III shows the internal hybridization probes for detection of *tuf* sequences.
- (iv) Annex IV illustrates the strategy used for the selection of the amplification primers specific for *atpD* sequences of the F-type.
- (v) Annex V illustrates the strategy used for the selection of the amplification primers specific for *atpD* sequences of the V-type.
- (vi) Annex VI illustrates the strategy used for the selection of the amplification primers specific for the *tuf* sequences of organelle lineage (M, the letter M is used to indicate that in most cases, the organelle is the mitochondria).
- (vii) Annex VII illustrates the strategy used for the selection of the amplification primers specific for the *tuf* sequences of eukaryotes (EF-1).
- (viii) Annex VIII illustrates the strategy for the selection of *Streptococcus agalactiae*-specific amplification primers from *tuf* sequences.
- (ix) Annex IX illustrates the strategy for the selection of *Streptococcus agalactiae*-specific hybridization probes from *tuf* sequences.
- (x) Annex X illustrates the strategy for the selection of *Streptococcus agalactiae*-specific amplification primers from *atpD* sequences.
- (xi) Annex XI illustrates the strategy for the selection from *tuf* sequences of *Candida albicans/dubliniensis*-specific amplification primers, *Candida albicans*-specific hybridization probe and *Candida dubliniensis*-specific hybridization probe.

- (xii) Annex XII illustrates the strategy for the selection of *Staphylococcus*-specific amplification primers from *tuf* sequences.
- (xiii) Annex XIII illustrates the strategy for the selection of the *Staphylococcus*-specific hybridization probe from *tuf* sequences.
- (xiv) Annex XIV illustrates the strategy for the selection of *Staphylococcus saprophyticus*-specific and *Staphylococcus haemolyticus*-specific hybridization probes from *tuf* sequences.
- (xv) Annex XV illustrates the strategy for the selection of *Staphylococcus aureus*-specific and *Staphylococcus epidermidis*-specific hybridization probes from *tuf* sequences.
- (xvi) Annex XVI illustrates the strategy for the selection of the *Staphylococcus hominis*-specific hybridization probe from *tuf* sequences.
- (xvii) Annex XVII illustrates the strategy for the selection of the *Enterococcus*-specific amplification primers from *tuf* sequences.
- (xviii) Annex XVIII illustrates the strategy for the selection of the *Enterococcus faecalis*-specific hybridization probe, of the *Enterococcus faecium*-specific hybridization probe and of the *Enterococcus casseliflavus-flavescens-gallinarum* group-specific hybridization probe from *tuf* sequences.
- (xix) Annex XIX illustrates the strategy for the selection of primers from *tuf* sequences for the identification of platelets contaminants.
- (xx) Annex XX illustrates the strategy for the selection of the universal amplification primers from *atpD* sequences.
- (xxi) Annex XXI shows the amplification primers used for nucleic acid amplification from *recA* sequences.
- (xxii) Annex XXII shows the specific and ubiquitous primers for nucleic acid amplification from *speA* sequences.
- (xxiii) Annex XXIII illustrates the first strategy for the selection of *Streptococcus pyogenes*-specific amplification primers from *speA* sequences.

- (xxiv) Annex XXIV illustrates the second strategy for the selection of *Streptococcus pyogenes*-specific amplification primers from *speA* sequences.
- (xxv) Annex XXV illustrates the strategy for the selection of *Streptococcus pyogenes*-specific amplification primers from *tuf* sequences.
- (xxvi) Annex XXVI illustrates the strategy for the selection of *stx*₁-specific amplification primers and hybridization probe.
- (xxvii) Annex XXVII illustrates the strategy for the selection of *stx*₂-specific amplification primers and hybridization probe.
- (xxviii) Annex XXVIII illustrates the strategy for the selection of *vanA*-specific amplification primers from *van* sequences.
- (xxix) Annex XXIX illustrates the strategy for the selection of *vanB*-specific amplification primers from *van* sequences.
- (xxx) Annex XXX illustrates the strategy for the selection of *vanC*-specific amplification primers from *vanC* sequences.
- (xxxi) Annex XXXI illustrates the strategy for the selection of *Streptococcus pneumoniae*-specific amplification primers and hybridization probes from *pbp1a* sequences.
- (xxxii) Annex XXXII shows the specific and ubiquitous primers for nucleic acid amplification from toxin gene sequences.
- (xxxiii) Annex XXXIII shows the molecular beacon internal hybridization probes for specific detection of toxin sequences.
- (xxxiv) Annex XXXIV shows the specific and ubiquitous primers for nucleic acid amplification from *van* sequences.
- (xxxv) Annex XXXV shows the internal hybridization probes for specific detection of *van* sequences.
- (xxxvi) Annex XXXVI shows the specific and ubiquitous primers for nucleic acid amplification from *pbp* sequences.
- (xxxvii) Annex XXXVII shows the internal hybridization probes for specific detection of *pbp* sequences.

- (xxxviii) Annex XXXVIII illustrates the strategy for the selection of *vanAB*-specific amplification primers and *vanA*- and *vanB*- specific hybridization probes from *van* sequences.
- (xxxix) Annex XXXIX shows the internal hybridization probe for specific detection of *mecA*.
- (xl) Annex XL shows the specific and ubiquitous primers for nucleic acid amplification from *hexA* sequences.
- (xli) Annex XLI shows the internal hybridization probe for specific detection of *hexA*.
- (xlii) Annex XLII illustrates the strategy for the selection of *Streptococcus pneumoniae* species-specific amplification primers and hybridization probe from *hexA* sequences.
- (xlili) Annex XLIII shows the specific and ubiquitous primers for nucleic acid amplification from *pcp* sequences.
- (xliv) Annex XLIV shows specific and ubiquitous primers for nucleic acid amplification of *S. saprophyticus* sequences of unknown coding potential.
- (xlv) Annex XLV shows the molecular beacon internal hybridization probes for specific detection of antimicrobial agents resistance gene sequences.
- (xlvi) Annex XLVI shows the molecular beacon internal hybridization probe for specific detection of *S. aureus* gene sequences of unknown coding potential.
- (xlvii) Annex XLVII shows the molecular beacon hybridization internal probe for specific detection of *tuf* sequences.
- (xlviii) Annex XLVIII shows the molecular beacon internal hybridization probes for specific detection of *ddl* and *mtl* sequences.
- (xlix) Annex XLIX shows the internal hybridization probe for specific detection of *S. aureus* sequences of unknown coding potential.
- (l) Annex L shows the amplification primers used for nucleic acid amplification from antimicrobial agents resistance genes sequences.

- (li) Annex LI shows the internal hybridization probes for specific detection of antimicrobial agents resistance genes sequences.
- (lii) Annex LII shows the molecular beacon internal hybridization probes for specific detection of *atpD* sequences.
- (liii) Annex LIII shows the internal hybridization probes for specific detection of *atpD* sequences.
- (liv) Annex LIV shows the internal hybridization probes for specific detection of *ddl* and *mtl* sequences.

As shown in these Annexes, the selected amplification primers may contain inosines and/or base ambiguities. Inosine is a nucleotide analog able to specifically bind to any of the four nucleotides A, C, G or T. Alternatively, degenerated oligonucleotides which consist of an oligonucleotide mix having two or more of the four nucleotides A, C, G or T at the site of mismatches were used. The inclusion of inosine and/or of degeneracies in the amplification primers allows mismatch tolerance thereby permitting the amplification of a wider array of target nucleotide sequences (Dieffenbach and Dveksler, 1995 PCR Primer: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Plainview, New York).

EXAMPLES

EXAMPLE 1:

Sequencing of bacterial *atpD* (F-type and V-type) gene fragments. As shown in Annex IV, the comparison of publicly available *atpD* (F-type) sequences from a variety of bacterial species revealed conserved regions allowing the design of PCR primers able to amplify *atpD* sequences (F-type) from a wide range of bacterial species. Using primers pairs SEQ ID NOs. 566 and 567, 566 and 814, 568 and 567, 570 and 567, 572 and 567, 569 and 567, 571 and 567, 700 and 567, it was possible to amplify and sequence *atpD* sequences SEQ ID NOs. 242-270, 272-398, 673-

674, 737-767, 866-867, 942-955, 1245-1254, 1256-1265, 1527, 1576, 1577, 1600-1604, 1640-1646, 1649, 1652, 1655, 1657, 1659-1660, 1671, 1844-1845, and 1849-1865.

Similarly, Annex V shows the strategy to design the PCR primers able to amplify *atpD* sequences of the V-type from a wide range of archaeal and bacterial species. Using primers SEQ ID NOs. 681-683, it was possible to amplify and sequence *atpD* sequences SEQ ID NOs. 827-832, 929-931, 958 and 966. As the gene was difficult to amplify for several species, additional amplification primers were designed inside the original amplicon (SEQ ID NOs. 1203-1207) in order to obtain sequence information for these species. Other primers (SEQ ID NO. 1212, 1213, 2282-2285) were also designed to amplify regions of the *atpD* gene (V-type) in archaeobacteria.

EXAMPLE 2:

Sequencing of eukaryotic *atpD* (F-type and V-type) gene fragments. The comparison of publicly available *atpD* (F-type) sequences from a variety of fungal and parasitical species revealed conserved regions allowing the design of PCR primers able to amplify *atpD* sequences from a wide range of fungal and parasitical species. Using primers pairs SEQ ID NOs. 568 and 573, 574 and 573, 574 and 708, and 566 and 567, it was possible to amplify and sequence *atpD* sequences SEQ ID NOs. 458-497, 530-538, 663, 667, 676, 678-680, 768-778, 856-862, 889-896, 941, 1638-1639, 1647, 1650-1651, 1653-1654, 1656, 1658, 1684, 1846-1848, and 2189-2192.

In the same manner, the primers described in Annex V (SEQ ID NOs. 681-683) could amplify the *atpD* (V-type) gene from various fungal and parasitical species. This strategy allowed to obtain SEQ ID NOs. 834-839, 956-957, and 959-965.

EXAMPLE 3:

Sequencing of eukaryotic *tuf* (EF-1) gene fragments. As shown in Annex VII, the comparison of publicly available *tuf* (EF-1) sequences from a variety of fungal and parasitical species revealed conserved regions allowing the design of PCR primers able to amplify *tuf* sequences from a wide range of fungal and parasitical species. Using primers pairs SEQ ID NOs. 558 and 559, 813 and 559, 558 and 815, 560 and 559, 653 and 559, 558 and 655, and 654 and 559, 1999 and 2000, 2001 and 2003, 2002 and 2003, it was possible to amplify and sequence *tuf* sequences SEQ ID NOs. 399-457, 509-529, 622-624, 677, 779-790, 840-842, 865, 897-903, 1266-1287, 1561-1571 and 1685.

EXAMPLE 4:

Sequencing of eukaryotic *tuf* (organelle origin, M) gene fragments. As shown in Annex VI, the comparison of publicly available *tuf* (organelle origin, M) sequences from a variety of fungal and parasitical organelles revealed conserved regions allowing the design of PCR primers able to amplify *tuf* sequences of several organelles belonging to a wide range fungal and parasitical species. Using primers pairs SEQ ID NOs. 664 and 652, 664 and 561, 911 and 914, 912 and 914, 913 and 915, 916 and 561, 664 and 917, it was possible to amplify and sequence *tuf* sequences SEQ ID NOs. 498-508, 791-792, 843-855, 904-910, 1664, 1666-1667, 1669-1670, 1673-1683, 1686-1689, 1874-1876, 1879, 1956-1960, and 2193-2199.

EXAMPLE 5:

Specific detection and identification of *Streptococcus agalactiae* using *tuf* sequences. As shown in Annex VIII, the comparison of *tuf* sequences from a variety of bacterial species allowed the selection of PCR primers specific for *S. agalactiae*. The strategy used to design the PCR primers was based on the analysis

of a multiple sequence alignment of various *tuf* sequences. The multiple sequence alignment includes the *tuf* sequences of four bacterial strains from the target species as well as *tuf* sequences from other species and bacterial genera, especially representatives of closely related species. A careful analysis of this alignment allowed the selection of oligonucleotide sequences which are conserved within the target species but which discriminate sequences from other species and genera, especially from the closely related species, thereby permitting the species-specific, ubiquitous and sensitive detection and identification of the target bacterial species.

The chosen primer pair, oligos SEQ ID NO. 549 and SEQ ID NO. 550, gives an amplification product of 252 bp. Standard PCR was carried out using 0.4 μ M of each primer, 2.5 mM $MgCl_2$, BSA 0.05 mM, 1X Taq Buffer (Promega), dNTP 0.2 mM (Pharmacia), 0.5 U *Taq* DNA polymerase (Promega) coupled with TaqStartTM antibody (Clontech Laboratories Inc., Palo Alto), 1 μ l of genomic DNA sample in a final volume of 20 μ l using a PTC-200 thermocycler (MJ Research Inc.). The optimal cycling conditions for maximum sensitivity and specificity were 3 minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 62 °C, followed by terminal extension at 72 °C for 2 minutes. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 μ g/ml of ethidium bromide.

Specificity of the assay was tested by adding into the PCR reactions, 0.1 ng of genomic DNA from each of the bacterial species listed in Table 8. Efficient amplification was observed only for the 5 *S. agalactiae* strains listed. Of the other bacterial species, including 32 species representative of the vaginal flora and 27 other streptococcal species, only *S. acidominimus* yielded amplification. The signal with 0.1 ng of *S. acidominimus* genomic DNA was weak and the detection limit for this species was 10 pg (corresponding to more than 4000 genome copies) while the detection limit for *S. agalactiae* was 2.5 fg (corresponding to one genome copy) of genomic DNA.

To increase the specificity of the assay, internal probes were designed for FRET (Fluorescence Resonance Energy Transfer) detection using the LightCycler™ (Idaho Technology). As illustrated in Annex IX, a multiple sequence alignment of streptococcal *tuf* sequence fragments corresponding to the 252 bp region amplified by primers SEQ ID NO. 549 and SEQ ID NO. 550, was used for the design of internal probes TSagHF436 (SEQ ID NO. 582) and TSagHF465 (SEQ ID NO. 583). The region of the amplicon selected for internal probes contained sequences unique and specific to *S. agalactiae*. SEQ ID NO. 583, the more specific probe, is labelled with fluorescein in 3', while SEQ ID NO. 582, the less discriminant probe, is labelled with CY5 in 5' and blocked in 3' with a phosphate group. However, since the FRET signal is only emitted if both probes are adjacently hybridized on the same target amplicon, detection is highly specific.

Real-time detection of PCR products using the LightCycler™ was carried out using 0.4 μ M of each primer (SEQ ID NO. 549-550), 0.2 μ M of each probe (SEQ ID NO. 582-583), 2.5 mM MgCl₂, BSA 450 μ g/ml, 1X PC2 Buffer (AB Peptides, St-Louis, MO), dNTP 0.2 mM (Pharmacia), 0.5 U KlenTaq1™ DNA polymerase (AB Peptides) coupled with TaqStart™ antibody (Clontech Laboratories Inc., Palo Alto), 0.7 μ l of genomic DNA sample in a final volume of 7 μ l using a LightCycler thermocycler (Idaho Technology). The optimal cycling conditions for maximum sensitivity and specificity were 3 minutes at 94 °C for initial denaturation, then forty cycles of three steps consisting of 0 second (this setting meaning the LightCycler will reach the target temperature and stay at it for its minimal amount of time) at 94 °C, 10 seconds at 64 °C, 20 seconds at 72 °C. Amplification was monitored during each annealing steps using the fluorescence ratio. The streptococcal species having close sequence homologies with the *tuf* sequence of *S. agalactiae* (*S. acidominimus*, *S. anginosus*, *S. bovis*, *S. dysgalactiae*, *S. equi*, *S. ferus*, *S. gordonii*, *S. intermedius*, *S. parasanguis*, *S. parauberis*, *S. salivarius*, *S. sanguis*, *S. suis*) as well as *S. agalactiae* were tested in the

LightCycler with 0.07 ng of genomic DNA per reaction. Only *S. agalactiae* yielded an amplification signal, hence demonstrating that the assay is species-specific. With the LightCycler™ assay using the internal FRET probes, the detection limit for *S. agalactiae* was 1-2 genome copies of genomic DNA.

EXAMPLE 6:

Specific detection and identification of *Streptococcus agalactiae* using *atpD* sequences. As shown in Annex X, the comparison of *atpD* sequences from a variety of bacterial species allowed the selection of PCR primers specific for *S. agalactiae*. The primer design strategy is similar to the strategy described in the preceding Example except that *atpD* sequences were used in the alignment.

Four primers were selected, ASag42 (SEQ ID NO. 627), ASag52 (SEQ ID NO. 628), ASag206 (SEQ ID NO. 625) and ASag371 (SEQ ID NO. 626). The following combinations of these four primers give four amplicons; SEQ ID NO. 627 + SEQ ID NO. 625 = 190 bp, SEQ ID NO. 628 + SEQ ID NO. 625 = 180 bp, SEQ ID NO. 627 + SEQ ID NO. 626 = 355 bp, and SEQ ID NO. 628 + SEQ ID NO. 626 = 345 bp.

Standard PCR was carried out on PTC-200 thermocyclers (MJ Research Inc) using 0.4 μ M of each primers pair, 2.5 mM MgCl₂, BSA 0.05 mM, 1X *taq* Buffer (Promega), dNTP 0.2 mM (Pharmacia), 0.5 U *Taq* DNA polymerase (Promega) coupled with TaqStart™ antibody (Clontech Laboratories Inc., Palo Alto), 1 μ l of genomic DNA sample in a final volume of 20 μ L. The optimal cycling conditions for maximum sensitivity and specificity were adjusted for each primer pair. Three minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at the optimal annealing temperature specified below were followed by terminal extension at 72 °C for 2 minutes. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing

0.25 µg/ml of ethidium bromide. Since *atpD* sequences are relatively more specific than *tuf* sequences, only the most closely related species namely, the streptococcal species listed in Table 9, were tested.

All four primer pairs only amplified the six *S. agalactiae* strains. With an annealing temperature of 63 °C, the primer pair SEQ ID NO. 627 + SEQ ID NO. 625 had a sensitivity of 1-5 fg (equivalent to 1-2 genome copies). At 55 °C, the primer pair SEQ ID NO. 628 + SEQ ID NO. 625 had a sensitivity of 2.5 fg (equivalent to 1 genome copy). At 60 °C, the primer pair SEQ ID NO. 627 + SEQ ID NO. 626 had a sensitivity of 10 fg (equivalent to 4 genome copies). At 58 °C, the primer pair SEQ ID NO. 628 + SEQ ID NO. 626 had a sensitivity of 2.5-5 fg (equivalent to 1-2 genome copies). This proves that all four primer pairs can detect *S. agalactiae* with high specificity and sensitivity. Together with Example 5, this example demonstrates that both *tuf* and *atpD* sequences are suitable and flexible targets for the identification of microorganisms at the species level. The fact that 4 different primer pairs based on *atpD* sequences led to efficient and specific amplification of *S. agalactiae* demonstrates that the challenge is to find target genes suitable for diagnostic purposes, rather than finding primer pairs from these target sequences.

EXAMPLE 7:

Development of a PCR assay for detection and identification of staphylococci at genus and species levels.

Materials and Methods

Bacterial strains. The specificity of the PCR assay was verified by using a panel of ATCC (America Type Culture Collection) and DSMZ (Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH; German Collection of

Microorganisms and Cell Cultures) reference strains consisting of 33 gram-negative and 47 gram-positive bacterial species (Table 12). In addition, 295 clinical isolates representing 11 different species of staphylococci from the microbiology laboratory of the Centre Hospitalier Universitaire de Québec, Pavillon Centre Hospitalier de l'Université Laval (CHUL) (Ste-Foy, Québec, Canada) were also tested to further validate the *Staphylococcus*-specific PCR assay. These strains were all identified by using (i) conventional methods or (ii) the automated MicroScan Autoscan-4 system equipped with the Positive BP Combo Panel Type 6 (Dade Diagnostics, Mississauga, Ontario, Canada). Bacterial strains from frozen stocks kept at -80°C in brain heart infusion (BHI) broth containing 10% glycerol were cultured on sheep blood agar or in BHI broth (Quelab Laboratories Inc, Montréal, Québec, Canada).

PCR primers and internal probes. Based on multiple sequence alignments, regions of the *tuf* gene unique to staphylococci were identified. *Staphylococcus*-specific PCR primers TStaG422 (SEQ ID NO. 553) and TStaG765 (SEQ ID NO. 575) were derived from these regions (Annex XII). These PCR primers are displaced by two nucleotide positions compared to original *Staphylococcus*-specific PCR primers described in our patent publication WO98/20157 (SEQ ID NOs. 17 and 20 in the said patent publication). These modifications were done to ensure specificity and ubiquity of the primer pair, in the light of new *tuf* sequence data revealed in the present patent application for several additional staphylococcal species and strains.

Similarly, sequence alignment analysis were performed to design genus and species-specific internal probes (see Annexes XIII to XVI). Two internal probes specific for *Staphylococcus* (SEQ ID NOs. 605-606), five specific for *S. aureus* (SEQ ID NOs. 584-588), five specific for *S. epidermidis* (SEQ ID NO. 589-593), two specific for *S. haemolyticus* (SEQ ID NOs. 594-595), three specific for *S. hominis* (SEQ ID NOs. 596-598), four specific for *S. saprophyticus* (SEQ ID NOs. 599-601 and 695), and two specific for coagulase-negative *Staphylococcus* species including

S. epidermidis, *S. hominis*, *S. saprophyticus*, *S. auricularis*, *S. capitis*, *S. haemolyticus*, *S. lugdunensis*, *S. simulans*, *S. cohnii* and *S. warneri* (SEQ ID NOs. 1175-1176) were designed. The range of mismatches between the *Staphylococcus*-specific 371-bp amplicon and each of the 20-mer species-specific internal probes was from 1 to 5, in the middle of the probe when possible. No mismatches were present in the two *Staphylococcus*-specific probes for the 11 species analyzed: *S. aureus*, *S. auricularis*, *S. capitis*, *S. cohnii*, *S. epidermidis*, *S. haemolyticus*, *S. hominis*, *S. lugdunensis*, *S. saprophyticus*, *S. simulans* and *S. warneri*. In order to verify the intra-specific sequence conservation of the nucleotide sequence, sequences were obtained for the 371-bp amplicon from five unrelated ATCC and clinical strains for each of the species *S. aureus*, *S. epidermidis*, *S. haemolyticus*, *S. hominis* and *S. saprophyticus*. The Oligo™ (version 5.0) primer analysis software (National Biosciences, Plymouth, Minn.) was used to confirm the absence of self-complementary regions within and between the primers or probes. When required, the primers contained inosines or degenerated nucleotides at one or more variable positions. Oligonucleotide primers and probes were synthesized on a model 394 DNA synthesizer (Applied Biosystems, Mississauga, Ontario, Canada). Detection of the hybridization was performed with the DIG-labeled dUTP incorporated during amplification with the *Staphylococcus*-specific PCR assay, and the hybridization signal was detected with a luminometer (Dynex Technologies) as described above in the section on luminescent detection of amplification products. Annexes XIII to XVI illustrate the strategy for the selection of several internal probes.

PCR amplification. For all bacterial species, amplification was performed from purified genomic DNA or from a bacterial suspension whose turbidity was adjusted to that of a 0.5 McFarland standard, which corresponds to approximately 1.5×10^8 bacteria per ml. One nanogram of genomic DNA or 1 μ l of the standardized bacterial suspension was transferred directly to a 19 μ l PCR mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM

MgCl₂, 0.2 µM (each) of the two *Staphylococcus* genus-specific primers (SEQ ID NOs. 553 and 575), 200 µM (each) of the four deoxynucleoside triphosphates (Pharmacia Biotech), 3.3 µg/µl bovine serum albumin (BSA) (Sigma-Aldrich Canada Ltd, Oakville, Ontario, Canada), and 0.5 U *Taq* polymerase (Promega) coupled with *TaqStart*TM Antibody (Clontech). The PCR amplification was performed as follows: 3 min. at 94 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 55 °C, plus a terminal extension at 72 °C for 2 minutes. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 µg/ml of ethidium bromide. Visualization of the PCR products was made under UV at 254 nm.

For determination of the sensitivities of the PCR assays, two-fold dilutions of purified genomic DNA were used to determine the minimal number of genome copies which can be detected.

Results

Amplifications with the *Staphylococcus* genus-specific PCR assay. The specificity of the assay was assessed by performing 30-cycle and 40-cycle PCR amplifications with the panel of gram-positive (47 species from 8 genera) and gram-negative (33 species from 22 genera) bacterial species listed in Table 12. The PCR assay was able to detect efficiently 27 of 27 staphylococcal species tested in both 30-cycle and 40-cycle regimens. For 30-cycle PCR, all bacterial species tested other than staphylococci were negative. For 40-cycle PCR, *Enterococcus faecalis* and *Macrococcus caseolyticus* were slightly positive for the *Staphylococcus*-specific PCR assay. The other species tested remained negative. Ubiquity tests performed on a collection of 295 clinical isolates provided by the microbiology laboratory of the Centre Hospitalier Universitaire de Québec, Pavillon Centre Hospitalier de l'Université Laval (CHUL), including *Staphylococcus aureus* (n=34), *S. auricularis* (n=2), *S. capitis* (n=19), *S. cohnii* (n=5), *S. epidermidis* (n=18), *S. haemolyticus*

(n=21), *S. hominis* (n=73), *S. lugdunensis* (n=17), *S. saprophyticus* (n=6), *S. simulans* (n=3), *S. warneri* (n=32) and *Staphylococcus* sp. (n=65), showed a uniform amplification signal with the 30-cycle PCR assays and a perfect relation between the genotype and classical identification schemes.

The sensitivity of the *Staphylococcus*-specific assay with 30-cycle and 40-cycle PCR protocols was determined by using purified genomic DNA from the 11 staphylococcal species previously mentioned. For PCR with 30 cycles, a detection limit of 50 copies of genomic DNA was consistently obtained. In order to enhance the sensitivity of the assay, the number of cycles was increased. For 40-cycle PCR assays, the detection limit was lowered to a range of 5-10 genome copies, depending on the staphylococcal species tested.

Hybridization between the *Staphylococcus*-specific 371-bp amplicon and species-specific or genus-specific internal probes. Inter-species polymorphism was sufficient to generate species-specific internal probes for each of the principal species involved in human diseases (*S. aureus*, *S. epidermidis*, *S. haemolyticus*, *S. hominis* and *S. saprophyticus*). In order to verify the intra-species sequence conservation of the nucleotide sequence, sequence comparisons were performed on the 371-bp amplicon from five unrelated ATCC and clinical strains for each of the 5 principal staphylococcal species: *S. aureus*, *S. epidermidis*, *S. haemolyticus*, *S. hominis* and *S. saprophyticus*. Results showed a high level of conservation of nucleotide sequence between different unrelated strains from the same species. This sequence information allowed the development of staphylococcal species identification assays using species-specific internal probes hybridizing to the 371-bp amplicon. These assays are specific and ubiquitous for those five staphylococcal species. In addition to the species-specific internal probes, the genus-specific internal probes were able to recognize all or most *Staphylococcus* species tested.

EXAMPLE 8:

Differentiating between the two closely related yeast species *Candida albicans* and *Candida dubliniensis*. It is often useful for the clinician to be able to differentiate between two very closely related species of microorganisms. *Candida albicans* is the most important cause of invasive human mycose. In recent years, a very closely related species, *Candida dubliniensis*, was isolated in immunosuppressed patients. These two species are difficult to distinguish by classic biochemical methods. This example demonstrates the use of *tuf* sequences to differentiate *Candida albicans* and *Candida dubliniensis*. PCR primers SEQ ID NOs. 11-12, from previous patent publication WO98/20157, were selected for their ability to specifically amplify a *tuf* (elongation factor 1 alpha type) fragment from both species (see Annex XI for primer positions). Within this *tuf* fragment, a region differentiating *C. albicans* and *C. dubliniensis* by two nucleotides was selected and used to design two internal probes (see Annex XI for probe design, SEQ ID NOs. 577 and 578) specific for each species. Amplification of genomic DNA from *C. albicans* and *C. dubliniensis* was carried out using DIG-11-dUTP as described above in the section on chemiluminescent detection of amplification products. Internal probes SEQ ID NOs. 577 and 578 were immobilized on the bottom of individual microtiter plates and hybridization was carried out as described above in the above section on chemiluminescent detection of amplification products. Luminometer data showed that the amplicon from *C. albicans* hybridized only to probe SEQ ID NO. 577 while the amplicon from *C. dubliniensis* hybridized only to probe SEQ ID NO. 578, thereby demonstrating that each probe was species-specific.

EXAMPLE 9:

Specific identification of *Entamoeba histolytica*. Upon analysis of *tuf* (elongation factor 1 alpha) sequence data, it was possible to find four regions where

Entamoeba histolytica sequences remained conserved while other parasitical and eukaryotic species have diverged. Primers TEntG38 (SEQ ID NO. 703), TEntG442 (SEQ ID NO. 704), TEntG534 (SEQ ID NO. 705), and TEntG768 (SEQ ID NO. 706) were designed so that SEQ ID NO. 703 could be paired with the three other primers. On PTC-200 thermocyclers (MJ Research), the cycling conditions for initial sensitivity and specificity testing were 3 min. at 94 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 55 °C, followed by terminal extension at 72 °C for 2 minutes. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 µg/ml of ethidium bromide. The three primer pairs could detect the equivalent of less than 200 *E. histolytica* genome copies. Specificity was tested using 0.5 ng of purified genomic DNA from a panel of microorganisms including *Babesia bovis*, *Babesia microtti*, *Candida albicans*, *Crithidia fasciculata*, *Leishmania major*, *Leishmania hertigi* and *Neospora caninum*. Only *E. histolytica* DNA could be amplified, thereby suggesting that the assay was species-specific.

EXAMPLE 10:

Sensitive identification of *Chlamydia trachomatis*. Upon analysis of *tuf* sequence data, it was possible to find two regions where *Chlamydia trachomatis* sequences remained conserved while other species have diverged. Primers Ctr82 (SEQ ID NO. 554) and Ctr249 (SEQ ID NO. 555) were designed. With the PTC-200 thermocyclers (MJ Research), the optimal cycling conditions for maximum sensitivity and specificity were determined to be 3 min. at 94 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 60 °C, followed by terminal extension at 72 °C for 2 minutes. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 µg/ml of ethidium bromide. The assay could detect the equivalent of 8 *C. trachomatis* genome copies. Specificity was tested with 0.1 ng of purified genomic DNA from a panel of microorganisms including 22 species commonly encountered

in the vaginal flora (*Bacillus subtilis*, *Bacteroides fragilis*, *Candida albicans*, *Clostridium difficile*, *Corynebacterium cervicis*, *Corynebacterium urealyticum*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Fusobacterium nucleatum*, *Gardnerella vaginalis*, *Haemophilus influenzae*, *Klebsiella oxytoca*, *Lactobacillus acidophilus*, *Peptococcus niger*, *Peptostreptococcus prevotii*, *Porphyromonas asaccharolytica*, *Prevotella melaninogenica*, *Propionibacterium acnes*, *Staphylococcus aureus*, *Streptococcus acidominimus*, and *Streptococcus agalactiae*). Only *C. trachomatis* DNA could be amplified, thereby suggesting that the assay was species-specific.

EXAMPLE 11:

Genus-specific detection and identification of enterococci. Upon analysis of *tuf* sequence data and comparison with the repertory of *tuf* sequences, it was possible to find two regions where *Enterococcus* sequences remained conserved while other genera have diverged (Annex XVII). Primer pair Encg313dF and Encg599c (SEQ ID NOs. 1137 and 1136) was tested for its specificity by using purified genomic DNA from a panel of bacteria listed in Table 10. Using the PTC-200 thermocycler (MJ Research), the optimal cycling conditions for maximum sensitivity and specificity were determined to be 3 min. at 94 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 55 °C, followed by terminal extension at 72 °C for 2 minutes. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 µg/ml of ethidium bromide. Visualization of the PCR products was made under UV at 254 nm. The 18 enterococcal species listed in Table 10 were all amplified efficiently. The only other species amplified were *Abiotrophia adiacens*, *Gemella haemolysans* and *Gemella morbillorum*, three gram-positive species. Sensitivity tested with several strains of *E. casseliflavus*, *E. faecium*, *E. faecalis*, *E. flavescens* and *E. gallinarum* and with one strain of each other *Enterococcus* species listed in Table 10 ranged from 1 to 10 copies of genomic DNA. The sequence variation

within the 308-bp amplicon was sufficient so that internal probes could be used to speciate the amplicon and differentiate enterococci from *Abiotrophia adiacens*, *Gemella haemolysans* and *Gemella morbillorum*, thereby allowing to achieve excellent specificity. Species-specific internal probes were generated for each of the clinically important species, *E. faecalis* (SEQ ID NO. 1174), *E. faecium* (SEQ ID NO. 602), and the group including *E. casseliflavus*, *E. flavescens* and *E. gallinarum* (SEQ ID NO. 1122) (Annex XVIII). The species-specific internal probes were able to differentiate their respective *Enterococcus* species from all other *Enterococcus* species. These assays are sensitive, specific and ubiquitous for those five *Enterococcus* species.

EXAMPLE 12:

Identification of the major bacterial platelets contaminants using *tuf* sequences with a multiplex PCR test. Blood platelets preparations need to be monitored for bacterial contaminations. The *tuf* sequences of 17 important bacterial contaminants of platelets were aligned. As shown in Annex XIX, analysis of these sequences allowed the design of PCR primers. Since in the case of contamination of platelet concentrates, detecting all species (not just the more frequently encountered ones) is desirable, perfect specificity of primers was not an issue in the design. However, sensitivity is important. That is why, to avoid having to put too much degeneracy, only the most frequent contaminants were included in primer design, knowing that the selected primers would anyway be able to amplify more species than the 17 used in the design because they target highly conserved regions of *tuf* sequences. Oligonucleotide sequences which are conserved in these 17 major bacterial contaminants of platelet concentrates were chosen (oligos Tplaq 769 and Tplaq 991, respectively SEQ ID NOs. 636 and 637) thereby permitting the detection of these bacterial species. However, sensitivity was slightly deficient with staphylococci. To ensure maximal sensitivity in the detection of all the more frequent bacterial contaminants, a multiplex assay also including oligonucleotide

primers targetting the *Staphylococcus* genera (oligos Stag 422, SEQ ID NO. 553; and Stag 765, SEQ ID NO. 575) was developed. The bacterial species detected with the assay are listed in Table 14.

The primer pairs, oligos SEQ ID NO. 636 and SEQ ID NO. 637 that give an amplification product of 245 pb, and oligos SEQ ID NO. 553 and SEQ ID NO. 575 that give an amplification product of 368 pb, were used simultaneously in the multiplex PCR assay. Detection of these PCR products was made on the LightCycler thermocycler (Idaho Technology) using SYBR[®] Green I (Molecular Probe Inc.). SYBR[®] Green I is a fluorescent dye that binds specifically to double-stranded DNA.

Fluorogenic detection of PCR products with the LightCycler was carried out using 1.0 μ M of both Tplaq primers (SEQ ID NOs. 636-637) and 0.4 μ M of both TStaG primers (SEQ ID NOs. 553 and 575), 2.5 mM MgCl₂, BSA 7.5 μ M, dNTP 0.2 mM (Pharmacia), 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 0.5 U *Taq* DNA polymerase (Boehringer Mannheim) coupled with TaqStart[™] antibody (Clontech), and 0.07 ng of genomic DNA sample in a final volume of 7 μ l. The optimal cycling conditions for maximum sensitivity and specificity were 1 minute at 94 °C for initial denaturation, then forty-five cycles of three steps consisting of 0 second at 95 °C, 5 seconds at 60 °C and 9 seconds at 72 °C. Amplification was monitored during each elongation cycle by measuring the level of SYBR[®] Green I. However, real analysis takes place after PCR. Melting curves are done for each sample and transformation of the melting peak allows determination of T_m. Thus primer-dimer and specific PCR product are discriminated. With this assay, all prominent bacterial contaminants of platelet concentrates listed in Annex XIX and Table 14 were detected. Sensitivity tests were performed on the 9 most frequent bacterial contaminants of platelets. The detection limit was less than 20 genome copies for *E. cloacae*, *B. cereus*, *S. choleraesuis* and *S. marcescens*; less than 15 genome copies for *P. aeruginosa*; and 2 to 3 copies were detected for *S. aureus*, *S.*

epidermidis, *E. coli* and *K. pneumoniae*. Further refinements of assay conditions should increase sensitivity levels.

EXAMPLE 13:

The resolving power of the *tuf* and *atpD* sequences databases is comparable to the biochemical methods for bacterial identification. The present gold standard for bacterial identification is mainly based on key morphological traits and batteries of biochemical tests. Here we demonstrate that the use of *tuf* and *atpD* sequences combined with simple phylogenetic analysis of databases formed by these sequences is comparable to the gold standard. In the process of acquiring data for the *tuf* sequences, we sequenced the *tuf* gene of a strain that was given to us labelled as *Staphylococcus hominis* ATCC 35982. That *tuf* sequence (SEQ ID NO. 192) was incorporated into the *tuf* sequences database and subjected to a basic phylogenetic analysis using the Pileup command from version 10 of the GCG package (Genetics Computer Group). This analysis indicated that SEQ ID NO. 192 is not associated with other *S. hominis* strains but rather with the *S. warneri* strains. The ATCC 35982 strain was sent to the reference laboratory of the Laboratoire de santé publique du Québec (LSPQ). They used the classic identification scheme for staphylococci (Kloos and Schleifer, 1975., J. Clin. Microbiol. 1:82-88). Their results shown that although the colonial morphology could correspond to *S. hominis*, the more precise biochemical assays did not. These assays included discriminant mannitol, mannose and ribose acidification tests as well as rapid and dense growth in deep thioglycolate agar. The LSPQ report identified strain ATCC 35982 as *S. warneri* which confirms our database analysis. The same thing happened for *S. warneri* (SEQ ID NO. 187) which had initially been identified as *S. haemolyticus* by a routine clinical laboratory using a low resolving power automated system (MicroScan, AutoScan-4™). Again, the *tuf* and LSPQ analysis agreed on its identification as *S. warneri*. In numerous other instances, in the course of acquiring *tuf* and *atpD* sequence data from various species and genera,

analysis of our *tuf* and/or *atpD* sequence databases permitted the exact identification of mislabelled or erroneously identified strains. These results clearly demonstrate the usefulness and the high resolving power of our sequence-based identification assays using the *tuf* and *atpD* sequences databases.

EXAMPLE 14:

Detection of group B streptococci from clinical specimens.

Introduction

Streptococcus agalactiae, the group B streptococcus (GBS), is responsible for a severe illness affecting neonate infants. The bacterium is passed from the healthy carrier mother to the baby during delivery. To prevent this infection, it is recommended to treat expectant mothers susceptible of carrying GBS in their vaginal/anal flora. Carrier status is often a transient condition and rigorous monitoring requires cultures and classic bacterial identification weeks before delivery. To improve the detection and identification of GBS we developed a rapid, specific and sensitive PCR test fast enough to be performed right at delivery.

Materials and Methods

GBS clinical specimens. A total of 66 duplicate vaginal/anal swabs were collected from 41 consenting pregnant women admitted for delivery at the Centre Hospitalier Universitaire de Québec, Pavillon Saint-François d'Assise following the CDC recommendations. The samples were obtained either before or after rupture of membranes. The swab samples were tested at the Centre de Recherche en Infectiologie de l'Université Laval within 24 hours of collection. Upon receipt, one swab was cut and then the tip of the swab was added to GNS selective broth for identification of group B streptococci (GBS) by the standard culture methods

recommended by the CDC. The other swab was processed following the instruction of the IDI DNA extraction kit (Infectio Diagnostics (IDI) Inc.) prior to PCR amplification.

Oligonucleotides. PCR primers, Tsag340 (SEQ ID NO. 549) and Tsag552 (SEQ ID NO. 550) complementary to the regions of the *tuf* gene unique for GBS were designed based upon a multiple sequence alignment using our repertory of *tuf* sequences. Oligo primer analysis software (version 5.0) (National Biosciences) was used to analyse primers annealing temperature, secondary structure potential as well as mispriming and dimerization potential. The primers were synthesized using a model 391 DNA synthesizer (Applied Biosystems).

A pair of fluorescently labeled adjacent hybridization probes Sag465-F (SEQ ID NO. 583) and Sag436-C (SEQ ID NO. 582) were synthesized and purified by Operon Technologies. They were designed to meet the recommendations of the manufacturer (Idaho Technology) and based upon multiple sequence alignment analysis using our repertory of *tuf* sequences to be specific and ubiquitous for GBS. These adjacent probes, which are separated by one nucleotide, allow fluorescence resonance energy transfer (FRET), generating an increased fluorescence signal when both hybridized simultaneously to their target sequences. The probe SEQ ID NO. 583 was labeled with FITC in 3 prime while SEQ ID NO. 582 was labeled with Cy5 in 5 prime. The Cy5-labeled probes contained a 3'-blocking phosphate group to prevent extension of the probes during the PCR reactions.

PCR amplification. Conventional amplifications were performed either from 2 μ l of a purified genomic DNA preparation or cell lysates of vaginal/anal specimens. The 20 μ l PCR mixture contained 0.4 μ M of each GBS-specific primer (SEQ ID NOs. 549-550), 200 μ M of each deoxyribonucleotide (Pharmacia Biotech), 10 mM Tris-HCl (pH 9.0), 50 mM KCl, 0.1% Triton X-100, 2.5 mM MgCl₂, 3.3 mg/ml bovine serum albumin (BSA) (Sigma), and 0.5 U of *Taq* polymerase (Promega) combined with the TaqStartTM antibody (Clontech). The TaqStartTM antibody, which is a neutralizing monoclonal antibody of *Taq* DNA

polymerase, was added to all PCR reactions to enhance the efficiency of the amplification. The PCR mixtures were subjected to thermal cycling (3 min at 95 °C and then 40 cycles of 1 s at 95 °C, and 30 s at 62 °C with a 2-min final extension at 72 °C) with a PTC-200 DNA Engine thermocycler (MJ research). The PCR-amplified reaction mixture was resolved by agarose gel electrophoresis.

The LightCyclerTM PCR amplifications were performed with 1 µl of a purified genomic DNA preparation or cell lysates of vaginal/anal specimens. The 10µl amplification mixture consisted of 0.4 µM each GBS-specific primer (SEQ ID NOs. 549-550), 200 µM each dNTP, 0.2 µM each fluorescently labeled probe (SEQ ID NOs. 582-583), 300 µg/ml BSA (Sigma), and 1 µl of 10x PC2 buffer (containing 50 mM Tris-HCl (pH 9.1), 16 mM ammonium sulfate, 3.5 mM Mg²⁺, and 150 µg/ml BSA) and 0.5 U KlenTaq1TM (AB Peptides) coupled with TaqStartTM antibody (Clontech). KlenTaq1TM is a highly active and more heat-stable DNA polymerase without 5'-exonuclease activity. This prevents hydrolysis of hybridized probes by the 5' to 3' exonuclease activity. A volume of 7 µl of the PCR mixture was transferred into a composite capillary tube (Idaho Technology). The tubes were then centrifuged to move the reaction mixture to the tips of the capillaries and then cleaned with optical-grade methanol. Subsequently the capillaries were loaded into the carousel of a LC32 LightCyclerTM (Idaho Technology), an instrument that combines rapid-cycle PCR with fluorescence analysis for continuous monitoring during amplification. The PCR reaction mixtures were subjected to a denaturation step at 94 °C for 3 min followed by 45 cycles of 0 s at 94 °C, 20 s at 64 °C and 10 s at 72 °C with a temperature transition rate of 20 °C/s. Fluorescence signals were obtained at each cycle by sequentially positioning each capillary on the carousel at the focus of optical elements affiliated to the built-in fluorimeter for 100 milliseconds. Complete amplification and analysis required about 35 min.

Specificity and sensitivity tests. The specificity of the conventional and LightCyclerTM PCR assays was verified by using purified genomic DNA (0.1 ng/reaction) from a battery of ATCC reference strains representing 35 clinically

relevant gram-positive species (*Abiotrophia defectiva* ATCC 49176, *Bifidobacterium breve* ATCC 15700, *Clostridium difficile* ATCC 9689, *Corynebacterium urealyticum* ATCC 43042, *Enterococcus casseliflavus* ATCC 25788, *Enterococcus durans* ATCC 19432, *Enterococcus faecalis* ATCC 29212, *Enterococcus faecium* ATCC 19434, *Enterococcus gallinarum* ATCC 49573, *Enterococcus raffinosus* ATCC 49427, *Lactobacillus reuteri* ATCC 23273, *Lactococcus lactis* ATCC 19435, *Listeria monocytogenes* ATCC 15313, *Peptococcus niger* ATCC 27731, *Peptostreptococcus anaerobius* ATCC 27337, *Peptostreptococcus prevotii* ATCC 9321, *Staphylococcus aureus* ATCC 25923, *Staphylococcus epidermidis* ATCC 14990, *Staphylococcus haemolyticus* ATCC 29970, *Staphylococcus saprophyticus* ATCC 15305, *Streptococcus agalactiae* ATCC 27591, *Streptococcus anginosus* ATCC 33397, *Streptococcus bovis* ATCC 33317, *Streptococcus constellatus* ATCC 27823, *Streptococcus dysgalactiae* ATCC 43078, *Streptococcus gordonii* ATCC 10558, *Streptococcus mitis* ATCC 33399, *Streptococcus mutans* ATCC 25175, *Streptococcus oralis* ATCC 35037, *Streptococcus parauberis* ATCC 6631, *Streptococcus pneumoniae* ATCC 6303, *Streptococcus pyogenes* ATCC 19615, *Streptococcus salivarius* ATCC 7073, *Streptococcus sanguinis* ATCC 10556, *Streptococcus uberis* ATCC 19436). These microbial species included 15 species of streptococci and many members of the normal vaginal and anal floras. In addition, 40 GBS isolates of human origin, whose identification was confirmed by a latex agglutination test (Streptex, Murex), were also used to evaluate the ubiquity of the assay.

For determination of the sensitivities (i.e., the minimal number of genome copies that could be detected) for conventional and LightCyclerTM PCR assays, serial 10-fold or 2-fold dilutions of purified genomic DNA from 5 GBS ATCC strains were used.

Results

Evaluation of the GBS-specific conventional and LightCyclerTM PCR assays. The specificity of the two assays demonstrated that only DNAs from GBS

strains could be amplified. Both PCR assays did not amplify DNAs from any other bacterial species tested including 14 streptococcal species other than GBS as well as phylogenetically related species belonging to the genera *Enterococcus*, *Peptostreptococcus* and *Lactococcus*. Important members of the vaginal or anal flora, including coagulase-negative staphylococci, *Lactobacillus* sp., and *Bacteriodes* sp. were also negative with the GBS-specific PCR assay. The LightCyclerTM PCR assays detected only GBS DNA by producing an increased fluorescence signal which was interpreted as a positive PCR result. Both PCR methods were able to amplify all of 40 GBS clinical isolates, showing a perfect correlation with the phenotypic identification methods.

The sensitivity of the assay was determined by using purified genomic DNA from the 5 ATCC strains of GBS. The detection limit for all of these 5 strains was one genome copy of GBS. The detection limit of the assay with the LightCyclerTM was 3.5 fg of genomic DNA (corresponding to 1-2 genome copies of GBS). These results confirmed the high sensitivity of our GBS-specific PCR assay.

Direct Detection of GBS from vaginal/anal specimens. Among 66 vaginal/anal specimens tested, 11 were positive for GBS by both culture and PCR. There was one sample positive by culture only. The sensitivity of both PCR methods with vaginal/anal specimens for identifying colonization status in pregnant women at delivery was 91.7% when compared to culture results. The specificity and positive predictive values were both 100% and the negative predictive value was 97.8%. The time for obtaining results was approximately 45 min for LightCyclerTM PCR, approximately 100 min for conventional PCR and 48 hours for culture.

Conclusion

We have developed two PCR assays (conventional and LightCyclerTM) for the detection of GBS, which are specific (i.e., no amplification of DNA from a variety of bacterial species other than GBS) and sensitive (i.e., able to detect around 1

genome copy for several reference ATCC strains of GBS). Both PCR assays are able to detect GBS directly from vaginal/anal specimens in a very short turnaround time. Using the real-time PCR assay on LightCycler™, we can detect GBS carriage in pregnant women at delivery within 45 minutes.

EXAMPLE 15:

Simultaneous detection and identification of *Streptococcus pyogenes* and its pyrogenic exotoxin A. The rapid detection of *Streptococcus pyogenes* and of its pyrogenic exotoxin A is of clinical importance. We developed a multiplex assay which permits the detection of strains of *S. pyogenes* carrying the pyrogenic toxin A gene, which is associated with scarlet fever and other pathologies. In order to specifically detect *S. pyogenes*, nucleotide sequences of the pyrrolidone carboxyl peptide (pcp) gene were aligned to design PCR primers Spy291 (SEQ ID NO. 1211) and Spy473 (SEQ ID NO. 1210). Next, we designed primers for the specific detection of the pyrogenic exotoxin A. Nucleotide sequences of the *speA* gene, carried on the bacteriophage T12, were aligned as shown in Annex XXIII to design PCR primers Spytx814 (SEQ ID NO. 994) and Spytx 927 (SEQ ID NO. 995).

The primer pairs: oligos SEQ ID NOs. 1210-1211, yielding an amplification product of 207 bp, and oligos SEQ ID NOs. 994-995, yielding an amplification product of 135 bp, were used in a multiplex PCR assay.

PCR amplification was carried out using 0.4 μ M of both pairs of primers, 2.5 mM MgCl₂, BSA 0.05 μ M, dNTP 0.2 μ M (Pharmacia), 10mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl₂, 0.5 U *Taq* DNA polymerase (Promega) coupled with TaqStart™ antibody (Clontech Laboratories Inc.), and 1 μ l of genomic DNA sample in a final volume of 20 μ l. PCR amplification was performed using a PTC-200 thermal cycler (MJ Research). The optimal cycling conditions for maximum specificity and sensitivity were 3 minutes at 94 °C for

initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 63 °C, followed by a final step of 2 minutes at 72 °C. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 µg/ml of ethidium bromide. Visualization of the PCR products was made under UV at 254 nm.

The detection limit was less than 5 genome copies for both *S. pyogenes* and its pyrogenic exotoxin A. The assay was specific for pyrogenic exotoxin A-producing *S. pyogenes*: strains of the 27 other species of *Streptococcus* tested, as well as 20 strains of various gram-positive and gram-negative bacterial species were all negative.

A similar approach was used to design an alternative set of *speA*-specific primers (SEQ ID NOs. 996 to 998, see Annex XXIV). In addition, another set of primers based on the *tuf* gene (SEQ ID NOs. 999 to 1001, see Annex XXV) could be used to specifically detect *Streptococcus pyogenes*.

EXAMPLE 16:

Real-time detection and identification of Shiga toxin-producing bacteria. Shiga toxin-producing *Escherichia coli* and *Shigella dysenteriae* cause bloody diarrhea. Currently, identification relies mainly on the phenotypic identification of *S. dysenteriae* and *E. coli* serotype O157:H7. However, other serotypes of *E. coli* are increasingly found to be producers of type 1 and/or type 2 Shiga toxins. Two pairs of PCR primers targeting highly conserved regions present in each of the Shiga toxin genes *stx*₁ and *stx*₂ were designed to amplify all variants of those genes (see Annexes XXVI and XXVII). The first primer pair, oligonucleotides 1SLT224 (SEQ ID NO. 1081) and 1SLT385 (SEQ ID NO. 1080), yields an amplification product of 186 bp from the *stx*₁ gene. For this amplicon, the 1SLTB1-Fam (SEQ ID NO. 1084) molecular beacon was designed for the specific detection of *stx*₁.

using the fluorescent label 6-carboxy-fluorescein. The 1SltS1-FAM (SEQ ID NO. 2012) molecular scorpion was also designed as an alternate way for the specific detection of *stx*₁. A second pair of PCR primers, oligonucleotides 2SLT537 (SEQ ID NO. 1078) and 2SLT678b (SEQ ID NO. 1079), yields an amplification product of 160 bp from the *stx*₂ gene. Molecular beacon 2SLTB1-Tet (SEQ ID NO. 1085) was designed for the specific detection of *stx*₂ using the fluorescent label 5-tetrachloro-fluorescein. Both primer pairs were combined in a multiplex PCR assay.

PCR amplification was carried out using 0.8 μ M of primer pair SEQ ID NOs. 1080-1081, 0.5 μ M of primer pair SEQ ID NOs. 1078-1079, 0.3 μ M of each molecular beacon, 8 mM MgCl₂, 490 μ g/mL BSA, 0.2 mM dNTPs (Pharmacia), 50 mM Tris-HCl, 16 mM NH₄SO₄, 1X TaqMaster (Eppendorf), 2.5 U KlenTaq1 DNA polymerase (AB Peptides) coupled with TaqStartTM antibody (Clontech Laboratories Inc.), and 1 μ l of genomic DNA sample in a final volume of 25 μ l. PCR amplification was performed using a SmartCycler thermal cycler (Cepheid). The optimal cycling conditions for maximum sensitivity and specificity were 60 seconds at 95 °C for initial denaturation, then 45 cycles of three steps consisting of 10 seconds at 95 °C, 15 seconds at 56 °C and 5 seconds at 72 °C. Detection of the PCR products was made in real-time by measuring the fluorescent signal emitted by the molecular beacon when it hybridizes to its target at the end of the annealing step at 56 °C.

The detection limit was the equivalent of less than 5 genome copies. The assay was specific for the detection of both toxins, as demonstrated by the perfect correlation between PCR results and the phenotypic characterization performed using antibodies specific for each Shiga toxin type. The assay was successfully performed on several Shiga toxin-producing strains isolated from various geographic areas of the world, including 10 O157:H7 *E. coli*, 5 non-O157:H7 *E. coli* and 4 *S. dysenteriae*.

EXAMPLE 17:

Development of a PCR assay for the detection and identification of staphylococci at genus and species levels and its associated *mecA* gene. The *Staphylococcus*-specific PCR primers described in Example 7 (SEQ ID NOs. 553 and 575) were used in multiplex with the *mecA*-specific PCR primers and the *S. aureus*-specific primers described in our assigned US patent no. 5,994,066 (SEQ ID NOs. 261 and 262 for *mecA* and SEQ ID NOs. 152 and 153 for *S.aureus* in the said patent). Sequence alignment analysis of 10 publicly available *mecA* gene sequences allowed to design an internal probe specific to *mecA* (SEQ ID NO. 1177). An internal probe was also designed for the *S. aureus*-specific amplicon (SEQ ID NO 1234). PCR amplification and agarose gel electrophoresis of the amplified products were performed as described in Example 7, with the exception that 0.4 μ M (each) of the two *Staphylococcus*-specific primers (SEQ ID NOs. 553 and 575) and 0.4 μ M (each) of the *mecA*-specific primers and 0.4 μ M (each) of the *S. aureus*-specific primers were used in the PCR mixture. The specificity of the multiplex assay with 40-cycle PCR protocols was verified by using purified genomic DNA from five methicillin-resistant and fifteen methicillin-sensitive staphylococcal strains. The sensitivity of the multiplex assay with 40-cycle PCR protocols was determined by using purified genomic DNA from twenty-three - methicillin-resistant and twenty-eight methicillin-sensitive staphylococcal strains. The detection limit was 2 to 10 genome copies of genomic DNA, depending on the staphylococcal species tested. Furthermore, the *mecA*-specific internal probe, the *S. aureus*-specific internal probe and the coagulase-negative staphylococci-specific internal probe (described in Example 7) were able to recognize twenty-three methicillin-resistant staphylococcal strains and twenty-eight methicillin-sensitive staphylococcal strains with high sensitivity and specificity.

The format of the assay is not limited to the one described above. A person skilled in the art could adapt the assay for different formats such as PCR with real-time detection using molecular beacon probes. Molecular beacon probes designed to be used in this assay include, but are not limited to, SEQ ID NO. 1232 for detection of the *S. aureus*-specific amplicon, SEQ ID NO. 1233 for detection of coagulase-negative staphylococci and SEQ ID NO. 1231 for detection of *mecA*.

Alternatively, a multiplex PCR assay containing the *Staphylococcus*-specific PCR primers described in Example 7 (SEQ ID NOs. 553 and 575) and the *mecA*-specific PCR primers described in our assigned US patent no. 5,994,066 (SEQ ID NOs. 261 and 262 in the said patent) were developed. PCR amplification and agarose gel electrophoresis of the amplified products were performed as described in Example 7, with the exception that 0.4 μ M (each) of the *Staphylococcus*-specific primers (SEQ ID NOs. 553 and 575) and 0.4 μ M (each) of the *mecA*-specific primers described in our assigned US patent no. 5,994,066 (SEQ ID NOs. 261 and 262 in the said patent) were used in the PCR mixture. The sensitivity of the multiplex assay with 40-cycle PCR protocols was determined by using purified genomic DNA from two methicillin-resistant and five methicillin-sensitive staphylococcal strains. The detection limit was 2 to 5 copies of genomic DNA, depending on the staphylococcal species tested. The specificity of the multiplex PCR assay coupled with capture-probe hybridization was tested with two strains of methicillin-resistant *S. aureus*, two strains of methicillin-sensitive *S. aureus* and seven strains of methicillin-sensitive coagulase-negative staphylococci. The *mecA*-specific internal probe (SEQ ID NO. 1177) and the *S. aureus*-specific internal probe (SEQ ID NO. 587) described in Example 7 were able to recognize all the strains with high specificity showing a perfect correlation with susceptibility to methicillin. The sensitivity of the PCR assay coupled with capture-probe hybridization was tested with one strain of methicillin-resistant *S. aureus*. The detection limit was around 10 copies of genomic DNA.

EXAMPLE 18:Sequencing of *pbp1a*, *pbp2b* and *pbp2x* genes of *Streptococcus pneumoniae*.

Penicillin resistance in *Streptococcus pneumoniae* involves the sequential alteration of up to five penicillin-binding proteins (PBPs) 1A, 1B, 2A, 2X and 2B in such a way that their affinity is greatly reduced toward the antibiotic molecule. The altered PBP genes have arisen as the result of interspecies recombination events from related streptococcal species. Among the PBPs usually found in *S. pneumoniae*, PBPs 1A, 2B, and 2X play the most important role in the development of penicillin resistance. Alterations in PBP 2B and 2X mediate low-level resistance to penicillin while additional alterations in PBP 1A play a significant role in full penicillin resistance.

In order to generate a database for *pbp* sequences that can be used for design of primers and/or probes for the specific and ubiquitous detection of β -lactam resistance in *S. pneumoniae*, *pbp1a*, *pbp2b* and *pbp2x* DNA fragments sequenced by us or selected from public databases (GenBank and EMBL) from a variety of *S. pneumoniae* strains were used to design oligonucleotide primers. This database is essential for the design of specific and ubiquitous primers and/or probes for detection of β -lactam resistance in *S. pneumoniae* since the altered PBP 1A, PBP 2B and PBP 2X of β -lactam resistant *S. pneumoniae* are encoded by mosaic genes with numerous sequence variations among resistant isolates. The PCR primers were located in conserved regions of *pbp* genes and were able to amplify *pbp1a*, *pbp2b*, and *pbp2x* sequences of several strains of *S. pneumoniae* having various levels of resistance to penicillin and third-generation cephalosporins. Using primer pairs SEQ ID NOs. 1125 and 1126, SEQ ID NOs. 1142 and 1143, SEQ ID NOs. 1146 and 1147, it was possible to amplify and determine *pbp1a* sequences SEQ ID NOs. 1004-1018, 1648, 2056-2060 and 2062-2064, *pbp2b* sequences SEQ ID NOs. 1019-1033, and *pbp2x* sequences SEQ ID NOs. 1034-1048. Six other PCR primers

(SEQ ID NOs. 1127-1128, 1144-1145, 1148-1149) were also designed and used to complete the sequencing of *pbp1a*, *pbp2b* and *pbp2x* amplification products. The described primers (SEQ ID NOs. 1125 and 1126, SEQ ID NOs. 1142 and 1143, SEQ ID NOs. 1146 and 1147, SEQ ID NOs. 1127-1128, 1144-1145, 1148-1149) represent a powerful tool for generating new *pbp* sequences for design of primers and/or probes for detection of β -lactam resistance in *S. pneumoniae*.

EXAMPLE 19:

Sequencing of *hexA* genes of *Streptococcus* species. The *hexA* sequence of *S. pneumoniae* described in our assigned US patent no. 5,994,066 (SEQ ID NO. 31 in the said patent, SEQ ID NO. 1183 in the present application) allowed the design of a PCR primer (SEQ ID NO. 1182) which was used with primer Spn1401 described in our assigned US patent no. 5,994,066 (SEQ ID NO. 156 in the said patent, SEQ ID NO. 1179 in the present application) to generate a database for *hexA* sequences that can be used to design primers and/or probes for the specific identification and detection of *S. pneumoniae* (Annex XLII). Using primers SEQ ID NO. 1179 and SEQ ID NO. 1182 (Annex XLII), it was possible to amplify and determine the *hexA* sequence from *S. pneumoniae* (4 strains) (SEQ ID NOs. 1184-1187), *S. mitis* (three strains) (SEQ ID NOs. 1189-1191) and *S. oralis* (SEQ ID NO. 1188).

EXAMPLE 20:

Development of multiplex PCR assays coupled with capture probe hybridization for the detection and identification of *Streptococcus pneumoniae* and its penicillin resistance genes.

Two different assays were developed to identify *S. pneumoniae* and its susceptibility to penicillin.

ASSAY I:

Bacterial strains. The specificity of the multiplex PCR assay was verified by using a panel of ATCC (American Type Culture Collection) reference strains consisting of 33 gram-negative and 67 gram-positive bacterial species (Table 13). In addition, a total of 98 strains of *S. pneumoniae*, 16 strains of *S. mitis* and 3 strains of *S. oralis* from the American Type Culture Collection, the microbiology laboratory of the Centre Hospitalier Universitaire de Québec, Pavillon Centre Hospitalier de l'Université Laval (CHUL), (Ste-Foy, Québec, Canada), the Laboratoire de santé publique du Québec, (Sainte-Anne-de-Bellevue, Québec, Canada), the Sunnybrook and Women's College Health Sciences Centre (Toronto, Canada), the Infectious Diseases Section, Department of Veterans Affairs Medical Center, (Houston, USA) were also tested to further validate the *Streptococcus pneumoniae*-specific PCR assay. The penicillin MICs (minimal inhibitory concentrations) were measured by the broth dilution method according to the recommended protocol of NCCLS.

PCR primers and internal probes. The analysis of *hexA* sequences from a variety of streptococcal species from the publicly available *hexA* sequence and from the database described in Example 19 (SEQ ID NOs. 1184-1191) allowed the selection of a PCR primer specific to *S. pneumoniae*, SEQ ID NO. 1181. This primer was used with the *S. pneumoniae*-specific primer SEQ ID NO. 1179 to generate an amplification product of 241 bp (Annex XLII). The PCR primer SEQ ID NO. 1181 is located 127 nucleotides downstream on the *hexA* sequence compared to the original *S. pneumoniae*-specific PCR primer Spn1515 described in our assigned US patent no. 5,994,066 (SEQ ID NO. 157 in the said patent). These modifications were done to ensure the design of the *S. pneumoniae*-specific internal probe according to the new *hexA* sequences of several streptococcal species from the database described in Example 19 (SEQ ID NOs. 1184-1191).

The analysis of *pbp1a* sequences from *S. pneumoniae* strains with various levels of penicillin resistance from public databases and from the database described in Example 18 allowed the identification of amino acid substitutions Ile-459 to Met and Ser-462 to Ala that occur in isolates with high-level penicillin resistance (MICs $\geq 1\mu\text{g/ml}$), and amino acid substitutions Ser-575 to Thr, Gln-576 to Gly and Phe-577 to Tyr that are common to all penicillin-resistant isolates with MICs $\geq 0.25\mu\text{g/ml}$. As shown in Annex XXXI, PCR primer pair SEQ ID NOs. 1130 and 1131 were designed to detect high-level penicillin resistance (MICs $\geq 1\mu\text{g/ml}$), whereas PCR primer pair SEQ ID NOs. 1129 and 1131 were designed to detect intermediate- and high-level penicillin resistance (MICs $\geq 0.25\mu\text{g/ml}$).

The analysis of *hexA* sequences from the publicly available *hexA* sequence and from the database described in Example 19 allowed the design of an internal probe specific to *S. pneumoniae* (SEQ ID NO. 1180) (Annex XLII). The range of mismatches between the *S. pneumoniae*-specific 241-bp amplicon was from 2 to 5, in the middle of the 19-bp probe. The analysis of *pbp1a* sequences from public databases and from the database described in Example 18 allowed the design of five internal probes containing all possible mutations to detect the high-level penicillin resistance 383-bp amplicon (SEQ ID NOs. 1197, 1217-1220). Alternatively, two other internal probes (SEQ ID NOs. 2024-2025) can also be used to detect the high-level penicillin resistance 383-bp amplicon. Five internal probes containing all possible mutations to detect the 157-bp amplicon which includes intermediate- and high-level penicillin resistance were also designed (SEQ ID NOs. 1094, 1192-1193, 1214 and 1216). Design and synthesis of primers and probes, and detection of the probe hybridization were performed as described in Example 7. Annex XXXI illustrates one of the internal probe for detection of the high-level penicillin resistance 383-bp amplicon (SEQ ID NO. 1197) and one of the internal probe for detection of the intermediate- and high-level penicillin resistance 157-bp amplicon (SEQ ID NO. 1193).

PCR amplification. For all bacterial species, amplification was performed from purified genomic DNA using a PTC-200 thermocycler (MJ Research). 1 μ l of genomic DNA at 0.1 ng/ μ l, or 1 μ l of a bacterial lysate, was transferred to a 19 μ l PCR mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (H 9.0), 0.1% Triton X-100, 2.5 mM MgCl₂, 0.1 μ M (each) of the *S. pneumoniae*-specific primers SEQ ID NO. 1179 and SEQ ID NO. 1181, 0.2 μ M of primer SEQ ID NO. 1129, 0.7 μ M of primer SEQ ID NO. 1131, and 0.6 μ M of primer SEQ ID NO. 1130, 0.05 mM bovine serum albumin (BSA), and 0.5 U *Taq* polymerase (Promega) coupled with TaqStartTM antibody. In order to generate Digoxigenin (DIG)-labeled amplicons for capture probe hybridization, 0.1X PCR DIG labeling four deoxynucleoside triphosphates mix (Boehringer Mannheim GmbH) was used for amplification.

For determination of the sensitivity of the PCR assays, 10-fold dilutions of purified genomic DNA were used to determine the minimal number of genome copies which can be detected.

Capture probe hybridization. The DIG-labeled amplicons were hybridized to the capture probes bound to 96-well plates. The plates were incubated with anti-DIG-alkaline phosphatase and the chemiluminescence was measured by using a luminometer (MLX, Dynex Technologies Inc.) after incubation with CSPD and recorded as Relative Light Unit (RLU). The RLU ratio of tested sample with and without captures probes was then calculated. A ratio ≥ 2.0 was defined as a positive hybridization signal. All reactions were performed in duplicate.

Results

Amplifications with the multiplex PCR assay. The specificity of the assay was assessed by performing 40-cycle PCR amplifications with the panel of gram-positive (67 species from 12 genera) and gram-negative (33 species from 17

genera) bacterial species listed in Table 13. All bacterial species tested other than *S. pneumoniae* were negative except *S. mitis* and *S. oralis*. Ubiquity tests were performed using a collection of 98 *S. pneumoniae* strains including high-level penicillin resistance (n=53), intermediate resistance (n=12) and sensitive (n=33) strains. There was a perfect correlation between PCR and standard susceptibility testing for 33 penicillin-sensitive isolates. Among 12 *S. pneumoniae* isolates with intermediate penicillin resistance based on susceptibility testing, 11 had intermediate resistance based on PCR, but one *S. pneumoniae* isolate with penicillin MIC of 0.25 µg/ml showed a high-level penicillin resistance based on genotyping. Among 53 isolates with high-level penicillin resistance based on susceptibility testing, 51 had high-level penicillin resistance based on PCR but two isolates with penicillin MIC > 1 µg/ml showed an intermediate penicillin resistance based on genotyping. In general, there was a good correlation between the genotype and classical culture method for bacterial identification and susceptibility testing.

The sensitivity of the *S. pneumoniae*-specific assay with 40-cycle PCR protocols was determined by using purified genomic DNA from 9 isolates of *S. pneumoniae*. The detection limit was around 10 copies of genomic DNA for all of them.

Post-PCR hybridization with internal probes. The specificity of the multiplex PCR assay coupled with capture-probe hybridization was tested with 98 strains of *S. pneumoniae*, 16 strains of *S. mitis* and 3 strains of *S. oralis*. The internal probe specific to *S. pneumoniae* (SEQ ID NO. 1180) detected all 98 *S. pneumoniae* strains but did not hybridize to the *S. mitis* and *S. oralis* amplicons. The five internal probes specific to the high-level resistance amplicon (SEQ ID NOs. 1197, 1217-1220) detected all amplification patterns corresponding to high-level resistance. The two *S. pneumoniae* strains with penicillin MIC > 1 µg/ml that showed an intermediate penicillin resistance based on PCR amplification were also intermediate resistance based on probe hybridization. Similarly, among 12 strains

with intermediate-penicillin resistance based on susceptibility testing, 11 showed intermediate-penicillin resistance based on hybridization with the five internal probes specific to the intermediate and high-level resistance amplicon (SEQ ID NOs. 1094, 1192-1193, 1214 and 1216). The strain described above having a penicillin MIC of 0.25 µg/ml which was high-level penicillin resistance based on PCR amplification was also high-level resistance based on probe hybridization. In summary, the combination of the multiplex PCR and hybridization assays results in a highly specific test for the detection of penicillin-resistant *Streptococcus pneumoniae*.

ASSAY II:

Bacterial strains. The specificity of the multiplex PCR assay was verified by using the same strains as those used for the development of Assay I. The penicillin MICs (minimal inhibitory concentrations) were measured by the broth dilution method according to the recommended protocol of NCCLS.

PCR primers and internal probes. The analysis of *pbpla* sequences from *S. pneumoniae* strains with various levels of penicillin resistance from public databases and from the database described in Example 18 allowed the design of two primers located in the constant region of *pbpla*. PCR primer pair (SEQ ID NOs. 2015 and 2016) was designed to amplify a 888-bp variable region of *pbpla* from all *S. pneumoniae* strains. A series of internal probes were designed for identification of the *pbpla* mutations associated with penicillin resistance in *S. pneumoniae*. For detection of high-level penicillin resistance (MICs $\geq 1\mu\text{g/ml}$), three internal probes were designed (SEQ ID NOs. 2017-2019). Alternatively, ten other internal probes were designed that can also be used for detection of high-level resistance within the 888-bp *pbpla* amplicon: (1) three internal probes for identification of the amino acid substitutions Thr-371 to Ser or Ala within the motif S370TMK (SEQ ID NOs. 2031-2033); (2) two internal probes for detection

of the amino acid substitutions Ile-459 to Met and Ser-462 to Ala near the motif S428RN (SEQ ID NOs. 1135 and 2026); (3) two internal probes for identification of the amino acid substitutions Asn-443 to Asp (SEQ ID NOs. 1134 and 2027); and (4) three internal probes for detection of all sequence variations within another region (SEQ ID NOs. 2028-2030). For detection of high-level and intermediate penicillin resistance (MICs ≥ 0.25 $\mu\text{g/ml}$), four internal probes were designed (SEQ ID NOs. 2020-2023). Alternatively, six other internal probes were designed for detection of the four consecutive amino acid substitutions T574SQF to A574TGY near the motif K557TG (SEQ ID NOs. 2034-2039) that can also be used for detection of intermediate- and high-level resistance within the 888-bp *pbp1a* amplicon.

PCR amplification. For all bacterial species, amplification was performed from purified genomic DNA using a PTC-200 thermocycler (MJ Research). 1 μl of genomic DNA at 0.1 ng/ μl , or 1 μl of a bacterial lysate, was transferred to a 19 μl PCR mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl_2 , 0.08 μM (each) of the *S. pneumoniae*-specific primers SEQ ID NO. 1179 and SEQ ID NO. 1181, 0.4 μM of the *pbp1a*-specific primer SEQ ID NO. 2015, 1.2 μM of *pbp1a*-specific primer SEQ ID NO. 2016, 0.05 mM bovine serum albumin (BSA), and 0.5 U *Taq* polymerase (Promega) coupled with TaqStartTM antibody. In order to generate Digoxigenin (DIG)-labeled amplicons for capture probe hybridization, 0.1X PCR DIG labeling four deoxynucleoside triphosphates mix (Boehringer Mannheim GmbH) was used for amplification.

For determination of the sensitivities of the PCR assays, 10-fold dilutions of purified genomic DNA were used to determine the minimal number of genome copies which can be detected.

Capture probe hybridization. The DIG-labeled amplicons were hybridized to the capture probes bound to 96-well plates as described for Assay I.

Results

Amplifications with the multiplex PCR assay. The specificity of the assay was assessed by performing 40-cycle PCR amplifications with the panel of gram-positive (67 species from 12 genera) and gram-negative (33 species from 17 genera) bacterial species listed in Table 13. All bacterial species tested other than *S. pneumoniae* were negative except *S. mitis* and *S. oralis*. Ubiquity tests were performed using a collection of 98 *S. pneumoniae* strains including high-level penicillin resistance (n=53), intermediate resistance (n=12) and sensitive (n=33) strains. All the above *S. pneumoniae* strains produced the 888-bp amplicon corresponding to *pbp1a* and the 241-bp fragment corresponding to *hexA*.

The sensitivity of the *S. pneumoniae*-specific assay with 40-cycle PCR protocols was determined by using purified genomic DNA from 9 isolates of *S. pneumoniae*. The detection limit was around 10 copies of genomic DNA for all of them.

Post-PCR hybridization with internal probes. The specificity of the multiplex PCR assay coupled with capture-probe hybridization was tested with 98 strains of *S. pneumoniae*, 16 strains of *S. mitis* and 3 strains of *S. oralis*. The internal probe specific to *S. pneumoniae* (SEQ ID NO. 1180) detected all 98 *S. pneumoniae* strains but did not hybridize to the *S. mitis* and *S. oralis* amplicons. The three internal probes (SEQ ID NOs 2017-2019) specific to high-level resistance detected all the 43 strains with high-level penicillin resistance based on susceptibility testing. Among 12 isolates with intermediate-penicillin resistance based on susceptibility testing, 11 showed intermediate-penicillin resistance based on hybridization with 4 internal probes (SEQ ID NOs. 2020-2023) and one strain

having penicillin MIC of 0.25 µg/ml was misclassified as high-level penicillin resistance. In summary, the combination of the multiplex PCR and hybridization assays results in a highly specific test for the detection of penicillin-resistant *Streptococcus pneumoniae*.

EXAMPLE 21:

Sequencing of the vancomycin resistance *vanA*, *vanC1*, *vanC2* and *vanC3* genes.

The publicly available sequences of the *vanH-vanA-vanX-vanY* locus of transposon Tn1546 from *E. faecalis*, *vanC1* sequence from one strain of *E. gallinarum*, *vanC2* and *vanC3* sequences from a variety of *E. casseliflavus* and *E. flavescens* strains, respectively, allowed the design of PCR primers able to amplify the *vanA*, *vanC1*, *vanC2* and *vanC3* sequences of several *Enterococcus* species. Using primer pairs van6877 and van9106 (SEQ ID NOs. 1150 and 1155), vanC1-122 and vanC1-1315 (SEQ ID NOs. 1110 and 1109), and vanC2C3-1 and vanC2C3-1064 (SEQ ID NOs. 1108 and 1107), it was possible to amplify and determine *vanA* sequences SEQ ID NOs. 1049-1057, *vanC1* sequences SEQ ID NOs. 1058-1059, *vanC2* sequences SEQ ID NOs. 1060-1063 and *vanC3* sequences SEQ ID NOs. 1064-1066, respectively. Four other PCR primers (SEQ ID NOs. 1151-1154) were also designed and used to complete the sequencing of *vanA* amplification products.

EXAMPLE 22:

Development of a PCR assay for the detection and identification of enterococci at genus and species levels and its associated resistance genes *vanA* and *vanB*.

The comparison of *vanA* and *vanB* sequences revealed conserved regions allowing the design of PCR primers specific to both *vanA* and *vanB* sequences (Annex XXXVIII). The PCR primer pair vanAB459 and vanAB830R (SEQ ID NOs. 1112 and 1111) was used in multiplex with the *Enterococcus*-specific primers Encg313dF and Encg599c (SEQ ID NOs. 1137 and 1136) described in Example

11. Sequence alignment analysis of *vanA* and *vanB* sequences revealed regions suitable for the design of internal probes specific to *vanA* (SEQ ID NO. 1170) and *vanB* (SEQ ID NO. 1171). PCR amplification and agarose gel electrophoresis of the amplified products were performed as described in Example 11. The optimal cycling conditions for maximum sensitivity and specificity were found to be 3 min. at 94 °C, followed by forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 62°C, plus a terminal extension at 72 °C for 2 minutes. The specificity of the multiplex assay with 40-cycle PCR was verified by using 0.1 nanogram of purified genomic DNA from a panel of bacteria listed in Table 10. The sensitivity of the multiplex assay with 40-cycle PCR was verified with three strains of *E. casseliflavus*, eight strains of *E. gallinarum*, two strains of *E. flavescens*, two vancomycin-resistant strains of *E. faecalis* and one vancomycin-sensitive strain of *E. faecalis*, three vancomycin-resistant strains of *E. faecium*, one vancomycin-sensitive strain of *E. faecium* and one strain of each of the other enterococcal species listed in Table 10. The detection limit was 1 to 10 copies of genomic DNA, depending on the enterococcal species tested. The *vanA*- and *vanB*-specific internal probes (SEQ ID NOs. 1170 and 1171), as well as the *E. faecalis*- and *E. faecium*-specific internal probes (SEQ ID NOs. 1174 and 602) and the internal probe specific to the group including *E. casseliflavus*, *E. gallinarum* and *E. flavescens* (SEQ ID NO. 1122) described in Example 11, were able to recognize vancomycin-resistant enterococcal species with high sensitivity, specificity and ubiquity showing a perfect correlation between the genotypic and phenotypic analysis.

The format of the assay is not limited to the one described above. A person skilled in the art could adapt the assay for different formats such as PCR with real-time detection using molecular beacon probes. Molecular beacon probes designed to be used in this assay include, but are not limited to, SEQ ID NO. 1236 for the detection of *E. faecalis*, SEQ ID NO. 1235 for the detection of *E. faecium*, SEQ ID NO. 1240 for the detection of *vanA*, and SEQ ID NO. 1241 for the detection of *vanB*.

EXAMPLE 23:

Development of a multiplex PCR assay for detection and identification of vancomycin-resistant *Enterococcus faecalis*, *Enterococcus faecium* and the group including *Enterococcus gallinarum*, *Enterococcus casseliflavus*, and *Enterococcus flavescens*. The analysis of *vanA* and *vanB* sequences revealed conserved regions allowing design of a PCR primer pair (SEQ ID NOs. 1089 and 1090) specific to *vanA* sequences (Annex XXVIII) and a PCR primer pair (SEQ ID NOs. 1095 and 1096) specific to *vanB* sequences (Annex XXIX). The *vanA*-specific PCR primer pair (SEQ ID NOs. 1089 and 1090) was used in multiplex with the *vanB*-specific PCR primer pair described in our assigned US patent 5,994,066 (SEQ ID NOs. 1095 and 1096 in the present patent and SEQ ID NOs. 231 and 232 in the said patent). The comparison of *vanC1*, *vanC2* and *vanC3* sequences revealed conserved regions allowing design of PCR primers (SEQ ID NOs. 1101 and 1102) able to generate a 158-bp amplicon specific to the group including *E. gallinarum*, *E. casseliflavus* and *E. flavescens* (Annex XXX). The *vanC*-specific PCR primer pair (SEQ ID NOs. 1101 and 1102) was used in multiplex with the *E. faecalis*-specific PCR primer pair described in our assigned US patent 5,994,066 (SEQ ID NOs. 40 and 41 in the said patent) and with the *E. faecium*-specific PCR primer pair described in our patent publication WO98/20157 (SEQ ID NOs. 1 and 2 in the said publication). For both multiplexes, the optimal cycling conditions for maximum sensitivity and specificity were found to be 3 min. at 94 °C, followed by forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 58 °C, plus a terminal extension at 72 °C for 2 minutes. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 µg/ml of ethidium bromide. The *vanA*-specific PCR primer pair (SEQ ID NOs. 1089 and 1090), the *vanB*-specific primer pair (SEQ ID NOs. 1095 and 1096) and the *vanC*-specific primer pair (SEQ ID NOs. 1101 and 1102) were tested for their specificity by using 0.1 nanogram of purified genomic DNA from a panel of 5 vancomycin-

sensitive *Enterococcus* species, 3 vancomycin-resistant *Enterococcus* species, 13 other gram-positive bacteria and one gram-negative bacterium. Specificity tests were performed with the *E. faecium*-specific PCR primer pair described in our patent publication WO98/20157 (SEQ ID NOs. 1 and 2 in the said publication) and with the *E. faecalis*-specific PCR primer pair described in our assigned US patent 5,994,066 (SEQ ID NOs. 40 and 41 in the said patent) on a panel of 37 gram-positive bacterial species. All *Enterococcus* strains were amplified with high specificity showing a perfect correlation between the genotypic and phenotypic analysis. The sensitivity of the assays was determined for several strains of *E. gallinarum*, *E. casseliflavus*, *E. flavescens* and vancomycin-resistant *E. faecalis* and *E. faecium*. Using each of the *E. faecalis*- and *E. faecium*-specific PCR primer pairs as well as *vanA*-, *vanB*- and *vanC*-specific PCR primers used alone or in multiplex as described above, the sensitivity ranged from 1 to 10 copies of genomic DNA.

The format of the assay is not limited to the one described above. A person skilled in the art could adapt the assay for different formats such as PCR with real-time detection using molecular beacon probes. Molecular beacon probes designed to be used in this assay include, but are not limited to, SEQ ID NO. 1238 for the detection of *E. faecalis*, SEQ ID NO. 1237 for the detection of *E. faecium*, SEQ ID NO. 1239 for the detection of *vanA*, and SEQ ID NO. 1241 for the detection of *vanB*.

Alternatively, another PCR assay was developed for the detection of vancomycin-resistant *E. faecium* and vancomycin-resistant *E. faecalis*. This assay included two multiplex: (1) the first multiplex contained the *vanA*-specific primer pair (SEQ ID NOs. 1090-1091) and the *vanB*-specific PCR primer pair described in our assigned US patent 5,994,066 (SEQ ID NOs. 1095 and 1096 in the present patent and SEQ ID NOs. 231 and 232 in the said patent), and (2) the second multiplex contained the *E. faecalis*-specific PCR primer pair described in our assigned US patent 5,994,066 (SEQ ID NOs. 40 and 41 in the said patent) and the *E. faecium*-specific PCR primer pair described in our patent publication WO98/20157 (SEQ ID NOs. 1

and 2 in the said publication). For both multiplexes, the optimal cycling conditions for maximum sensitivity and specificity were found to be 3 min. at 94 °C, followed by forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 58 °C, plus a terminal extension at 72 °C for 2 minutes. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 µg/ml of ethidium bromide. The two multiplexes were tested for their specificity by using 0.1 nanogram of purified genomic DNA from a panel of two vancomycin-sensitive *E. faecalis* strains, two vancomycin-resistant *E. faecalis* strains, two vancomycin-sensitive *E. faecium* strains, two vancomycin-resistant *E. faecium* strains, 16 other enterococcal species and 31 other gram-positive bacterial species. All the *E. faecium* and *E. faecalis* strains were amplified with high specificity showing a perfect correlation between the genotypic analysis and the susceptibility to glycopeptide antibiotics (vancomycin and teicoplanin). The sensitivity of the assay was determined for two vancomycin-resistant *E. faecalis* strains and two vancomycin-resistant *E. faecium* strains. The detection limit was 5 copies of genomic DNA for all the strains.

This multiplex PCR assay was coupled with capture-probe hybridization. Four internal probes were designed: one specific to the *vanA* amplicon (SEQ ID NO. 2292), one specific to the *vanB* amplicon (SEQ ID NO. 2294), one specific to the *E. faecalis* amplicon (SEQ ID NO. 2291) and one specific to the *E. faecium* amplicon (SEQ ID NO. 2287). Each of the internal probes detected their specific amplicons with high specificity and sensitivity.

EXAMPLE 24:

Universal amplification involving the EF-G (*fusA*) subdivision of *tuf* sequences. As shown in Figure 3, primers SEQ ID NOs. 1228 and 1229 were designed to amplify the region between the end of *fusA* and the beginning of *tuf* genes in the *str* operon. Genomic DNAs from a panel of 35 strains were tested for PCR amplification with those primers. In the initial experiment, the following strains showed a positive

result: *Abiotrophia adiacens* ATCC 49175, *Abiotrophia defectiva* ATCC 49176, *Bacillus subtilis* ATCC 27370, *Clostridium difficile* ATCC 9689, *Enterococcus avium* ATCC 14025, *Enterococcus casseliflavus* ATCC 25788, *Enterococcus cecorum* ATCC 43198, *Enterococcus faecalis* ATCC 29212, *Enterococcus faecium* ATCC 19434, *Enterococcus flavescens* ATCC 49996, *Enterococcus gallinarum* ATCC 49573, *Enterococcus solitarius* ATCC 49428, *Escherichia coli* ATCC 11775, *Haemophilus influenzae* ATCC 9006, *Lactobacillus acidophilus* ATCC 4356, *Peptococcus niger* ATCC 27731, *Proteus mirabilis* ATCC 25933, *Staphylococcus aureus* ATCC 43300, *Staphylococcus auricularis* ATCC 33753, *Staphylococcus capitis* ATCC 27840, *Staphylococcus epidemidis* ATCC 14990, *Staphylococcus haemolyticus* ATCC 29970, *Staphylococcus hominis* ATCC 27844, *Staphylococcus lugdunensis* ATCC 43809, *Staphylococcus saprophyticus* ATCC 15305, *Staphylococcus simulans* ATCC 27848, and *Staphylococcus warneri* ATCC 27836. This primer pair could amplify additional bacterial species; however, there was no amplification for some species, suggesting that the PCR cycling conditions could be optimized or the primers modified. For example, SEQ ID NO. 1227 was designed to amplify a broader range of species.

In addition to other possible primer combinations to amplify the region covering *fusA* and *tuf*, Figure 3 illustrates the positions of amplification primers SEQ ID NOs. 1221-1227 which could be used for universal amplification of *fusA* segments. All of the above mentioned primers (SEQ ID NOs. 1221-1229) could be useful for the universal and/or the specific detection of bacteria.

Moreover, different combinations of primers SEQ ID NOs. 1221-1229, sometimes in combination with *tuf* sequencing primer SEQ ID NO. 697, were used to sequence portions of the *str* operon, including the intergenic region. In this manner, the following sequences were generated: SEQ ID NOs. 1518-1526, 1578-1580, 1786-1821, 1822-1834, 1838-1843, 2184, 2187, 2188, 2214-2249, and 2255-2269.

EXAMPLE 25:

DNA fragment isolation from *Staphylococcus saprophyticus* by arbitrarily primed PCR. DNA sequences of unknown coding potential for the species-specific detection and identification of *Staphylococcus saprophyticus* were obtained by the method of arbitrarily primed PCR (AP-PCR).

AP-PCR is a method which can be used to generate specific DNA probes for microorganisms (Fani *et al.*, 1993, *Molecular Ecology* 2:243-250). A description of the AP-PCR protocol used to isolate a species-specific genomic DNA fragment from *Staphylococcus saprophyticus* follows. Twenty different oligonucleotide primers of 10 nucleotides in length (all included in the AP-PCR kit OPAD (Operon Technologies, Inc., Alameda, CA)) were tested systematically with DNAs from 5 bacterial strains of *Staphylococcus saprophyticus* as well as with bacterial strains of 27 other staphylococcal (non-*S. saprophyticus*) species. For all bacterial species, amplification was performed directly from one μL (0.1 ng/ μL) of purified genomic DNA. The 25 μL PCR reaction mixture contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl_2 , 1.2 μM of only one of the 20 different AP-PCR primers OPAD, 200 μM of each of the four dNTPs, 0.5 U of *Taq* DNA polymerase (Promega Corp., Madison, Wis.) coupled with TaqStartTM antibody (Clontech Laboratories Inc., Palo Alto, CA). PCR reactions were subjected to cycling using a MJ Research PTC-200 thermal cycler as follows: 3 min at 96 °C followed by 42 cycles of 1 min at 94 °C for the denaturation step, 1 min at 31 °C for the annealing step and 2 min at 72 °C for the extension step. A final extension step of 7 min at 72 °C followed the 42 cycles to ensure complete extension of PCR products. Subsequently, twenty microliters of the PCR-amplified mixture were resolved by electrophoresis on a 1.5 % agarose gel containing 0.25 $\mu\text{g}/\text{ml}$ of ethidium bromide. The size of the amplification products was estimated by comparison with a 50-bp molecular weight ladder.

Amplification patterns specific for *Staphylococcus saprophyticus* were observed with the AP-PCR primer OPAD-16 (sequence: 5'-AACGGGCGTC-3'). Amplification with this primer consistently showed a band corresponding to a

DNA fragment of approximately 380 bp for all *Staphylococcus saprophyticus* strains tested but not for any of the other staphylococcal species tested.

The band corresponding to the 380 bp amplicon, specific and ubiquitous for *S. saprophyticus* based on AP-PCR, was excised from the agarose gel and purified using the QIAquickTM gel extraction kit (QIAGEN Inc.). The gel-purified DNA fragment was cloned into the T/A cloning site of the pCR 2.1TM plasmid vector (Invitrogen Inc.) using T4 DNA ligase (New England BioLabs). Recombinant plasmids were transformed into *E. coli* DH5 α competent cells using standard procedures. All reactions were performed according to the manufacturer's instructions. Plasmid DNA isolation was done by the method of Birnboim and Doly (Nucleic Acid Res., 1979, 7:1513-1523) for small-scale preparations. All plasmid DNA preparations were digested with the EcoRI restriction endonuclease to ensure the presence of the approximately 380 bp AP-PCR insert into the plasmid. Subsequently, a large-scale and highly purified plasmid DNA preparation was performed from two selected clones shown to carry the AP-PCR insert by using the QIAGEN plasmid purification kit (midi format). These large-scale plasmid preparations were used for automated DNA sequencing.

The 380 bp nucleotide sequence was determined for three strains of *S. saprophyticus* (SEQ ID NOs. 74, 1093, and 1198). Both strands of the AP-PCR insert from the two selected clones were sequenced by the dideoxynucleotide chain termination sequencing method with SP6 and T7 sequencing primers by using the Applied Biosystems automated DNA sequencer (model 373A) with their PRISMTM Sequenase^{RTM} Terminator Double-stranded DNA Sequencing Kit (Applied Biosystems, Foster City, CA).

Optimal species-specific amplification primers (SEQ ID NOs. 1208 and 1209) have been selected from the sequenced AP-PCR *Staphylococcus saprophyticus* DNA fragments with the help of the primer analysis software OligoTM 5.0 (National BioSciences Inc.). The selected primers were tested in PCR assays to verify their specificity and ubiquity. Data obtained with DNA preparations from reference ATCC strains of 49 gram-positive and 31 gram-negative bacterial

species, including 28 different staphylococcal species, indicate that the selected primer pairs are specific for *Staphylococcus saprophyticus* since no amplification signal has been observed with DNAs from the other staphylococcal or bacterial species tested. This assay was able to amplify efficiently DNA from all 60 strains of *S. saprophyticus* from various origins tested. The sensitivity level achieved for three *S. saprophyticus* reference ATCC strains was around 6 genome copies.

EXAMPLE 26:

Sequencing of prokaryotic *tuf* gene fragments. The comparison of publicly available *tuf* sequences from a variety of bacterial species revealed conserved regions, allowing the design of PCR primers able to amplify *tuf* sequences from a wide range of bacterial species. Using primer pair SEQ ID NOs. 664 and 697, it was possible to amplify and determine *tuf* sequences SEQ ID NOs.: 1-73, 75-241, 607-618, 621, 662, 675, 717-736, 868-888, 932, 967-989, 992, 1002, 1572-1575, 1662-1663, 1715-1733, 1835-1837, 1877-1878, 1880-1881, 2183, 2185, 2200, 2201, and 2270-2272.

EXAMPLE 27:

Sequencing of procaryotic *recA* gene fragments. The comparison of publicly available *recA* sequences from a variety of bacterial species revealed conserved regions, allowing the design of PCR primers able to amplify *recA* sequences from a wide range of bacterial species. Using primer pairs SEQ ID NOs. 921-922 and 1605-1606, it was possible to amplify and determine *recA* sequences SEQ ID NOs.: 990-991, 1003, 1288-1289, 1714, 1756-1763, 1866-1873 and 2202-2212.

EXAMPLE 28:

Specific detection and identification of *Escherichia coli/Shigella* sp. using *tuf* sequences. The analysis of *tuf* sequences from a variety of bacterial species allowed the selection of PCR primers (SEQ ID NOs. 1661 and 1665) and of an internal probe (SEQ ID NO. 2168) specific to *Escherichia coli/Shigella* sp. The strategy used to design the PCR primers was based on the analysis of a multiple sequence alignment of various *tuf* sequences. The multiple sequence alignment included the *tuf* sequences of *Escherichia coli/Shigella* sp. as well as *tuf* sequences from other species and bacterial genera, especially representatives of closely related species. A careful analysis of this alignment allowed the selection of oligonucleotide sequences which are conserved within the target species but which discriminate sequences from other species, especially from the closely related species, thereby permitting the species-specific and ubiquitous detection and identification of the target bacterial species.

The chosen primer pair, oligos SEQ ID NOs. 1661 and 1665, gives an amplification product of 219 bp. Standard PCR was carried out using 0.4 μ M of each primer, 2.5 mM MgCl₂, BSA 0.05 mM, 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1 % Triton X-100, dNTPs 0.2 mM (Pharmacia), 0.5 U *Taq* DNA polymerase (Promega) coupled with TaqStartTM antibody (Clontech Laboratories Inc.), 1 μ l of genomic DNA sample in a final volume of 20 μ l using a PTC-200 thermocycler (MJ Research). The optimal cycling conditions for maximum sensitivity and specificity were 3 minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 60 °C, followed by terminal extension at 72 °C for 2 minutes. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 μ g/ml of ethidium bromide. Visualization of the PCR products was made under UV at 254 nm.

Specificity of the assay was tested by adding to the PCR reactions 0.1 ng of genomic DNA from each of the following bacterial species: *Escherichia coli* (7

strains), *Shigella sonnei*, *Shigella flexneri*, *Shigella dysenteriae*, *Salmonella typhimurium*, *Salmonella typhi*, *Salmonella enteritidis*, *Tatumella ptyseos*, *Klebsiella pneumoniae* (2 strains), *Enterobacter aerogenes*, *Citrobacter farmeri*, *Campylobacter jejuni*, *Serratia marcescens*. Amplification was observed only for the *Escherichia coli* and *Shigella* sp. strains listed and *Escherichia fergusonii*. The sensitivity of the assay with 40-cycle PCR was verified with one strain of *E. coli* and three strains of *Shigella* sp. The detection limit for *E. coli* and *Shigella* sp. was 1 to 10 copies of genomic DNA, depending on the strains tested.

EXAMPLE 29:

Specific detection and identification of *Klebsiella pneumoniae* using *atpD* sequences. The analysis of *atpD* sequences from a variety of bacterial species allowed the selection of PCR primers specific to *K. pneumoniae*. The primer design strategy is similar to the strategy described in Example 28 except that *atpD* sequences were used in the alignment.

Two *K. pneumoniae*-specific primers were selected, (SEQ ID NOs. 1331 and 1332) which give an amplification product of 115 bp. Standard PCR was carried out on PTC-200 thermocyclers (MJ Research) using 0.4 μ M of each primer as described in Example 28. The optimal cycling conditions for maximum sensitivity and specificity were as follow: three minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 55°C, followed by terminal extension at 72 °C for 2 minutes.

Specificity of the assay was tested by adding to the PCR reactions 0.1 ng of genomic DNA from each of the following bacterial species: *Klebsiella pneumoniae* (2 strains), *Klebsiella ornitholytica*, *Klebsiella oxytoca* (2 strains), *Klebsiella planticola*, *Klebsiella terrigena*, *Citrobacter freundii*, *Escherichia coli*, *Salmonella cholerasuis typhi*, *Serratia marcescens*, *Enterobacter aerogenes*, *Proteus vulgaris*,

Kluyvera ascorbata, *Kluyvera georgiana*, *Kluyvera cryocrescens* and *Yersinia enterocolitica*. Amplification was detected for the two *K. pneumoniae* strains, *K. planticola*, *K. terrigena* and the three *Kluyvera* species tested. Analysis of the multiple alignment sequence of the *atpD* gene allowed the design of an internal probe SEQ ID NO. 2167 which can discriminate *Klebsiella pneumoniae* from other *Klebsiella* sp. and *Kluyvera* sp. The sensitivity of the assay with 40-cycle PCR was verified with one strain of *K. pneumoniae*. The detection limit for *K. pneumoniae* was around 10 copies of genomic DNA.

EXAMPLE 30:

Specific detection and identification of *Acinetobacter baumannii* using *atpD* sequences. The analysis of *atpD* sequences from a variety of bacterial species allowed the selection of PCR primers specific to *Acinetobacter baumannii*. The primer design strategy is similar to the strategy described in Example 28.

Two *A. baumannii*-specific primers were selected, SEQ ID NOs. 1690 and 1691, which give an amplification product of 233 bp. Standard PCR was carried out on PTC-200 thermocyclers (MJ Research) using 0.4 μ M of each primer as described in Example 28. The optimal cycling conditions for maximum sensitivity and specificity were as follow: three minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 60°C, followed by terminal extension at 72 °C for 2 minutes.

Specificity of the assay was tested by adding to the PCR reactions 0.1 ng of genomic DNA from each of the following bacterial species: *Acinetobacter baumannii* (3 strains), *Acinetobacter anitratus*, *Acinetobacter lwöffi*, *Serratia marcescens*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Pseudomonas aeruginosa*, *Psychrobacter phenylpyruvicus*, *Neisseria gonorrhoeae*, *Haemophilus haemoliticus*, *Yersinia enterocolitica*, *Proteus vulgaris*, *Eikenella corrodens*,

Escherichia coli. Amplification was detected only for *A. baumannii*, *A. anitratus* and *A. lwoffii*. The sensitivity of the assay with 40-cycle PCR was verified with two strains of *A. baumannii*. The detection limit for the two *A. baumannii* strains tested was 5 copies of genomic DNA. Analysis of the multiple alignment sequence of the *atpD* gene allowed the design of a *A. baumannii*-specific internal probe (SEQ ID NO. 2169).

EXAMPLE 31:

Specific detection and identification of *Neisseria gonorrhoeae* using *tuf* sequences.

The analysis of *tuf* sequences from a variety of bacterial species allowed the selection of PCR primers specific to *Neisseria gonorrhoeae*. The primer design strategy is similar to the strategy described in Example 28.

Two *N. gonorrhoeae*-specific primers were selected, SEQ ID NOs. 551 and 552, which give an amplification product of 139 bp. PCR amplification was carried out on PTC-200 thermocyclers (MJ Research) using 0.4 μ M of each primer as described in Example 28. The optimal cycling conditions for maximum sensitivity and specificity were as follow: three minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 65°C, followed by terminal extension at 72 °C for 2 minutes.

Specificity of the assay was tested by adding into the PCR reactions, 0.1 ng of genomic DNA from each of the following bacterial species: *Neisseria gonorrhoeae* (19 strains), *Neisseria meningitidis* (2 strains), *Neisseria lactamica*, *Neisseria flavescens*, *Neisseria animalis*, *Neisseria canis*, *Neisseria cuniculi*, *Neisseria elongata*, *Neisseria mucosa*, *Neisseria polysaccharea*, *Neisseria sicca*, *Neisseria subflava*, *Neisseria weaveri*. Amplification was detected only for *N. gonorrhoeae*, *N. sicca* and *N. polysaccharea*. The sensitivity of the assay with 40-cycle PCR was verified with two strains of *N. gonorrhoeae*. The detection limit for the *N.*

gonorrhoeae strains tested was 5 copies of genomic DNA. Analysis of the multiple alignment sequence of the *tuf* gene allowed the design of an internal probe, SEQ ID NO. 2166, which can discriminate *N. gonorrhoeae* from *N. sicca* and *N. polysaccharea*.

EXAMPLE 32:

Sequencing of bacterial *gyrA* and *parC* gene fragments. Sequencing of bacterial *gyrA* and *parC* fragments. One of the major mechanism of resistance to quinolone in various bacterial species is mediated by target changes (DNA gyrase and/or topoisomerase IV). These enzymes control DNA topology and are vital for chromosome function and replication. Each of these enzymes is a tetramer composed of two subunits: GyrA and GyrB forming A₂B₂ complex in DNA gyrase; and ParC and ParE forming C₂E₂ complex in DNA topoisomerase IV. It has been shown that they are hotspots, called the quinolone-resistance-determining region (QRDR) for mutations within *gyrA* that encodes for the GyrA subunit of DNA gyrase and within *parC* that encodes the *parC* subunit of topoisomerase IV.

In order to generate a database for *gyrA* and *parC* sequences that can be used for design of primers and/or probes for the specific detection of quinolone resistance in various bacterial species, *gyrA* and *parC* DNA fragments selected from public database (GenBank and EMBL) from a variety of bacterial species were used to design oligonucleotide primers.

Using primer pair SEQ ID NOs. 1297 and 1298, it was possible to amplify and determine *gyrA* sequences from *Klebsiella oxytoca* (SEQ ID NO. 1764), *Klebsiella pneumoniae* subsp. *ozaneae* (SEQ ID NO. 1765), *Klebsiella planticola* (SEQ ID NO. 1766), *Klebsiella pneumoniae* (SEQ ID NO. 1767), *Klebsiella pneumoniae* subsp. *pneumoniae* (two strains) (SEQ ID NOs. 1768-1769), *Klebsiella*

pneumoniae subsp. *rhinoscleromatis* (SEQ ID NO. 1770), *Klebsiella terrigena* (SEQ ID NO. 1771), *Kluyvera ascorbata* (SEQ ID NO. 2013), *Kluyvera georgiana* (SEQ ID NO. 2014) and *Escherichia coli* (4 strains) (SEQ ID NOs. 2277-2280). Using primer pair SEQ ID NOs. 1291 and 1292, it was possible to amplify and determine *gyrA* sequences from *Legionella pneumophila* subsp. *pneumophila* (SEQ ID NO. 1772), *Proteus mirabilis* (SEQ ID NO. 1773), *Providencia rettgeri* (SEQ ID NO. 1774), *Proteus vulgaris* (SEQ ID NO. 1775) and *Yersinia enterocolitica* (SEQ ID NO. 1776). Using primer pair SEQ ID NOs. 1340 and 1341, it was possible to amplify and determine *gyrA* sequence from *Staphylococcus aureus* (SEQ ID NO. 1255).

Using primers SEQ ID NOs. 1318 and 1319, it was possible to amplify and determine *parC* sequences from *K. oxytoca* (two strains) (SEQ ID NOs. 1777-1778), *Klebsiella pneumoniae* subsp. *ozaenae* (SEQ ID NO. 1779), *Klebsiella planticola* (SEQ ID NO. 1780), *Klebsiella pneumoniae* (SEQ ID NO. 1781), *Klebsiella pneumoniae* subsp. *pneumoniae* (two strains) (SEQ ID NOs. 1782-1783), *Klebsiella pneumoniae* subsp. *rhinoscleromatis* (SEQ ID NO. 1784) and *Klebsiella terrigena* (SEQ ID NO. 1785).

EXAMPLE 33:

Development of a PCR assay for the specific detection and identification of *Staphylococcus aureus* and its quinolone resistance genes *gyrA* and *parC*. The analysis of *gyrA* and *parC* sequences from a variety of bacterial species revealed conserved regions allowing the design of PCR primers specific to the quinolone-resistance-determining region (QRDR) of *gyrA* and *parC* from *Staphylococcus aureus*. PCR primer pair SEQ ID NOs. 1340 and 1341 was designed to amplify the *gyrA* sequence of *S. aureus*, whereas PCR primer pair SEQ ID NOs. 1342 and 1343 was designed to amplify *S. aureus parC*. The comparison of *gyrA* and *parC* sequences from *S. aureus* strains with various levels of quinolone resistance

allowed the identification of amino acid substitutions Ser-84 to Leu, Glu-88 to Gly or Lys in the GyrA subunit of DNA gyrase encoded by *gyrA* and amino acid changes Ser-80 to Phe or Tyr and Ala-116 to Glu in the ParC subunit of topoisomerase IV encoded by *parC*. These amino acid substitutions in GyrA and ParC subunits occur in isolates with intermediate- or high-level quinolone resistance. Internal probes for the specific detection of wild-type *S. aureus gyrA* (SEQ ID NO. 1940) and wild-type *S. aureus parC* (SEQ ID NO. 1941) as well as internal probes for the specific detection of each of the *gyrA* (SEQ ID NOs. 1333-1335) and *parC* mutations identified in quinolone-resistant *S. aureus* (SEQ ID NOs. 1336-1339) were designed.

The *gyrA*- and *parC*-specific primer pairs (SEQ ID NOs. 1340-1341 and SEQ ID NOs. 1342-1343) were used in multiplex. PCR amplification was carried out on PTC-200 thermocyclers (MJ Research) using 0.3, 0.3, 0.6 and 0.6 μ M of each primers, respectively, as described in Example 28. The optimal cycling conditions for maximum sensitivity and specificity were 3 minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 62 °C, followed by terminal extension at 72 °C for 2 minutes. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 μ g/ml of ethidium bromide. The specificity of the multiplex assay with 40-cycle PCR was verified by using 0.1 ng of purified genomic DNA from a panel of gram-positive bacteria. The list included the following: *Abiotrophia adiacens*, *Abiotrophia defectiva*, *Bacillus cereus*, *Bacillus mycoides*, *Enterococcus faecalis* (2 strains), *Enterococcus flavescens*, *Gemella morbillorum*, *Lactococcus lactis*, *Listeria innocua*, *Listeria monocytogenes*, *Staphylococcus aureus* (5 strains), *Staphylococcus auricularis*, *Staphylococcus capitis* subsp. *urealyticus*, *Staphylococcus carnosus*, *Staphylococcus chromogenes*, *Staphylococcus epidermidis* (3 strains), *Staphylococcus gallinarum*, *Staphylococcus haemolyticus* (2 strains), *Staphylococcus hominis*, *Staphylococcus hominis* subsp. *hominis*, *Staphylococcus lentus*, *Staphylococcus lugdunensis*, *Staphylococcus*

saccharolyticus, *Staphylococcus saprophyticus* (3 strains), *Staphylococcus simulans*, *Staphylococcus warneri*, *Staphylococcus xylosus*, *Streptococcus agalactiae*, *Streptococcus pneumoniae*. Strong amplification of both *gyrA* and *parC* genes was only detected for the *S. aureus* strains tested. The sensitivity of the multiplex assay with 40-cycle PCR was verified with one quinolone-sensitive and four quinolone-resistant strains of *S. aureus*. The detection limit was 2 to 10 copies of genomic DNA, depending on the strains tested.

Detection of the hybridization with the internal probes was performed as described in Example 7. The internal probes specific to wild-type *gyrA* and *parC* of *S. aureus* and to the *gyrA* and *parC* variants of *S. aureus* were able to recognize two quinolone-resistant and one quinolone-sensitive *S. aureus* strains showing a perfect correlation with the susceptibility to quinolones.

The complete assay for the specific detection of *S. aureus* and its susceptibility to quinolone contains the *Staphylococcus*-specific primers (SEQ ID NOs. 553 and 575) described in Example 7 and the multiplex containing the *S. aureus gyrA*- and *parC*-specific primer pairs (SEQ ID NOs. 1340-1341 and SEQ ID NOs. 1342-1343). Amplification is coupled with post-PCR hybridization with the internal probe specific to *S. aureus* (SEQ ID NO. 587) described in Example 7 and the internal probes specific to wild-type *S. aureus gyrA* and *parC* (SEQ ID NOs. 1940-1941) and to the *S. aureus gyrA* and *parC* variants (SEQ ID NOs. 1333-1338).

An assay was also developed for the detection of quinolone-resistant *S. aureus* using the SmartCycler (Cepheid). Real-time detection is based on the use of *S. aureus parC*-specific primers (SEQ ID NOs. 1342 and 1343) and the *Staphylococcus*-specific primers (SEQ ID NOs. 553 and 575) described in Example 7. Internal probes were designed for molecular beacon detection of the wild-type *S. aureus parC* (SEQ ID NO.1939), for detection of the Ser-80 to Tyr or

Phe amino acid substitutions in the ParC subunit encoded by *S. aureus parC* (SEQ ID NOs. 1938 and 1955) and for detection of *S. aureus* (SEQ ID NO. 2282) .

EXAMPLE 34:

Development of a PCR assay for the detection and identification of *Klebsiella pneumoniae* and its quinolone resistance genes *gyrA* and *parC*. The analysis of *gyrA* and *parC* sequences from a variety of bacterial species from the public databases and from the database described in Example 32 revealed conserved regions allowing the design of PCR primers specific to the quinolone-resistance-determining region (QRDR) of *gyrA* and *parC* from *K. pneumoniae*. PCR primer pair SEQ ID NOs. 1936 and 1937, or pair SEQ ID NOs. 1937 and 1942, were designed to amplify the *gyrA* sequence of *K. pneumoniae*, whereas PCR primer pair SEQ ID NOs. 1934 and 1935 was designed to amplify *K. pneumoniae parC* sequence. An alternative pair, SEQ ID NOs. 1935 and 1936, can also amplify *K. pneumoniae parC*. The comparison of *gyrA* and *parC* sequences from *K. pneumoniae* strains with various levels of quinolone resistance allowed the identification of amino acid substitutions Ser-83 to Tyr or Phe and Asp-87 to Gly or Ala and Asp-87 to Asn in the GyrA subunit of DNA gyrase encoded by *gyrA* and amino acid changes Ser-80 to Ile or Arg and Glu-84 to Gly or Lys in the ParC subunit of topoisomerase IV encoded by *parC*. These amino acid substitutions in the GyrA and ParC subunits occur in isolates with intermediate- or high-level quinolone resistance. Internal probes for the specific detection of wild-type *K. pneumoniae gyrA* (SEQ ID NO. 1943) and wild-type *K. pneumoniae parC* (SEQ ID NO. 1944) as well as internal probes for the specific detection of each of the *gyrA* (SEQ ID NOs. 1945-1949) and *parC* mutations identified in quinolone-resistant *K. pneumoniae* (SEQ ID NOs. 1950-1953) were designed.

Two multiplex using the *K. pneumoniae gyrA*- and *parC*-specific primer pairs were used: the first multiplex contained *K. pneumoniae gyrA*-specific primers (SEQ ID

NOs. 1937 and 1942) and *K. pneumoniae parC*-specific primers (SEQ ID NOs. 1934 and 1935) and the second multiplex contained *K. pneumoniae gyrA/parC*-specific primer (SEQ ID NOs. 1936), *K. pneumoniae gyrA*-specific primer (SEQ ID NO. 1937) and *K. pneumoniae parC*-specific primer (SEQ ID NO. 1935). Standard PCR was carried out on PTC-200 thermocyclers (MJ Research) using for the first multiplex 0.6, 0.6, 0.4, 0.4 μM of each primer, respectively, and for the second multiplex 0.8, 0.4, 0.4 μM of each primer, respectively. PCR amplification and agarose gel electrophoresis of the amplified products were performed as described in Example 28. The optimal cycling conditions for maximum sensitivity and specificity were 3 minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 62 °C, followed by terminal extension at 72 °C for 2 minutes. The specificity of the two multiplex assays with 40-cycle PCR was verified by using 0.1 ng of purified genomic DNA from a panel of gram-negative bacteria. The list included: *Acinetobacter baumannii*, *Citrobacter freundii*, *Eikenella corrodens*, *Enterobacter aerogenes*, *Enterobacter cancerogenes*, *Enterobacter cloacae*, *Escherichia coli* (10 strains), *Haemophilus influenzae*, *Klebsiella pneumoniae*, *Klebsiella ornitholytica*, *Klebsiella oxytoca* (2 strains), *Klebsiella planticola*, *Klebsiella terrigena*, *Kluyvera ascorbata*, *Kluyvera cryocrescens*, *Kluyvera georgiana*, *Neisseria gonorrhoeae*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis* subsp. *typhimurium*, *Salmonella enteritidis*, *Serratia liquefaciens*, *Serratia marcescens* and *Yersinia enterocolytica*. For both multiplex, strong amplification of both *gyrA* and *parC* was observed only for the *K. pneumoniae* strain tested. The sensitivity of the two multiplex assays with 40-cycle PCR was verified with one quinolone-sensitive strain of *K. pneumoniae*. The detection limit was around 10 copies of genomic DNA.

The complete assay for the specific detection of *K. pneumoniae* and its susceptibility to quinolone contains the *Klebsiella*-specific primers (SEQ ID NOs. 1331 and 1332) described in Example 29 and either the multiplex containing the *K.*

pneumoniae gyrA- and *parC*-specific primers (SEQ ID NOs. 1935, 1936, 1937) or the multiplex containing the *K. pneumoniae gyrA*- and *parC*-specific primers (SEQ ID NOs. 1934, 1937, 1939, 1942). Amplification is coupled with post-PCR hybridization with the internal probe specific to *K. pneumoniae* (SEQ ID NO. 2167) described in Example 29 and the internal probes specific to wild-type *K. pneumoniae gyrA* and *parC* (SEQ ID NOs. 1943, 1944) and to the *K. pneumoniae gyrA* and *parC* variants (SEQ ID NOs. 1945-1949 and 1950-1953).

An assay was also developed for the detection of quinolone-resistant *K. pneumoniae* using the SmartCycler (Cepheid). Real-time detection is based on the use of resistant *K. pneumoniae gyrA*-specific primers (SEQ ID NOs. 1936 and 1937) and the *K. pneumoniae*-specific primers (SEQ ID NOs. 1331 and 1332) described in Example 29. Internal probes were designed for molecular beacon detection of the wild-type *K. pneumoniae gyrA* (SEQ ID NO. 2251), for detection of the Ser-83 to Tyr or Phe and/or Asp-87 to Gly or Asn in the GyrA subunit of DNA gyrase encoded by *gyrA* (SEQ ID NOs. 2250) and for detection of *K. pneumoniae* (SEQ ID NO. 2281).

EXAMPLE 35:

Development of a PCR assay for detection and identification of *S. pneumoniae* and its quinolone resistance genes *gyrA* and *parC*. The analysis of *gyrA* and *parC* sequences from a variety of bacterial species revealed conserved regions allowing the design of PCR primers able to amplify the quinolone-resistance-determining region (QRDR) of *gyrA* and *parC* from all *S. pneumoniae* strains. PCR primer pair SEQ ID NOs. 2040 and 2041 was designed to amplify the QRDR of *S. pneumoniae gyrA*, whereas PCR primer pair SEQ ID NOs. 2044 and 2045 was designed to amplify the QRDR of *S. pneumoniae parC*. The comparison of *gyrA* and *parC* sequences from *S. pneumoniae* strains with various levels of quinolone resistance allowed the identification of amino acid substitutions Ser-81 to Phe or

Tyr in the GyrA subunit of DNA gyrase encoded by *gyrA* and amino acid changes Ser-79 to Phe in the ParC subunit of topoisomerase IV encoded by *parC*. These amino acid substitutions in the GyrA and ParC subunits occur in isolates with intermediate- or high-level quinolone resistance. Internal probes for the specific detection of each of the *gyrA* (SEQ ID NOs. 2042 and 2043) and *parC* (SEQ ID NO. 2046) mutations identified in quinolone-resistant *S. pneumoniae* were designed.

For all bacterial species, amplification was performed from purified genomic DNA. 1 μ l of genomic DNA at 0.1 ng/ μ L was transferred directly to a 19 μ l PCR mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl₂, 0.4 μ M (each) of the above primers SEQ ID NOs. 2040, 2041, 2044 and 2045, 0.05 mM bovine serum albumin (BSA) and 0.5 U *Taq* polymerase coupled with TaqStartTM antibody. The optimal cycling conditions for maximum sensitivity and specificity were 3 minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 58 °C, followed by terminal extension at 72 °C for 2 minutes. In order to generate Digoxigenin (DIG)-labeled amplicons for capture probe hybridization, 0.1X PCR DIG labeling four deoxynucleoside triphosphates mix (Boehringer Mannheim GmbH) was used for amplification.

The DIG-labeled amplicons were hybridized to the capture probes bound to 96-well plates. The plates were incubated with anti-DIG-alkaline phosphatase and the chemiluminescence was measured by using a luminometer (MLX, Dynex Technologies Inc.) after incubation with CSPD and recorded as Relative Light Unit (RLU). The RLU ratio of tested sample with and without captures probes was then calculated. A ratio ≥ 2.0 was defined as a positive hybridization signal. All reactions were performed in duplicate.

The specificity of the multiplex assay with 40-cycle PCR was verified by using 0.1 ng of purified genomic DNA from a panel of bacteria listed in Table 13. Strong amplification of both *gyrA* and *parC* was detected only for the *S. pneumoniae* strains tested. Weak amplification of both *gyrA* and *parC* genes was detected for *Staphylococcus simulans*. The detection limit tested with purified genomic DNA from 5 strains of *S. pneumoniae* was 1 to 10 genome copies. In addition, 5 quinolone-resistant and 2 quinolone-sensitive clinical isolates of *S. pneumoniae* were tested to further validate the developed multiplex PCR coupled with capture probe hybridization assays. There was a perfect correlation between detection of *S. pneumoniae gyrA* and *parC* mutations and the susceptibility to quinolone.

The complete assay for the specific detection of *S. pneumoniae* and its susceptibility to quinolone contains the *S. pneumoniae*-specific primers (SEQ ID NOs. 1179 and 1181) described in Exemple 20 and the multiplex containing the *S. pneumoniae gyrA*-specific and *parC*-specific primer pairs (SEQ ID NOS. 2040 and 2041 and SEQ ID NOs. 2044 and 2045). Amplification is coupled with post-PCR hybridization with the internal probe specific to *S. pneumoniae* (SEQ ID NO. 1180) described in Example and the internal probes specific to each of the *S. pneumoniae gyrA* and *parC* variants (SEQ ID NOs. 2042, 2043 and 2046).

EXAMPLE 36:

Detection of extended-spectrum TEM-type β -lactamases in *Escherichia coli*. The analysis of TEM sequences which confer resistance to third-generation cephalosporins and to β -lactamase inhibitors allowed the identification of amino acid substitutions Met-69 to Ile or Leu or Val, Ser-130 to Gly, Arg-164 to Ser or His, Gly-238 to Ser, Glu-240 to Lys and Arg-244 to Ser or Cys or Thr or His or Leu. PCR primers SEQ ID NOs. 1907 and 1908 were designed to amplify TEM sequences. Internal probes for the specific detection of wild-type TEM (SEQ ID NO. 2141) and for each of the amino acid substitutions (SEQ ID NOs. 1909-1926) identified in TEM variants were designed to detect resistance to third-generation

cephalosporins and to β -lactamase inhibitors. Design and synthesis of primers and probes, and detection of the hybridization were performed as described in Example 7.

For all bacterial species, amplification was performed from purified genomic DNA. One μ l of genomic DNA at 0.1ng/ μ l was transferred directly to a 19 μ l PCR mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0); 0.1% Triton X-100, 2.5 mM MgCl₂, 0.4 μ M of the TEM-specific primers SEQ ID NOs. 1907 and 1908, 200 μ M (each) of the four deoxynucleoside triphosphates, 0.05 mM bovine serum albumin (BSA) and 0.5 U *Taq* polymerase (Promega) coupled with TaqStartTM antibody. PCR amplification and agarose gel analysis of the amplified products were performed as described in Example 28. The optimal cycling conditions for maximum sensitivity and specificity were 3 minutes at 95 °C for initial denaturation, then forty cycles of three steps consisting of 5 seconds at 95 °C, 30 seconds at 55 °C and 30 seconds at 72 °C, followed by terminal extension at 72 °C for 2 minutes.

The specificity of the TEM-specific primers with 40-cycle PCR was verified by using 0.1 ng of purified genomic from the following bacteria: three third-generation cephalosporin-resistant *Escherichia coli* strains (one with TEM-10, one with TEM-28 and the other with TEM-49), two third-generation cephalosporin-sensitive *Escherichia coli* strain (one with TEM-1 and the other without TEM), one third-generation cephalosporin-resistant *Klebsiella pneumoniae* strain (with TEM-47), and one β -lactamase-inhibitor-resistant *Proteus mirabilis* strain (with TEM-39). Amplification with the TEM-specific primers was detected only for strains containing TEM.

The sensitivity of the assay with 40-cycle PCR was verified with three *E. coli* strains containing TEM-1 or TEM-10 or TEM-49, one *K. pneumoniae* strain containing TEM-47 and one *P. mirabilis* strain containing TEM-39. The detection

limit was 5 to 100 copies of genomic DNA, depending on the TEM-containing strains tested.

The TEM-specific primers SEQ ID NOs. 1907 and 1908 were used in multiplex with the *Escherichia coli/Shigella sp.*-specific primers SEQ ID NOs. 1661 and 1665 described in Example 28 to allow the complete identification of *Escherichia coli/Shigella sp.* and the susceptibility to β -lactams. PCR amplification with 0.4 μ M of each of the primers and agarose gel analysis of the amplified products was performed as described above.

The specificity of the multiplex with 40-cycle PCR was verified by using 0.1 ng of purified genomic DNA from the following bacteria: three third-generation cephalosporin-resistant *Escherichia coli* strains (one with TEM-10, one with TEM-28 and the other with TEM-49), two third-generation cephalosporin-sensitive *Escherichia coli* strain (one with TEM-1 and the other without TEM), one third-generation cephalosporin-resistant *Klebsiella pneumoniae* strain (with TEM-47), and one β -lactamase-inhibitor-resistant *Proteus mirabilis* strain (with TEM-39). The multiplex was highly specific to *Escherichia coli* strains containing TEM.

The complete assay for detection of TEM-type β -lactamases in *E. coli* includes PCR amplification using the multiplex containing the TEM-specific primers (SEQ ID NOs. 1907 and 1908) and the *Escherichia coli/Shigella sp.*-specific primers (SEQ ID NOs. 1661 and 1665) coupled with post PCR-hybridization with the internal probes specific to wild-type TEM (SEQ ID NO. 2141) and to the TEM variants (SEQ ID NOs. 1909-1926).

EXAMPLE 37:

Detection of extended-spectrum SHV-type β -lactamases in *Klebsiella pneumoniae*.

The comparison of SHV sequences, which confer resistance to third-generation

cephalosporins and to β -lactamase inhibitors, allowed the identification of amino acid substitutions Ser-130 to Gly, Asp-179 to Ala or Asn, Gly-238 to Ser, and Glu-240 to Lys. PCR primer pair SEQ ID NOs. 1884 and 1885 was designed to amplify SHV sequences. Internal probes for the specific identification of wild-type SHV (SEQ ID NO. 1896) and for each of the amino acid substitutions (SEQ ID NOs. 1886-1895 and 1897-1898) identified in SHV variants were designed to detect resistance to third-generation cephalosporins and to β -lactamase inhibitors. Design and synthesis of primers and probes, and detection of the hybridization were performed as described in Example 7.

For all bacterial species, amplification was performed from purified genomic DNA. One μ l of genomic DNA at 0.1ng/ μ l was transferred directly to a 19 μ l PCR mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl₂, 0.4 μ M of the SHV-specific primers SEQ ID NO. 1884 and 1885, 200 μ M (each) of the four deoxynucleoside triphosphates, 0.05 mM bovine serum albumin (BSA) and 0.5 U *Taq* polymerase (Promega) coupled with TaqStartTM antibody. PCR amplification and agarose gel analysis of the amplified products were performed as described in Example 28. The optimal cycling conditions for maximum sensitivity and specificity were 3 minutes at 95 °C for initial denaturation, then forty cycles of three steps consisting of 5 seconds at 95 °C, 30 seconds at 55 °C and 30 seconds at 72 °C, followed by terminal extension at 72 °C for 2 minutes.

The specificity of the SHV-specific primers with 40-cycle PCR was verified by using 0.1 ng of purified genomic from the following bacteria: two third-generation cephalosporin-resistant *Klebsiella pneumoniae* strains (one with SHV-2a and the other with SHV-12), one third-generation cephalosporin-sensitive *Klebsiella pneumoniae* strain (with SHV-1), two third-generation cephalosporin-resistant *Escherichia coli* strains (one with SHV-8 and the other with SHV-7), and two third-generation cephalosporin-sensitive *Escherichia coli* strains (one with SHV-1

and the other without any SHV). Amplification with the SHV-specific primers was detected only for strains containing SHV.

The sensitivity of the assay with 40-cycle PCR was verified with four strains containing SHV. The detection limit was 10 to 100 copies of genomic DNA, depending on the SHV-containing strains tested.

The amplification was coupled with post-PCR hybridization with the internal probes specific for identification of wild-type SHV (SEQ ID NO. 1896) and for each of the amino acid substitutions (SEQ ID NOs. 1886-1895 and 1897-1898) identified in SHV variants. The specificity of the probes was verified with six strains containing various SHV enzymes, one *Klebsiella pneumoniae* strain containing SHV-1, one *Klebsiella pneumoniae* strain containing SHV-2a, one *Klebsiella pneumoniae* strain containing SHV-12, one *Escherichia coli* strain containing SHV-1, one *Escherichia coli* strain containing SHV-7 and one *Escherichia coli* strain containing SHV-8. The probes correctly detected each of the SHV genes and their specific mutations. There was a perfect correlation between the SHV genotype of the strains and the susceptibility to β -lactam antibiotics.

The SHV-specific primers SEQ ID NOs. 1884 and 1885 were used in multiplex with the *K. pneumoniae*-specific primers SEQ ID NOs. 1331 and 1332 described in Example 29 to allow the complete identification of *K. pneumoniae* and the susceptibility to β -lactams. PCR amplification with 0.4 μ M of each of the primers and agarose gel analysis of the amplified products were performed as described above.

The specificity of the multiplex with 40-cycle PCR was verified by using 0.1 ng of purified genomic DNA from the following bacteria: three *K. pneumoniae* strains containing SHV-1, one *Klebsiella pneumoniae* strain containing SHV-2a, one

Klebsiella pneumoniae strain containing SHV-12, one *K. rhinoscleromatis* strain containing SHV-1, one *Escherichia coli* strain without SHV. The multiplex was highly specific to *Klebsiella pneumoniae* strain containing SHV.

EXAMPLE 38:

Development of a PCR assay for the detection and identification of *Neisseria gonorrhoeae* and its associated tetracycline resistance gene *tetM*. The analysis of publicly available *tetM* sequences revealed conserved regions allowing the design of PCR primers specific to *tetM* sequences. The PCR primer pair SEQ ID NOs. 1588 and 1589 was used in multiplex with the *Neisseria gonorrhoeae*-specific primers SEQ ID NOs. 551 and 552 described in Example 31. Sequence alignment analysis of *tetM* sequences revealed regions suitable for the design of an internal probe specific to *tetM* (SEQ ID NO. 2254). PCR amplification was carried out on PTC-200 thermocyclers (MJ Research) using 0.4 μ M of each primer pair as described in Example 28. The optimal cycling conditions for maximum sensitivity and specificity were as follow: three minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 60°C, followed by terminal extension at 72 °C for 2 minutes.

The specificity of the multiplex PCR assay with 40-cycle PCR was verified by using 0.1 ng of purified genomic DNA from the following bacteria: two tetracycline-resistant *Escherichia coli* strains (one containing the tetracycline-resistant gene *tetB* and the other containing the tetracycline-resistant gene *tetC*), one tetracycline-resistant *Pseudomonas aeruginosa* strain (containing the tetracycline-resistant gene *tetA*), nine tetracycline-resistant *Neisseria gonorrhoeae* strains, two tetracycline-sensitive *Neisseria meningitidis* strains, one tetracycline-sensitive *Neisseria polysaccharea* strain, one tetracycline-sensitive *Neisseria sicca* strain and one tetracycline-sensitive *Neisseria subflava* strain. Amplification with both the *tetM*-specific and *Neisseria gonorrhoeae*-specific primers was detected

only for *N. gonorrhoeae* strains containing *tetM*. There was a weak amplification signal using *Neisseria gonorrhoeae*-specific primers for the following species: *Neisseria sicca*, *Neisseria polysaccharea* and *Neisseria meningitidis*. There was a perfect correlation between the *tetM* genotype and the tetracycline susceptibility pattern of the *Neisseria gonorrhoeae* strains tested. The internal probe specific to *N. gonorrhoeae* SEQ ID NO. 2166 described in Example 31 can discriminate *Neisseria gonorrhoeae* from the other *Neisseria* sp.

The sensitivity of the assay with 40-cycle PCR was verified with two tetracycline resistant strains of *N. gonorrhoeae*. The detection limit was 5 copies of genomic DNA for both strains.

EXAMPLE 39:

Development of a PCR assay for the detection and identification of *Shigella* sp. and their associated trimethoprim resistance gene *dhfrIa*. The analysis of publicly available *dhfrIa* and other *dhfr* sequences revealed regions allowing the design of PCR primers specific to *dhfrIa* sequences. The PCR primer pair (SEQ ID NOs. 1459 and 1460) was used in multiplex with the *Escherichia coli/Shigella* sp.-specific primers SEQ ID NOs. 1661 and 1665 described in Example 28. Sequence alignment analysis of *dhfrIa* sequences revealed regions suitable for the design of an internal probe specific to *dhfrIa* (SEQ ID NO. 2253). PCR amplification and agarose gel analysis of the amplified products were performed as described in Example 28 with an annealing temperature of 60 °C. The specificity of the multiplex assay with 40-cycle PCR was verified by using 0.1 ng of purified genomic DNA from a panel of bacteria. The list included the following trimethoprim-sensitive strains, *Salmonella typhimurium*, *Salmonella typhi*, *Salmonella enteritidis*, *Tatumella ptyseos*, *Klebsiella pneumoniae*, *Enterobacter aerogenes*, *Citrobacter farmeri*, *Campylobacter jejuni*, *Serratia marcescens*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, six trimethoprim-resistant *Escherichia coli* strains (containing *dhfrIa* or *dhfrV* or *dhfrVII* or *dhfrXII* or

dhfrXIII or *dhfrXV*), four trimethoprim-resistant strains containing *dhfrIa* (*Shigella sonnei*, *Shigella flexneri*, *Shigella dysenteriae* and *Escherichia coli*). There was a perfect correlation between the *dhfrIa* genotype and the trimethoprim susceptibility pattern of the *Escherichia coli* and *Shigella* sp. strains tested. The *dhfrIa* primers were specific to the *dhfrIa* gene and did not amplify any of the other trimethoprim-resistant *dhfr* genes tested. The sensitivity of the multiplex assay with 40-cycle PCR was verified with three strains of trimethoprim-resistant strains of *Shigella* sp. The detection limit was 5 to 10 genome copies of DNA, depending on the *Shigella* sp. strains tested.

EXAMPLE 40:

Development of a PCR assay for the detection and identification of *Acinetobacter baumannii* and its associated aminoglycoside resistance gene *aph(3')-Vla*. The comparison of publicly available *aph(3')-Vla* sequence revealed regions allowing the design of PCR primers specific to *aph(3')-Vla*. The PCR primer pair (SEQ ID NOs. 1404 and 1405) was used in multiplex with the *Acinetobacter baumannii*-specific primers SEQ ID NOs. 1692 and 1693 described in Example 30. Analysis of the *aph(3')-Vla* sequence revealed region suitable for the design of an internal probe specific to *aph(3')-Vla* (SEQ ID NO. 2252). PCR amplification and agarose gel analysis of the amplified products were performed as described in Example 28. The specificity of the multiplex assay with 40-cycle PCR was verified by using 0.1 ng of purified genomic DNA from a panel of bacteria including: two aminoglycoside-resistant *A. baumannii* strains (containing *aph(3')-Vla*), one aminoglycoside-sensitive *A. baumannii* strain, one of each of the following aminoglycoside-resistant bacteria, one *Serratia marcescens* strain containing the aminoglycoside-resistant gene *aacC1*, one *Serratia marcescens* strain containing the aminoglycoside-resistant gene *aacC4*, one *Enterobacter cloacae* strain containing the aminoglycoside-resistant gene *aacC2*, one *Enterococcus faecalis* containing the aminoglycoside-resistant gene *aacA-aphD*, one *Pseudomonas*

aeruginosa strain containing the aminoglycoside-resistant gene *aac6IIa* and one of each of the following aminoglycoside-sensitive bacterial species, *Acinetobacter anitratus*, *Acinetobacter lwoffii*, *Psychobacter phenylpyruvian*, *Neisseria gonorrhoeae*, *Haemophilus haemolyticus*, *Haemophilus influenzae*, *Yersinia enterocolitica*, *Proteus vulgaris*, *Eikenella corrodens*, *Escherichia coli*. There was a perfect correlation between the *aph(3')-VIa* genotype and the aminoglycoside susceptibility pattern of the *A. baumannii* strains tested. The *aph(3')-VIa*-specific primers were specific to the *aph(3')-VIa* gene and did not amplify any of the other aminoglycoside-resistant genes tested. The sensitivity of the multiplex assay with 40-cycle PCR was verified with two strains of aminoglycoside-resistant strains of *A. baumannii*. The detection limit was 5 genome copies of DNA for both *A. baumannii* strains tested.

EXAMPLE 41:

Specific identification of *Bacteroides fragilis* using *atpD* (V-type) sequences. The comparison of *atpD* (V-type) sequences from a variety of bacterial species allowed the selection of PCR primers for *Bacteroides fragilis*. The strategy used to design the PCR primers was based on the analysis of a multiple sequence alignment of various *atpD* sequences from *B. fragilis*, as well as *atpD* sequences from the related species *B. dispar*, bacterial genera and archaea, especially representatives with phylogenetically related *atpD* sequences. A careful analysis of this alignment allowed the selection of oligonucleotide sequences which are conserved within the target species but which discriminate sequences from other species, especially from closely related species *B. dispar*, thereby permitting the species-specific and ubiquitous detection and identification of the target bacterial species.

The chosen primer pair, SEQ ID NOs. 2134-2135, produces an amplification product of 231 bp. Standard PCR was carried out on PTC-200 thermocyclers (MJ Research Inc.) using 0.4 μ M of each primers pair as described in Example 28. The

optimal cycling conditions for maximum sensitivity and specificity were as follows: three minutes at 95°C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95°C and 30 seconds at 60°C, followed by terminal extension at 72°C for 2 minutes.

The format of this assay is not limited to the one described above. A person skilled in the art could adapt the assay for different formats such as PCR with real-time detection using molecular beacon probes. Molecular beacon probes designed to be used in this assay include, but are not limited to, SEQ ID NO. 2136 for the detection of the *B. fragilis* amplicon.

EXAMPLE 42:

Evidence for horizontal gene transfer in the evolution of the elongation factor Tu in Enterococci.

ABSTRACT

The elongation factor Tu, encoded by *tuf* genes, is a GTP binding protein that plays a central role in protein synthesis. One to three *tuf* genes per genome are present depending on the bacterial species. Most low G+C gram-positive bacteria carry only one *tuf* gene. We have designed degenerate PCR primers derived from consensus sequences of the *tuf* gene to amplify partial *tuf* sequences from 17 enterococcal species and other phylogenetically related species. The amplified DNA fragments were sequenced either by direct sequencing or by sequencing cloned inserts containing putative amplicons. Two different *tuf* genes (*tufA* and *tufB*) were found in 11 enterococcal species, including *Enterococcus avium*, *E. casseliflavus*, *E. dispar*, *E. durans*, *E. faecium*, *E. gallinarum*, *E. hirae*, *E. malodoratus*, *E. mundtii*, *E. pseudoavium*, and *E. raffinosus*. For the other six enterococcal species (*E. cecorum*, *E. columbae*, *E. faecalis*, *E. sulfureus*, *E.*

saccharolyticus, and *E. solitarius*), only the *tufA* gene was present. Based on 16S rRNA gene sequence analysis, the 11 species having two *tuf* genes all share a common ancestor, while the six species having only one copy diverged from the enterococcal lineage before that common ancestor. The presence of one or two copies of the *tuf* gene in enterococci was confirmed by Southern hybridization. Phylogenetic analysis of *tuf* sequences demonstrated that the enterococcal *tufA* gene branches with the *Bacillus*, *Listeria* and *Staphylococcus* genera, while the enterococcal *tufB* gene clusters with the genera *Streptococcus* and *Lactococcus*. Primary structure analysis showed that four amino acid residues within the sequenced regions are conserved and unique to the enterococcal *tufB* genes and the *tuf* genes of streptococci and *L. lactis*. The data suggest that an ancestral streptococcus or a streptococcus-related species may have horizontally transferred a *tuf* gene to the common ancestor of the 11 enterococcal species which now carry two *tuf* genes.

INTRODUCTION

The elongation factor Tu (EF-Tu) is a GTP binding protein playing a central role in protein synthesis. It mediates the recognition and transport of aminoacyl-tRNAs and their positioning to the A-site of the ribosome. The highly conserved function and ubiquitous distribution render the elongation factor a valuable phylogenetic marker among eubacteria and even throughout the archaeobacterial and eukaryotic kingdoms. The *tuf* genes encoding elongation factor Tu are present in various copy numbers per bacterial genome. Most gram-negative bacteria contain two *tuf* genes. As found in *Escherichia coli*, the two genes, while being almost identical in sequence, are located in different parts of the bacterial chromosome. However, recently completed microbial genomes revealed that only one *tuf* gene is found in *Helicobacter pylori* as well as in some obligate parasitic bacteria, such as *Borrelia burgdorferi*, *Rickettsia prowazekii*, and *Treponema pallidum*, and in some cyanobacteria. In most gram-positive bacteria studied so far, only one *tuf* gene was found. However, Southern hybridization showed that there are two *tuf* genes in

some clostridia as well as in *Streptomyces coelicolor* and *S. lividans*. Up to three *tuf*-like genes have been identified in *S. ramocissimus*.

Although massive prokaryotic gene transfer is suggested to be one of the factors responsible for the evolution of bacterial genomes, the genes encoding components of the translation machinery are thought to be highly conserved and difficult to be transferred horizontally due to the complexity of their interactions. However, a few recent studies demonstrated evidence that horizontal gene transfer has also occurred in the evolution of some genes coding for the translation apparatus, namely, 16S rRNA and some aminoacyl-tRNA synthetases. No further data suggest that such a mechanism is involved in the evolution of the elongation factors. Previous studies concluded that the two copies of *tuf* genes in the genomes of some bacteria resulted from an ancient event of gene duplication. Moreover, a study of the *tuf* gene in *R. prowazekii* suggested that intrachromosomal recombination has taken place in the evolution of the genome of this organism.

To date, little is known about the *tuf* genes of enterococcal species. In this study, we analyzed partial sequences of *tuf* genes in 17 enterococcal species, namely, *E. avium*, *E. casseliflavus*, *E. cecorum*, *E. columbae*, *E. dispar*, *E. durans*, *E. faecalis*, *E. faecium*, *E. gallinarum*, *E. hirae*, *E. malodoratus*, *E. mundtii*, *E. pseudoavium*, *E. raffinosus*, *E. saccharolyticus*, *E. solitarius*, and *E. sulfureus*. We report here the presence of two divergent copies of *tuf* genes in 11 of these enterococcal species. The 6 other species carried a single *tuf* gene. The evolutionary implications are discussed.

MATERIALS AND METHODS

Bacterial strains. Seventeen enterococcal strains and other gram-positive bacterial strains obtained from the American Type Culture Collection (ATCC, Manassas, Va.) were used in this study (Table 16). All strains were grown on sheep blood agar or in brain-heart infusion broth prior to DNA isolation.

DNA isolation. Bacterial DNAs were prepared using the G NOME DNA extraction kit (Bio101, Vista, Calif.) as previously described.

Sequencing of putative *tuf* genes. In order to obtain the *tuf* gene sequences of enterococci and other gram-positive bacteria, two sequencing approaches were used: 1) sequencing of cloned PCR products and 2) direct sequencing of PCR products. A pair of degenerate primers (SEQ ID NOs. 664 and 697) were used to amplify an 886-bp portion of the *tuf* genes from enterococcal species and other gram-positive bacteria as previously described. For *E. avium*, *E. casseliflavus*, *E. dispar*, *E. durans*, *E. faecium*, *E. gallinarum*, *E. hirae*, *E. mundtii*, *E. pseudoavium*, and *E. raffinosus*, the amplicons were cloned using the Original TA cloning kit (Invitrogen, Carlsbad, Calif.) as previously described. Five clones for each species were selected for sequencing. For *E. cecorum*, *E. faecalis*, *E. saccharolyticus*, and *E. solitarius* as well as the other gram-positive bacteria, the sequences of the 886-bp amplicons were obtained by direct sequencing. Based on the results obtained from the earlier rounds of sequencing, two pairs of primers were designed for obtaining the partial *tuf* sequences from the other enterococcal species by direct sequencing. One pair of primers (SEQ ID NOs. 543 and 660) were used to amplify the enterococcal *tuf* gene fragments from *E. columbae*, *E. malodoratus*, and *E. sulfureus*. Another pair of primers (SEQ ID NOs. 664 and 661) were used to amplify the second *tuf* gene fragments from *E. avium*, *E. malodoratus*, and *E. pseudoavium*.

Prior to direct sequencing, PCR products were electrophoresed on 1% agarose gel at 120V for 2 hours. The gel was then stained with 0.02% methylene blue for 30 minutes and washed twice with autoclaved distilled water for 15 minutes. The gel slices containing PCR products of the expected sizes were cut out and purified with the QIAquick gel extraction kit (QIAGEN Inc., Mississauga, Ontario, Canada) according to the manufacturer's instructions. PCR mixtures for sequencing were prepared as described previously. DNA sequencing was carried out with the Big DyeTM Terminator Ready Reaction cycle sequencing kit using a 377 DNA sequencer (PE Applied Biosystems, Foster City, Calif.). Both strands of the

amplified DNA were sequenced. The sequence data were verified using the SequencerTM 3.0 software (Gene Codes Corp., Ann Arbor, Mich.).

Sequence analysis and phylogenetic study. Nucleotide sequences of the *tuf* genes and their respective flanking regions for *E. faecalis*, *Staphylococcus aureus*, and *Streptococcus pneumoniae*, were retrieved from the TIGR microbial genome database and *S. pyogenes* from the University of Oklahoma database. DNA sequences and deduced protein sequences obtained in this study were compared with those in all publicly available databases using the BLAST and FASTA programs. Unless specified, sequence analysis was conducted with the programs from GCG package (Version 10; Genetics Computer Group, Madison, Wisc.). Sequence alignment of the *tuf* genes from 74 species representing all three kingdoms of life (Tables 16 and 17) were carried out by use of Pileup and corrected upon visual analysis. The N- and C-termini extremities of the sequences were trimmed to yield a common block of 201 amino acids sequences and equivocal residues were removed. Phylogenetic analysis was performed with the aid of PAUP 4.0b4 written by Dr. David L. Swofford (Sinauer Associates, Inc., Publishers, Sunderland, Mass.). The distance matrix and maximum parsimony were used to generate phylogenetic trees and bootstrap resampling procedures were performed using 500 and 100 replications in each analysis, respectively.

Protein structure analysis. The crystal structures of (i) *Thermus aquaticus* EF-Tu in complex with Phe-tRNA^{Phe} and a GTP analog and (ii) *E. coli* EF-Tu in complex with GDP served as templates for constructing the equivalent models for enterococcal EF-Tu. Homology modeling of protein structure was performed using the SWISS-MODEL server and inspected using the SWISS-PDB viewer version 3.1.

Southern hybridization. In a previous study, we amplified and cloned an 803-bp PCR product of the *tuf* gene fragment from *E. faecium*. Two divergent sequences of the inserts, which we assumed to be *tufA* and *tufB* genes, were obtained. The recombinant plasmid carrying either *tufA* or *tufB* sequence was used to generate two probes labeled with Digoxigenin (DIG)-11-dUTP by PCR

incorporation following the instructions of the manufacturer (Boehringer Mannheim, Laval, Québec, Canada). Enterococcal genomic DNA samples (1-2 µg) were digested to completion with restriction endonucleases *Bgl*III and *Xba*I as recommended by the supplier (Amersham Pharmacia Biotech, Mississauga, Ontario, Canada). These restriction enzymes were chosen because no restriction sites were observed within the amplified *tuf* gene fragments of most enterococci. Southern blotting and filter hybridization were performed using positively charged nylon membranes (Boehringer Mannheim) and QuikHyb hybridization solution (Stratagene Cloning Systems, La Jolla, Calif.) according to the manufacturers' instructions with modifications. Twenty µl of each digestion were electrophoresed for 2 h at 120V on a 0.8% agarose gel. The DNA fragments were denatured with 0.5 M NaOH and transferred by Southern blotting onto a positively charged nylon membrane (Boehringer Mannheim). The filters were pre-hybridized for 15 min and then hybridized for 2 h in the QuikHyb solution at 68°C with either DIG-labeled probe. Posthybridization washings were performed twice with 0.5x SSC, 1% SDS at room temperature for 15 min and twice in the same solution at 60°C for 15 min. Detection of bound probes was achieved using disodium 3- (4-methoxyspiro (1,2-dioxetane-3,2'- (5'-chloro) tricyclo(3,3.1.1^{3,7}) decan)-4-yl) phenyl phosphate (CSPD) (Boehringer Mannheim) as specified by the manufacturer.

GenBank submission. The GenBank accession numbers for partial *tuf* gene sequences generated in this study are given in Table 16.

RESULTS

Sequencing and nucleotide sequence analysis. In this study, all gram-positive bacteria other than enterococci yielded a single *tuf* sequence of 886 bp using primers SEQ ID NOs. 664 and 697 (Table 16). Each of four enterococcal species including *E. cecorum*, *E. faecalis*, *E. saccharolyticus*, and *E. solitarius* also yielded one 886-bp *tuf* sequence. On the other hand, for *E. avium*, *E. casseliflavus*, *E. dispar*, *E. durans*, *E. faecium*, *E. gallinarum*, *E. hirae*, *E. mundtii*, *E. pseudoavium*,

and *E. raffinosus*, direct sequencing of the 886-bp fragments revealed overlapping peaks according to their sequence chromatograms, suggesting the presence of additional copies of the *tuf* gene. Therefore, the *tuf* gene fragments of these 10 species were cloned first and then sequenced. Sequencing data revealed that two different types of *tuf* sequences (*tufA* and *tufB*) are found in eight of these species including *E. casseliflavus*, *E. dispar*, *E. durans*, *E. faecium*, *E. gallinarum*, *E. hirae*, *E. mundtii*, and *E. raffinosus*. Five clones from *E. avium* and *E. pseudoavium* yielded only a single *tuf* sequence. These new sequence data allowed the design of new primers specific for the enterococcal *tufA* or *tufB* sequences. Primers SEQ ID NOs. 543 and 660 were designed to amplify only enterococcal *tufA* sequences and a 694-bp fragment was amplified from all 17 enterococcal species. The 694-bp sequences of *tufA* genes from *E. columbae*, *E. malodoratus*, and *E. sulfureus* were obtained by direct sequencing using these primers. Primers SEQ ID NOs. 664 and 661 were designed for the amplification of 730-bp portion of *tufB* genes and yielded the expected fragments from 11 enterococcal species, including *E. malodoratus* and the 10 enterococcal species in which heterogeneous *tuf* sequences were initially found. The sequences of the *tufB* fragments for *E. avium*, *E. malodoratus* and *E. pseudoavium* were determined by direct sequencing using the primers SEQ ID NOs. 664 and 661. Overall, *tufA* gene fragments were obtained from all 17 enterococcal species but *tufB* gene fragments were obtained with only 11 enterococcal species (Table 16).

The identities between *tufA* and *tufB* for each enterococcal species were 68-79% at the nucleotide level and 81 to 89% at the amino acid level. The *tufA* gene is highly conserved among all enterococcal species with identities varying from 87% to 99% for DNA and 93% to 99% for amino acid sequences, while the identities among *tufB* genes of enterococci varies from 77% to 92% for DNA and 91% to 99% for amino acid sequences, indicating their different origins and evolution (Table 18). Since *E. solitarius* has been transferred to the genus *Tetragenococcus*, which is also a low G+C gram-positive bacterium, our sequence comparison did not include this species as an enterococcus. G+C content of enterococcal *tufA*

sequences ranged from 40.8% to 43.1%, while that of enterococcal *tufB* sequences varied from 37.8% to 46.3%. Based on amino acid sequence comparison, the enterococcal *tufA* gene products share higher identities with those of *Abiotrophia adiacens*, *Bacillus subtilis*, *Listeria monocytogenes*, *S. aureus*, and *S. epidermidis*. On the other hand, the enterococcal *tufB* gene products share higher percentages of amino acid identity with the *tuf* genes of *S. pneumoniae*, *S. pyogenes* and *Lactococcus lactis* (Table 18).

In order to elucidate whether the two enterococcal *tuf* sequences encode genuine EF-Tu, the deduced amino acid sequences of both genes were aligned with other EF-Tu sequences available in SWISSPROT (Release 38). Sequence alignment demonstrated that both gene products are highly conserved and carry all conserved residues present in this portion of prokaryotic EF-Tu (Figure 4). Therefore, it appears that both gene products could fulfill the function of EF-Tu. The partial *tuf* gene sequences encode the portion of EF-Tu from residues 117 to 317, numbered as in *E. coli*. This portion makes up of the last four α -helices and two β -strands of domain I, the entire domain II and the N-terminal part of domain III on the basis of the determined structures of *E. coli* EF-Tu.

Based on the deduced amino acid sequences, the enterococcal *tufB* genes have unique conserved residues Lys129, Leu140, Ser230, and Asp234 (*E. coli* numbering) that are also conserved in streptococci and *L. lactis*, but not in the other bacteria (Figure 4). All these residues are located in loops except for Ser230. In other bacteria the residue Ser230 is substituted for highly conserved Thr, which is the 5th residue of the third β -strand of domain II. This region is partially responsible for the interaction between the EF-Tu and aminoacyl-tRNA by the formation of a deep pocket for any of the 20 naturally occurring amino acids. According to our three-dimensional model (data not illustrated), the substitution Thr230→Ser in domain II of EF-Tu may have little impact on the capability of the pocket to accommodate any amino acid. However, the high conservation of Thr230 comparing to the unique Ser substitution found only in streptococci and 11 enterococci could suggest a subtle functional role for this residue.

The *tuf* gene sequences obtained for *E. faecalis*, *S. aureus*, *S. pneumoniae* and *S. pyogenes* were compared with their respective incomplete genome sequence. Contigs with more than 99% identity were identified. Analysis of the *E. faecalis* genome data revealed that the single *E. faecalis tuf* gene is located within an *str* operon where *tuf* is preceded by *fus* that encodes the elongation factor G. This *str* operon is present in *S. aureus* and *B. subtilis* but not in the two streptococcal genomes examined. The 700-bp or so sequence upstream the *S. pneumoniae tuf* gene has no homology with any known gene sequences. In *S. pyogenes*, the gene upstream of *tuf* is similar to a cell division gene, *ftsW*, suggesting that the *tuf* genes in streptococci are not arranged in a *str* operon.

Phylogenetic analysis. Phylogenetic analysis of the *tuf* amino acid sequences with representatives of eubacteria, archeabacteria, and eukaryotes using neighbor-joining and maximum parsimony methods showed three major clusters representing the three kingdoms of life. Both methods gave similar topologies consistent with the rRNA gene data (data not shown). Within the bacterial clade, the tree is polyphyletic but *tufA* genes from all enterococcal species always clustered with those from other low G+C gram-positive bacteria (except for streptococci and lactococci), while the *tufB* genes of the 11 enterococcal species form a distinct cluster with streptococci and *L. lactis* (Figure 5). Duplicated genes from the same organism do not cluster together, thereby not suggesting evolution by recent gene duplication.

Southern hybridization. Southern hybridization of *Bgl*III/*Xba*I digested genomic DNA from 12 enterococcal species tested with the *tufA* probe (DIG-labeled *tufA* fragment from *E. faecium*) yielded two bands of different sizes in 9 species, which also carried two divergent *tuf* sequences according to their sequencing data. For *E. faecalis* and *E. solitarius*, a single band was observed indicating that one *tuf* gene is present (Figure 6). A single band was also found when digested genomic DNA from *S. aureus*, *S. pneumoniae*, and *S. pyogenes* were hybridized with the *tufA* probe (data not shown). For *E. faecium*, the presence of three bands can be explained by the existence of a *Xba*I restriction site in the

middle of the *tufA* sequence, which was confirmed by sequencing data. Hybridization with the *tufB* probe (DIG-labeled *tufB* fragment of *E. faecium*) showed a banding profile similar to the one obtained with the *tufA* probe (data not shown).

DISCUSSION

In this study, we have shown that two divergent copies of genes encoding the elongation factor Tu are present in some enterococcal species. Sequence data revealed that both genes are highly conserved at the amino acid level. One copy (*tufA*) is present in all enterococcal species, while the other (*tufB*) is present only in 11 of the 17 enterococcal species studied. Based on 16S rRNA sequence analysis, these 11 species are members of three different enterococcal subgroups (*E. avium*, *E. faecium*, and *E. gallinarum* species groups) and a distinct species (*E. dispar*). Moreover, 16S rDNA phylogeny suggests that these 11 species possessing 2 *tuf* genes all share a common ancestor before they further evolved to become the modern species. Since the six other species having only one copy diverged from the enterococcal lineage before that common ancestor, it appears that the presence of one *tuf* gene in these six species is not attributable to gene loss.

Two clusters of low G+C gram-positive bacteria were observed in the phylogenetic tree of the *tuf* genes: one contains a majority of low G+C gram-positive bacteria and the other contains lactococci and streptococci. This is similar to the finding on the basis of phylogenetic analysis of the 16S rRNA gene and the *hrcA* gene coding for a unique heat-shock regulatory protein. The enterococcal *tufA* genes branched with most of the low G+C gram-positive bacteria, suggesting that they originated from a common ancestor. On the other hand, the enterococcal *tufB* genes branched with the genera *Streptococcus* and *Lactococcus* that form a distinct lineage separated from other low G+C gram-positive bacteria (Figure 5). The finding that these EF-Tu proteins share some conserved amino acid residues unique to this branch also supports the idea that they may share a common ancestor. Although these conserved residues might result from convergent

evolution upon a specialized function, such convergence at the sequence level, even for a few residues, seems to be rare, making it an unlikely event. Moreover, no currently known selective pressure, if any, would account for keeping one versus two *tuf* genes in bacteria. The G+C contents of enterococcal *tufA* and *tufB* sequences are similar, indicating that they both originated from low G+C gram-positive bacteria, in accordance with the phylogenetic analysis.

The *tuf* genes are present in various copy numbers in different bacteria. Furthermore, the two *tuf* genes are normally associated with characteristic flanking genes. The two *tuf* gene copies commonly encountered within gram-negative bacteria are part of the bacterial *str* operon and tRNA-*tufB* operon, respectively. The arrangement of *tufA* in the *str* operon was also found in a variety of bacteria, including *Thermotoga maritima*, the most ancient bacteria sequenced so far, *Aquifex aeolicus*, cyanobacteria, *Bacillus* sp., *Micrococcus luteus*, *Mycobacterium tuberculosis*, and *Streptomyces* sp. Furthermore, the tRNA-*tufB* operon has also been identified in *Aquifex aeolicus*, *Thermus thermophilus*, and *Chlamydia trachomatis*. The two widespread *tuf* gene arrangements argue in favor of their ancient origins. It is noteworthy that most obligate intracellular parasites, such as *Mycoplasma* sp., *R. prowazekii*, *B. burgdorferi*, and *T. pallidum*, contain only one *tuf* gene. Their flanking sequences are distinct from the two conserved patterns as a result of selection for effective propagation by an extensive reduction in genome size by intragenomic recombination and rearrangement.

Most gram-positive bacteria with low G+C content sequenced to date contain only a single copy of the *tuf* gene as a part of the *str* operon. This is the case for *B. subtilis*, *S. aureus* and *E. faecalis*. PCR amplification using a primer targeting a conserved region of the *fus* gene and the *tufA*-specific primer SEQ ID NO. 660, but not the *tufB*-specific primer SEQ ID NO. 661, yielded the expected amplicons for all 17 enterococcal species tested, indicating the presence of the *fus-tuf* organization in all enterococci (data not shown). However, in the genomes of *S. pneumoniae* and *S. pyogenes*, the sequences flanking the *tuf* genes varies although the *tuf* gene itself remains highly conserved. The enterococcal *tufB* genes are

clustered with streptococci, but at present we do not have enough data to identify the genes flanking the enterococcal *tufB* genes. Furthermore, the functional role of the enterococcal *tufB* genes remains unknown. One can only postulate that the two divergent gene copies are expressed under different conditions.

The amino acid sequence identities between the enterococcal *tufA* and *tufB* genes are lower than either i) those between the enterococcal *tufA* and the *tuf* genes from other low G+C gram-positive bacteria (streptococci and lactococci excluded) or ii) those between the enterococcal *tufB* and streptococcal and lactococcal *tuf* genes. These findings suggest that the enterococcal *tufA* genes share a common ancestor with other low G+C gram-positive bacteria via the simple scheme of vertical evolution, while the enterococcal *tufB* genes are more closely related to those of streptococci and lactococci. The facts that some enterococci possess an additional *tuf* gene and that the single streptococcal *tuf* gene is not clustered with other low G+C gram-positive bacteria cannot be explained by the mechanism of gene duplication or intrachromosomal recombination. According to sequence and phylogenetic analysis, we propose that the presence of the additional copy of the *tuf* genes in 11 enterococcal species is due to horizontal gene transfer. The common ancestor of the 11 enterococcal species now carrying *tufB* genes acquired a *tuf* gene from an ancestral streptococcus or a streptococcus-related species during enterococcal evolution through gene transfer before the diversification of modern enterococci. Further study of the flanking regions of the gene may provide more clues for the origin and function of this gene in enterococci.

Recent studies of genes and genomes have demonstrated that considerable horizontal transfer occurred in the evolution of aminoacyl-tRNA synthetases in all three kingdoms of life. The heterogeneity of 16S rRNA is also attributable to horizontal gene transfer in some bacteria, such as *Streptomyces*, *Thermomonospora chromogena* and *Mycobacterium celatum*. In this study, we provide the first example in support of a likely horizontal transfer of the *tuf* gene encoding the elongation factor Tu. This may be an exception since stringent functional constraints do not allow for frequent horizontal transfer of the *tuf* gene as with

other genes. However, enterococcal *tuf* genes should not be the only such exception as we have noticed that the phylogeny of *Streptomyces tuf* genes is equally or more complex than that of enterococci. For example, the three *tuf*-like genes in a high G+C gram-positive bacterium, *S. ramocissimus*, branched with the *tuf* genes of phylogenetically divergent groups of bacteria (Figure 5). Another example may be the *tuf* genes in clostridia, which represent a phylogenetically very broad range of organisms and form a plethora of lines and groups of various complexities and depths. Four species belonging to three different clusters within the genus *Clostridium* have been shown by Southern hybridization to carry two copies of the *tuf* gene. Further sequence data and phylogenetic analysis may help interpreting the evolution of the elongation factor Tu in these gram-positive bacteria. Since the *tuf* genes and 16S rRNA genes are often used for phylogenetic study, the existence of duplicate genes originating from horizontal gene transfer may alter the phylogeny of microorganisms when the laterally acquired copy of the gene is used for such analysis. Hence, caution should be taken in interpreting phylogenetic data. In addition, the two *tuf* genes in enterococci have evolved separately and are distantly related to each other phylogenetically. The enterococcal *tufB* genes are less conserved and unique to the 11 enterococcal species only. We previously demonstrated that the enterococcal *tufA* genes could serve as a target to develop a DNA-based assay for identification of enterococci. The enterococcal *tufB* genes would also be useful in identification of these 11 enterococcal species.

EXAMPLE 43:

Elongation Factor Tu (*tuf*) and the F-ATPase beta-subunit (*atpD*) as phylogenetic tools for species of the family *Enterobacteriaceae*.

SUMMARY

The phylogeny of enterobacterial species commonly found in clinical samples was analyzed by comparing partial sequences of their elongation factor Tu (*tuf*) genes and their F-ATPase beta-subunit (*atpD*) genes. A 884-bp fragment for *tuf* and a 884- or 871-bp fragment for *atpD* were sequenced for 88 strains of 72 species from 25 enterobacterial genera. The *atpD* sequence analysis revealed a specific indel to *Pantoea* and *Tatumella* species showing for the first time a tight phylogenetic affiliation between these two genera. Comprehensive *tuf* and *atpD* phylogenetic trees were constructed and are in agreement with each other. Monophyletic genera are *Yersinia*, *Pantoea*, *Edwardsiella*, *Cedecea*, *Salmonella*, *Serratia*, *Proteus*, and *Providencia*. Analogous trees were obtained based on available 16S rDNA sequences from databases. *tuf* and *atpD* phylogenies are in agreement with the 16S rDNA analysis despite the smaller resolution power for the latter. In fact, distance comparisons revealed that *tuf* and *atpD* genes provide a better resolution for pairs of species belonging to the family *Enterobacteriaceae*. However, 16S rDNA distances are better resolved for pairs of species belonging to different families. In conclusion, *tuf* and *atpD* conserved genes are sufficiently divergent to discriminate different species inside the family *Enterobacteriaceae* and offer potential for the development of diagnostic tests based on DNA to identify enterobacterial species.

INTRODUCTION

Members of the family *Enterobacteriaceae* are facultatively anaerobic gram-negative rods, catalase-positive and oxydase-positive (Brenner, 1984). They are found in soil, water, plants, and in animals from insects to man. Many enterobacteria are opportunistic pathogens. In fact, members of this family are responsible for about 50 % of nosocomial infections in the United States (Brenner, 1984). Therefore, this family is of considerable clinical importance.

Major classification studies on the family *Enterobacteriaceae* are based on phenotypic traits (Brenner *et al.*, 1999; Brenner *et al.*, 1980; Dickey & Zumoff,

1988; Farmer III *et al.*, 1980; Farmer III *et al.*, 1985b; Farmer III *et al.*, 1985a) such as biochemical reactions and physiological characteristics. However, phenotypically distinct strains may be closely related by genotypic criteria and may belong to the same genospecies (Bercovier *et al.*, 1980; Hartl & Dykhuizen, 1984). Also, phenotypically close strains (biogroups) may belong to different genospecies, like *Klebsiella pneumoniae* and *Enterobacter aerogenes* (Brenner, 1984) for example. Consequently, identification and classification of certain species may be ambiguous with techniques based on phenotypic tests (Janda *et al.*, 1999; Kitch *et al.*, 1994; Sharma *et al.*, 1990).

More advances in the classification of members of the family *Enterobacteriaceae* have come from DNA-DNA hybridization studies (Brenner *et al.*, 1993; Brenner *et al.*, 1986; Brenner, *et al.*, 1980; Farmer III, *et al.*, 1980; Farmer III, *et al.*, 1985b; Izard *et al.*, 1981; Steigerwalt *et al.*, 1976). Furthermore, the phylogenetic significance of bacterial classification based on 16S rDNA sequences has been recognized by many workers (Stackebrandt & Goebel, 1994; Wayne *et al.*, 1987). However, members of the family *Enterobacteriaceae* have not been subjected to extensive phylogenetic analysis of 16S rDNA (Sproer *et al.*, 1999). In fact, this molecule was not thought to solve taxonomic problems concerning closely related species because of its very high degree of conservation (Brenner, 1992; Sproer, *et al.*, 1999). Another drawback of the 16S rDNA gene is that it is found in several copies within the genome (seven in *Escherichia coli* and *Salmonella typhimurium*) (Hill & Harnish, 1981). Due to sequence divergence between the gene copies, direct sequencing of PCR products is often not suitable to achieve a representative sequence (Cilia *et al.*, 1996; Hill & Harnish, 1981). Other genes such as *gap* and *ompA* (Lawrence *et al.*, 1991), *rpoB* (Mollet *et al.*, 1997), and *infB* (Hedegaard *et al.*, 1999) were used to resolve the phylogeny of enterobacteria. However, none of these studies covered an extensive number of species.

tuf and *atpD* are the genes encoding the elongation factor Tu (EF-Tu) and the F-ATPase beta-subunit, respectively. EF-Tu is involved in peptide chain formation (Ludwig *et al.*, 1990). The two copies of the *tuf* gene (*tufA* and *tufB*) found in enterobacteria (Sela *et al.*, 1989) share high identity level (99 %) in *Salmonella typhimurium* and in *E. coli*. The recombination phenomenon could explain sequence homogenization between the two copies (Abdulkarim & Hughes, 1996; Grunberg-Manago, 1996). F-ATPase is present on the plasma membranes of eubacteria (Nelson & Taiz, 1989). It functions mainly in ATP synthesis (Nelson & Taiz, 1989) and the beta-subunit contains the catalytic site of the enzyme. EF-Tu and F-ATPase are highly conserved throughout evolution and shows functional constancy (Amann *et al.*, 1988; Ludwig, *et al.*, 1990). Recently, phylogenies based on protein sequences from EF-Tu and F-ATPase beta-subunit showed good agreement with each other and with the rDNA data (Ludwig *et al.*, 1993).

We elected to sequence 884-bp fragments of *tuf* and *atpD* from 88 clinically relevant enterobacterial strains representing 72 species from 25 genera. These sequences were used to create phylogenetic trees that were compared with 16S rDNA trees. These trees revealed good agreement with each others and demonstrated the high resolution of *tuf* and *atpD* phylogenies at the species level.

MATERIALS AND METHODS

Bacterial strains and genomic material. All bacterial strains used in this study were obtained from the American Type Culture Collection (ATCC) or the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ). These enterobacteria can all be recovered from clinical specimens, but not all are pathogens. Whenever possible, we choose type strains. Identification of all strains was confirmed by classical biochemical tests using the automated system MicroScan WalkAway-96 system equipped with a Negative BP Combo Panel Type 15 (Dade Behring Canada). Genomic DNA was purified using the G NOME

DNA kit (Bio 101). Genomic DNA from *Yersinia pestis* was kindly provided by Dr. Robert R. Brubaker. Strains used in this study and their descriptions are shown in Table 19.

PCR primers. The eubacterial *tuf* and *atpD* gene sequences available from public databases were analyzed using the GCG package (version 8.0) (Genetics Computer Group). Based on multiple sequence alignments, two highly conserved regions were chosen for each genes, and PCR primers were derived from these regions with the help of Oligo primer analysis software (version 5.0) (National Biosciences). A second 5' primer was design to amplify the gene *atpD* for few enterobacteria difficult to amplifiy with the first primer set. When required, the primers contained inosines or degeneracies to account for variable positions. Oligonucleotide primers were synthesized with a model 394 DNA/RNA synthesizer (PE Applied Biosystems). PCR primers used in this study are listed in Table 20.

DNA sequencing. An 884-bp portion of the *tuf* gene and an 884-bp portion (or alternatively an 871-bp portion for a few enterobacterial strains) of the *atpD* gene were sequenced for all enterobacteria listed in the first strain column of Table 19. Amplification was performed with 4 ng of genomic DNA. The 40- μ l PCR mixtures used to generate PCR products for sequencing contained 1.0 μ M each primer, 200 μ M each deoxyribonucleoside triphosphate (Pharmacia Biotech), 10 mM Tris-HCl (pH 9.0 at 25 °C), 50 mM KCl, 0.1 % (w/v) Triton X-100, 2.5 mM MgCl₂, 0.05 mM BSA, 0.3 U of *Taq* DNA polymerase (Promega) coupled with TaqStartTM antibody (Clontech Laboratories). The TaqStartTM neutralizing monoclonal antibody for *Taq* DNA polymerase was added to all PCR mixtures to enhance efficiency of amplification (Kellogg *et al.*, 1994). The PCR mixtures were subjected to thermal cycling (3 min at 95 °C and then 35 cycles of 1 min at 95 °C, 1 min at 55 °C for *tuf* or 50 °C for *atpD*, and 1 min at 72 °C, with a 7-min final extension at 72 °C) using a PTC-200 DNA Engine thermocycler (MJ Research).

PCR products having the predicted sizes were recovered from an agarose gel stained for 15 min with 0.02 % of methylene blue followed by washing in sterile distilled water for 15 min twice (Flores *et al.*, 1992). Subsequently, PCR products having the predicted sizes were recovered from gels using the QIAquick gel extraction kit (QIAGEN).

Both strands of the purified amplicons were sequenced using the ABI Prism BigDye Terminator Cycle Sequencing Ready Reaction Kit (PE Applied Biosystems) on an automated DNA sequencer (Model 377). Amplicons from two independent PCR amplifications were sequenced for each strain to ensure the absence of sequencing errors attributable to nucleotide misincorporations by the *Taq* DNA polymerase. Sequence assembly was performed with the aid of Sequencher 3.0 software (Gene Codes).

Phylogenetic analysis. Multiple sequence alignments were performed using PileUp from the GCG package (Version 10.0) (Genetics Computer Group) and checked by eye with the editor SeqLab to edit sequences if necessary and to note which regions were to be excluded for phylogenetic analysis. *Vibrio cholerae* and *Shewanella putrefaciens* were used as outgroups. Bootstrap subsets (750 sets) and phylogenetic trees were generated with the Neighbor Joining algorithm from Dr. David Swofford's PAUP (Phylogenetic Analysis Using Parsimony) Software version 4.0b4 (Sinauer Associates) and with tree-bisection branch-swapping. The distance model used was Kimura (1980) two-parameter. Relative rate test was performed with the aid of Phyltest program version 2.0 (c).

RESULTS AND DISCUSSION

DNA amplification, sequencing and sequence alignments

A PCR product of the expected size of 884 bp was obtained for *tuf* and of 884 or 871 bp for *atpD* from all bacterial strains tested. After subtracting for biased

primer regions and ambiguous single strand data, sequences of at least 721 bp for *tuf* and 713 bp for *atpD* were submitted to phylogenetic analyses. These sequences were aligned with *tuf* and *atpD* sequences available in databases to verify that the nucleotide sequences indeed encoded a part of tested genes. Gaps were excluded to perform phylogenetic analysis.

Signature sequences

From the sequence alignments obtained from both tested genes, only one insertion was observed. This five amino acids insertion is located between the positions 325 and 326 of *atpD* gene of *E. coli* strain K-12 (Saraste *et al.*, 1981) and can be considered a signature sequence of *Tatumella ptyseos* and *Pantoea* species (Fig. 7). The presence of a conserved indel of defined length and sequence and flanked by conserved regions could suggest a common ancestor, particularly when members of a given taxa share this indel (Gupta, 1998). To our knowledge, high relatedness between the genera *Tatumella* and *Pantoea* is demonstrated for the first time.

Enterobacter agglomerans ATCC 27989 sequence does not possess the five amino acid indel (Fig. 7). This indel could represent a useful marker to help resolve the *Enterobacter agglomerans* and *Pantoea* classification. Indeed, the transfer of *Enterobacter agglomerans* to *Pantoea agglomerans* was proposed in 1989 by Gavini *et al.* (Gavini *et al.*, 1989). However, some strains are provisionally classified as *Pantoea* sp. until their interrelatedness is elucidated (Gavini, *et al.*, 1989). Since the transfer was proposed, the change of nomenclature has not yet been made for all *Enterobacter agglomerans* in the ATCC database. The absence of the five amino acids indel suggests that some strains of *Enterobacter agglomerans* most likely do not belong to the genus *Pantoea*.

Phylogenetic trees based on partial *tuf* sequences, *atpD* sequences, and published 16S rDNA data of members of the *Enterobacteriaceae*.

Representative trees constructed from *tuf* and *atpD* sequences with the neighbor-joining method are shown in Fig. 8. The phylogenetic trees generated from partial *tuf* sequences and *atpD* sequences are very similar. Nevertheless, *atpD* tree shows more monophyletic groups corresponding to species that belong to the same genus. These groups are more consistent with the actual taxonomy. For both genes, some genera are not monophyletic. These results support previous phylogenies based on the genes *gap* and *ompA* (Lawrence, *et al.*, 1991), *rpoB* (Mollet, *et al.*, 1997), and *infB* (Hedegaard, *et al.*, 1999) which all showed that the genera *Escherichia* and *Klebsiella* are polyphyletic. There were few differences in branching between *tuf* and *atpD* genes.

Even though *Pantoea agglomerans* and *Pantoea dispersa* indels were excluded for phylogenetic analysis, these two species grouped together and were distant from *Enterobacter agglomerans* ATCC 27989, adding another evidence that the latter species is heterogenous and that not all members of this species belong to the genus *Pantoea*. In fact, the *E. agglomerans* strain ATCC 27989 exhibits branch lengths similar to others *Enterobacter* species with both genes. Therefore, we suggest that this strain belong to the genus *Enterobacter* until further reclassification of that genus.

tuf and *atpD* trees exhibit very short genetic distances between taxa belonging to the same genetic species including species segregated for clinical considerations. This first concern *E. coli* and *Shigella* species that were confirmed to be the same genetic species by hybridization studies (Brenner *et al.*, 1972; Brenner *et al.*, 1972; Brenner *et al.*, 1982) and phylogenies based on 16S rDNA (Wang *et al.*, 1997) and *rpoB* genes (Mollet, *et al.*, 1997). Hybridization studies (Bercovier, *et al.*, 1980) and phylogeny based on 16S rDNA genes (Ibrahim *et al.*, 1994) demonstrated also that *Yersinia pestis* and *Y. pseudotuberculosis* are the same genetic species. Among

Yersinia pestis and *Y. pseudotuberculosis*, the three *Klebsiella pneumoniae* subspecies, *E. coli-Shigella* species, and *Salmonella choleraesuis* subspecies, *Salmonella* is a less tightly knit species than the other genetic species. The same is true for *E. coli* and *Shigella* species.

Escherichia fergusonii is very close to *E. coli-Shigella* genetic species. This observation is corroborated by 16S rDNA phylogeny (McLaughlin *et al.*, 2000) but not by DNA hybridization values. In fact, *E. fergusonii* is only 49% to 63% related to *E. coli-Shigella* (Farmer III, *et al.*, 1985b). It was previously observed that very recently diverged species may not be recognizable based on 16S rDNA sequences although DNA hybridization established them as different species (Fox *et al.*, 1992). Therefore, *E. fergusonii* could be a new “quasi-species”.

atpD phylogeny revealed *Salmonella* subspecies divisions consistent with the actual taxonomy. This result was already observed by Christensen *et al.* (Christensen & Olsen, 1998). Nevertheless, *tuf* partial sequences discriminate less than *atpD* between *Salmonella* subspecies.

Overall, *tuf* and *atpD* phylogenies exhibit enough divergence between species to ensure efficient discrimination. Therefore, it could be easy to distinguish phenotypically close enterobacteria belonging to different genetic species such as *Klebsiella pneumoniae* and *Enterobacter aerogenes*.

Phylogenetic relationships between *Salmonella*, *E. coli* and *C. freundii* are not well defined. 16S rDNA and 23S rDNA sequence data reveals a closer relationship between *Salmonella* and *E. coli* than between *Salmonella* and *C. freundii* (Christensen *et al.*, 1998), while DNA homology studies (Selander *et al.*, 1996) and *infB* phylogeny (Hedegaard, *et al.*, 1999) showed that *Salmonella* is more closely related to *C. freundii* than to *E. coli*. In that regard, *tuf* and *atpD* phylogenies are coherent with 16S rDNA and 23S rDNA sequence analysis.

Phylogenetic analyses were also performed using amino acids sequences. *tuf* tree based on amino acids is characterized by a better resolution between taxa outgroup and taxa ingroup (enterobacteria) than tree based on nucleic acids whereas *atpD* trees based on amino acids and nucleic acids give almost the same resolution between taxa outgroup and ingroup (data not shown).

Relative rate test (or two cluster test (Takezaki *et al.*, 1995)) evaluates if evolution is constant between two taxa. Before to apply the test, the topology of a tree is determined by tree-building method without the assumption of rate constancy. Therefore, two taxa (or two groups of taxa) are compared with a third taxon that is an outgroup of the first two taxa (Takezaki, *et al.*, 1995). Few pairs of taxa that exhibited a great difference between their branch lengths at particular nodes were chosen to perform the test. This test reveals that *tuf* and *atpD* are not constant in their evolution within the family *Enterobacteriaceae*. For *tuf*, for example, the hypothesis of rate constancy is rejected (Z value higher than 1.96) between *Yersinia* species. The same is true for *Proteus* species. For *atpD*, for example, evolution is not constant between *Proteus* species, between *Proteus* species and *Providencia* species, and between *Yersinia* species and *Escherichia coli*. For 16S rDNA, for example, evolution is not constant between two *E. coli*, between *E. coli* and *Enterobacter aerogenes*, and between *E. coli* and *Proteus vulgaris*. These results suggest that *tuf*, *atpD* and 16S rDNA could not serve as a molecular clock for the entire family *Enterobacteriaceae*.

Since the number and the nature of taxa can influence topology of trees, phylogenetic trees from *tuf* and *atpD* were reconstructed using sequences corresponding to strains for which 16S rDNA genes were published in GenEMBL. These trees were similar to those generated using 16S rDNA (Fig. 9). Nevertheless, 16S rDNA tree gave poorer resolution power than *tuf* and *atpD* gene trees. Indeed, these latter exhibited less multifurcation (polytomy) than the 16S rDNA tree.

Comparison of distances based on *tuf*, *atpD*, and 16S rDNA data.

tuf, *atpD*, and 16S rDNA distances (i.e. the number of differences per nucleotide site) were compared with each other for each pair of strains. We found that the *tuf* and *atpD* distances were respectively 2.268 ± 0.965 and 2.927 ± 0.896 times larger than 16S rDNA distances (Fig. 10a and b). *atpD* distances were 1.445 ± 0.570 times larger than *tuf* distances (Fig. 10c). Figure 10 also shows that the *tuf*, *atpD*, and 16S rDNA distances between members of different species of the same genus (0.053 ± 0.034 , 0.060 ± 0.020 , and 0.024 ± 0.010 , respectively) were in mean smaller than the distances between members of different genera belonging to the same family (0.103 ± 0.053 , 0.129 ± 0.051 , and 0.044 ± 0.013 , respectively). However, the overlap exhibits with standard deviations add to a focus of evidences that some enterobacterial genera are not well defined (Brenner, 1984). In fact, many distances for pairs of species especially belonging to the genera *Escherichia*, *Shigella*, *Enterobacter*, *Citrobacter*, *Klebsiella*, and *Kluyvera* overlap distances for pairs of species belonging to the same genus (Fig. 10). For example, distances for pairs composed by species of *Citrobacter* and species of *Klebsiella* overlap distances for pairs composed by two *Citrobacter* or by two *Klebsiella*.

Observing the distance distributions, 16S rDNA distances reveal a clear separation between the families *Enterobacteriaceae* and *Vibrionaceae* despite the fact that the family *Vibrionaceae* is genetically very close to the *Enterobacteriaceae* (Fig. 10a and b). Nevertheless, *tuf* and *atpD* show higher discriminating power below the family level (Fig. 10a and b).

There were some discrepancies in the relative distances for the same pairs of taxa between the two genes studied. First, distances between *Yersinia* species are at least two times lower for *atpD* than for *tuf* (Fig. 10c). Also, distances at the family level (between *Enterobacteriaceae* and *Vibrionaceae*) show that *Enterobacteriaceae* is a tightlier knit family with *atpD* gene (*Proteus* genus

excepted) than with *tuf* gene. Both genes well delineate taxa belonging to the same species. There is one exception with *atpD*: *Klebsiella planticola* and *K. ornithinolithica* belong to the same genus but fit with taxa belonging to the same species (Fig. 10a and c). These two species are also very close genotypically with *tuf* gene. This suggest that *Klebsiella planticola* and *K. ornithinolithica* could be two newborn species. *tuf* and *atpD* genes exhibit little distances between *Escherichia fergusonii* and *E. coli-Shigella* species. Unfortunately, comparison with 16S rDNA could not be achieved because the *E. fergusonii* 16S rDNA sequence is not yet accessible in GenEMBL database. Therefore, the majority of phenotypically close enterobacteria could be easily discriminated genotypically using *tuf* and *atpD* gene sequences.

In conclusion, *tuf* and *atpD* genes exhibit phylogenies consistent with 16S rDNA genes phylogeny. For example, they reveal that the family *Enterobacteriaceae* is monophyletic. Moreover, *tuf* and *atpD* distances provide a higher discriminating power than 16S rDNA distances. In fact, *tuf* and *atpD* genes discriminate well between different genospecies and are conserved between strains of the same genetic species in such a way that primers and molecular probes for diagnostic purposes could be designed. Preliminary studies support these observations and diagnostic tests based on *tuf* and *atpD* sequence data to identify enterobacteria are currently under development.

EXAMPLE 44:

Testing new pairs of PCR primers selected from two species-specific genomic DNA fragments which are objects of our assigned US patent 6,001,564

Objective: The goal of these experiments is to demonstrate that it is relatively easy for a person skilled in the art to find other PCR primer pairs from the species-specific

fragments used as targets for detection and identification of a variety of microorganisms. In fact, we wish to prove that the PCR primers previously tested by our group and which are objects of the present patent application are not the only possible good choices for diagnostic purposes. For this example, we used diagnostic targets described in our assigned US patent 6,001,564.

Experimental strategy: We have selected randomly two species-specific genomic DNA fragments for this experiment. The first one is the 705-bp fragment specific to *Staphylococcus epidermidis* (SEQ ID NO: 36 from US patent 6,001,564) while the second one is the 466-bp fragment specific to *Moraxella catarrhalis* (SEQ ID NO: 29 from US patent 6,001,564). Subsequently, we have selected from these two fragments a number of PCR primer pairs other than those previously tested. We have chosen 5 new primer pairs from each of these two sequences which are well dispersed along the DNA fragment (Figures 11 and 12). We have tested these primers for their specificity and compared them with the original primers previously tested. For the specificity tests, we have tested all bacterial species closely related to the target species based on phylogenetic analysis with three conserved genes (rRNA genes, *tuf* and *atpD*). The rationale for selecting a restricted number of bacterial species to evaluate the specificity of the new primer pairs is based on the fact that the lack of specificity of a DNA-based assay is attributable to the detection of closely related species which are more similar at the nucleotide level. Based on the phylogenetic analysis, we have selected (i) species from the closely related genus *Staphylococcus*, *Enterococcus*, *Streptococcus* and *Listeria* to test the specificity of the *S. epidermidis*-specific PCR assays and (ii) species from the closely related genus *Moraxella*, *Kingella* and *Neisseria* to test the specificity of the *M. catarrhalis*-specific PCR assays.

Materials and methods

Bacterial strains. All bacterial strains used for these experiments were obtained from the American Type Culture Collection (ATCC, Rockville, MD).

Genomic DNA isolation. Genomic DNA was purified from the ATCC reference strains by using the G-nome DNA kit (Bio 101 Inc., Vista, CA).

Oligonucleotide design and synthesis. PCR primers were designed with the help of the OligoTM primer analysis software Version 4.0 (National Biosciences Inc., Plymouth, Minn.) and synthesized using a model 391 DNA synthesizer (Applied Biosystems, Foster City, CA).

PCR assays. All PCR assays were performed by using genomic DNA purified from reference strains obtained from the ATCC. One μ l of purified DNA preparation (containing 0.01 to 1 ng of DNA per μ l) was added directly into the PCR reaction mixture. The 20 μ L PCR reactions contained final concentrations of 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl₂, 0.4 μ M of each primer, 200 μ M of each of the four dNTPs and 0.5 unit of *Taq* DNA polymerase (Promega, Madison, WI) combined with the TaqStartTM antibody (Clontech Laboratories Inc., Palo Alto, CA). An internal control was integrated into all amplification reactions to verify the efficiency of the amplification reaction as well as to ensure that significant PCR inhibition was absent. Primers amplifying a region of 252 bp from a control plasmid added to each amplification reaction were used to provide the internal control. PCR reactions were then subjected to thermal cycling (3 min at 95°C followed by 30 cycles of 1 second at 95°C for the denaturation step and 30 seconds at 50 to 65°C for the annealing-extension step) using a PTC-200 thermal cycler (MJ Research Inc., Watertown, MA). PCR amplification products were then analyzed by standard agarose gel (2%) electrophoresis. Amplification products were visualized in agarose gels containing 0.25 μ g/mL of ethidium bromide under UV at 254 nm.

Results

Tables 21 and 22 show the results of specificity tests with the 5 new primer pairs selected from SEQ ID NO: 29 (specific to *M. catarrhalis* from US patent 6,001,564) and SEQ ID NO: 36 (specific to *S. epidermidis* from US patent 6,001,564), respectively. In order to evaluate the performance of these new primers pairs, we compared them in parallel with the original primer pairs previously tested.

For *M. catarrhalis*, all of the 5 selected PCR primer pairs were specific for the target species because none of the closely related species could be amplified (Table 21). In fact, the comparison with the original primer pair SEQ ID NO: 118 + SEQ ID NO: 119 (from US patent 6,001,564) revealed that all new pairs showed identical results in terms of specificity and sensitivity thereby suggesting their suitability for diagnostic purposes.

For *S. epidermidis*, 4 of the 5 selected PCR primer pairs were specific for the target species (Table 22). It should be noted that for 3 of these four primer pairs the annealing temperature had to be increased from 55 °C to 60 or 65 °C to attain specificity for *S. epidermidis*. Again the comparison with the original primer pair SEQ ID NO: 145 + SEQ ID NO: 146 (from US patent 6,001,564) revealed that these four primer pairs were as good as the original pair. Increasing the annealing temperature for the PCR amplification is well known by persons skilled in the art to be a very effective way to improve the specificity of a PCR assay (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.; Ehrlich and Greenberg, 1994, PCR-based Diagnostics in Infectious Disease, Blackwell Scientific Publications, Boston, MA). In fact, those skilled in the art are well aware of the fact that the annealing temperature is critical for the optimization of PCR assays. Only the primer pair VBsep3 + VBsep4 amplified bacterial species other than *S. epidermidis* including the staphylococcal species *S. capitis*, *S. cohnii*, *S. aureus*, *S. haemolyticus* and *S. hominis* (Table 22). For this non-specific primer pair, increasing the annealing temperature

from 55 to 65 °C was not sufficient to attain the desired specificity. One possible explanation for the fact that it appears slightly easier to select species-specific primers for *M. catarrhalis* than for *S. epidermidis* is that *M. catarrhalis* is more isolated in phylogenetic trees than *S. epidermidis*. The large number of coagulase negative staphylococcal species such as *S. epidermidis* is largely responsible for this phylogenetic clustering.

Conclusion

These experiment clearly show that it is relatively easy for a person skilled in the art to select, from the species-specific DNA fragments selected as target for identification, PCR primer pairs suitable for diagnostic purposes other than those previously tested. The amplification conditions can be optimize by modifying critical variables such as the annealing temperature to attain the desired specificity and sensitivity. Consequently, we consider that it is legitimate to claim any possible primer sequences selected from the species-specific fragment and that it would be unfair to grant only the claims dealing with the primer pairs previously tested. By extrapolation, these results strongly suggest that it is also relatively easy for a person skilled in the art to select, from the species-specific DNA fragments, DNA probes suitable for diagnostic purposes other than those previously tested.

EXAMPLE 45:

Testing modified versions of PCR primers derived from the sequence of several primers which are objects of US patent 6,001,564.

Objective: The purpose of this project is to verify the efficiency of amplification by modified PCR primers derived from primers previously tested. The types of primer modifications to be tested include (i) variation of the sequence at one or more nucleotide positions and (ii) increasing or reducing the length of the primers. For this example, we used diagnostic targets described in US patent 6,001,564.

Experimental strategy:

a) Testing primers with nucleotide changes

We have designed 13 new primers which are derived from the *S. epidermidis*-specific SEQ ID NO: 146 from US patent 6,001,564 (Table 23). These primers have been modified at one or more nucleotide positions. As shown in Table 23, the nucleotide changes were introduced all along the primer sequence. Furthermore, instead of modifying the primer at any nucleotide position, the nucleotide changes were introduced at the third position of each codon to better reflect potential genetic variations *in vivo*. It should be noted that no nucleotide changes were introduced at the 3' end of the oligonucleotide primers because those skilled in the art are well aware of the fact that mismatches at the 3' end should be avoided (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). All of these modified primers were tested in PCR assays in combination with SEQ ID NO: 145 from US patent 6,001,564 and the efficiency of the amplification was compared with the original primer pair SEQ ID NO: 145 + SEQ ID NO: 146 previously tested in US patent 6,001,564.

b) Testing shorter or longer versions of primers

We have designed shorter and longer versions of the original *S. epidermidis*-specific PCR primer pair SEQ ID NO: 145 + 146 from US patent 6,001,564 (Table 24) as well as shorter versions of the original *P. aeruginosa*-specific primer pair SEQ ID NO: 83 + 84 from US patent 6,001,564 (Table 25). As shown in Tables 24 and 25, both primers of each pair were shortened or lengthen to the same length. Again, those skilled in the art know that the melting temperature of both primers from a pair should be similar to avoid preferential binding at one primer binding site which is

detrimental in PCR (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.; Ehrlich and Greenberg, 1994, PCR-based Diagnostics in Infectious Disease, Blackwell Scientific Publications, Boston, MA). All of these shorter or longer primer versions were tested in PCR assays and the efficiency of the amplification was compared with the original primer pair SEQ ID NOs 145 and 146.

Materials and methods

See the Materials and methods section of Example 44.

Results

a) Testing primers with nucleotide changes

The results of the PCR assays with the 13 modified versions of SEQ ID NO: 146 from US patent 6,001,564 are shown in Table 23. The 8 modified primers having a single nucleotide variation showed an efficiency of amplification identical to the original primer pair based on testing with 3 different dilutions of genomic DNA. The four primers having two nucleotide variations and primer VBmut12 having 3 nucleotide changes also showed PCR results identical to those obtained with the original pair. Finally, primer VBmut13 with four nucleotide changes showed a reduction in sensitivity by approximately one log as compared with the original primer pair. However, reducing the annealing temperature from 55 to 50 °C gave an efficiency of amplification very similar to that observed with the original primer pair (Table 23). In fact, reducing the annealing temperature of PCR cycles represents an effective way to reduce the stringency of hybridization for the primers and consequently allows the binding of probes with mismatches (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). Subsequently, we have confirmed the

specificity of the PCR assays with each of these 13 modified versions of SEQ ID NO: 146 from US patent 6,001,564 by performing amplifications from all bacterial species closely related to *S. epidermidis* which are listed in Table 22.

b) Testing shorter or longer versions of primers

For these experiments, two primer pairs were selected: i) SEQ ID NO: 145 + 146 from US patent 6,001,564 (specific to *S. epidermidis*) which are AT rich and ii) SEQ ID NO: 83 + 84 (specific to *P. aeruginosa*) which are GC rich. For the AT rich sequence, primers of 15 to 30 nucleotide in length were designed (Table 24) while for the GC rich sequences, primers of 13 to 19 nucleotide in length were designed (Table 25).

Table 24 shows that, for an annealing temperature of 55 °C, the 30- 25-, 20- and 17-nucleotide versions of SEQ ID NO: 145 and 146 from US patent 6,001,564 all showed identical results as compared with the original primer pair except that the 17-nucleotide version amplified slightly less efficiently the *S. epidermidis* DNA. Reducing the annealing temperature from 55 to 45 °C for the 17-nucleotide version allowed to increase the amplification efficiency to a level very similar to that with the original primer pair (SEQ ID NO: 145 + 146 from US patent 6,001,564). Regarding the 15-nucleotide version, there was amplification of *S. epidermidis* DNA only when the annealing temperature was reduced to 45 °C. Under those PCR conditions the assay remained *S. epidermidis*-specific but the amplification signal with *S. epidermidis* DNA was slightly lower as compared with the original primer pair. Subsequently, we have further confirmed the specificity of the shorter or longer versions by amplifying DNA from all bacterial species closely related to *S. epidermidis* which are listed in Table 22.

Table 25 shows that, for an annealing temperature of 55 °C, all shorter versions of SEQ ID NO: 83 and 84 from US patent 6,001,564 showed identical PCR results as

compared with the original primer pair. As expected, these results show that it is simpler to reduce the length of GC rich as compared with AT rich. This is attributable to the fact that GC binding is more stable than AT binding.

Conclusion

a) Testing primers with nucleotide changes

The above experiments clearly show that PCR primers may be modified at one or more nucleotide positions without affecting the specificity and the sensitivity of the PCR assay. These results strongly suggest that a given oligonucleotide can detect variant genomic sequences from the target species. In fact, the nucleotide changes in the selected primers were purposely introduced at the third position of each codon to mimic nucleotide variation in genomic DNA. Thus we conclude that it is justified to claim "a variant thereof" for i) the SEQ IDs of the fragments and oligonucleotides which are object of the present patent application and ii) genomic variants of the target species.

b) Testing shorter or longer versions of primers

The above experiments clearly show that PCR primers may be shorter or longer without affecting the specificity and the sensitivity of the PCR assay. We have showed that oligonucleotides ranging in sizes from 13 to 30 nucleotides may be as specific and sensitive as the original primer pair from which they were derived. Consequently, these results suggest that it is not exaggerated to claim sequences having at least 12 nucleotide in length.

This invention has been described herein above, and it is readily apparent that modifications can be made thereto without departing from the spirit of this invention. These modifications are under the scope of this invention, as defined in the appended claims.

Table 1. Distribution (%) of nosocomial pathogens for various human infections in USA (1990-1992)¹.

Pathogen	UTI ²	SSI ³	BSI ⁴	Pneumonia	CSF ⁵
<i>Escherichia coli</i>	27	9	5	4	2
<i>Staphylococcus aureus</i>	2	21	17	21	2
<i>Staphylococcus epidermidis</i>	2	6	20	0	1
<i>Enterococcus faecalis</i>	16	12	9	2	0
<i>Enterococcus faecium</i>	1	1	0	0	0
<i>Pseudomonas aeruginosa</i>	12	9	3	18	0
<i>Klebsiella pneumoniae</i>	7	3	4	9	0
<i>Proteus mirabilis</i>	5	3	1	2	0
<i>Streptococcus pneumoniae</i>	0	0	3	1	18
Group B <i>Streptococci</i>	1	1	2	1	6
Other streptococci	3	5	2	1	3
<i>Haemophilus influenzae</i>	0	0	0	6	45
<i>Neisseria meningitidis</i>	0	0	0	0	14
<i>Listeria monocytogenes</i>	0	0	0	0	3
Other enterococci	1	1	0	0	0
Other staphylococci	2	8	13	2	0
<i>Candida albicans</i>	9	3	5	5	0
Other <i>Candida</i>	2	1	3	1	0
<i>Enterobacter</i> sp.	5	7	4	12	2
<i>Acinetobacter</i> sp.	1	1	2	4	2
<i>Citrobacter</i> sp.	2	1	1	1	0
<i>Serratia marcescens</i>	1	1	1	3	1
Other <i>Klebsiella</i>	1	1	1	2	1
Others	0	6	4	5	0

¹ Data recorded by the National Nosocomial Infections Surveillance (NNIS) from 80 hospitals (Emori and Gaynes, 1993, *Clin. Microbiol. Rev.*, 6:428-442).

² Urinary tract infection.

³ Surgical site infection.

⁴ Bloodstream infection.

⁵ Cerebrospinal fluid.

Table 2. Distribution (%) of bloodstream infection pathogens in Quebec (1995), Canada (1992), UK (1969-1988) and USA (1990-1992).

5	Organism	Quebec ¹	Canada ²	UK ³	USA ⁴	
				Community-acquired	Hospital-acquired	Hospital-acquired
	<i>E. coli</i>	15.6	53.8	24.8	20.3	5.0
10	<i>S. epidermidis</i> and other CoNS ⁵	25.8	-	0.5	7.2	31.0
	<i>S. aureus</i>	9.6	-	9.7	19.4	16.0
	<i>S. pneumoniae</i>	6.3	-	22.5	2.2	-
	<i>E. faecalis</i>	3.0	-	1.0	4.2	-
15	<i>E. faecium</i>	2.6	-	0.2	0.5	-
	<i>Enterococcus</i> sp.	-	-	-	9.0	
	<i>H. influenzae</i>	1.5	-	3.4	0.4	-
	<i>P. aeruginosa</i>	1.5	8.2	1.0	8.2	3.0
	<i>K. pneumoniae</i>	3.0	11.2	3.0	9.2	4.0
20	<i>P. mirabilis</i>	-	3.9	2.8	5.3	1.0
	<i>S. pyogenes</i>	-	-	1.9	0.9	-
	<i>Enterobacter</i> sp.	4.1	5.5	0.5	2.3	4.0
	<i>Candida</i> sp.	8.5	-	-	1.0	8.0
	Others	18.5	17.4	28.7	18.9	19.0

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- ¹ Data obtained for 270 isolates collected at the Centre Hospitalier de l'Université Laval (CHUL) during a 5 month period (May to October 1995).
- ² Data from 10 hospitals throughout Canada representing 941 gram-negative isolates. (Chamberland *et al.*, 1992, *Clin. Infect. Dis.*, 15:615-628).
- 30 ³ Data from a 20-year study (1969-1988) for nearly 4000 isolates. (Eykyn *et al.*, 1990, *J. Antimicrob. Chemother.*, Suppl. C, 25:41-58).
- ⁴ Data recorded by the National Nosocomial Infections Surveillance (NNIS) from 80 hospitals (Emori and Gaynes, 1993, *Clin. Microbiol. Rev.*, 6:428-442).
- ⁵ Coagulase-negative staphylococci.

Table 3. Distribution of positive and negative clinical specimens tested at the microbiology laboratory of the CHUL (February 1994 – January 1995).

5	Clinical specimens and/or sites	No. of samples tested (%)	% of positive specimens	% of negative specimens
	Urine	17,981 (54.5)	19.4	80.6
	Blood culture/marrow	10,010 (30.4)	6.9	93.1
	Sputum	1,266 (3.8)	68.4	31.6
10	Superficial pus	1,136 (3.5)	72.3	27.7
	Cerebrospinal fluid	553 (1.7)	1.0	99.0
	Synovial fluid	523 (1.6)	2.7	97.3
	Respiratory tract	502 (1.5)	56.6	43.4
	Deep pus	473 (1.4)	56.8	43.2
15	Ears	289 (0.9)	47.1	52.9
	Pleural and pericardial fluid	132 (0.4)	1.0	99.0
	Peritoneal fluid	101(0.3)	28.6	71.4
	Total:	32,966 (100.0)	20.0	80.0

Table 4. Example of microbial species for which *tuf* and/or *atpD* and/or *recA* nucleic acids and/or sequences are used in the present invention.

5	Bacterial species	
	<i>Abiotrophia adiacens</i>	<i>Brevibacterium flavum</i>
	<i>Abiotrophia defectiva</i>	<i>Brevundimonas diminuta</i>
	<i>Achromobacter xylosoxidans</i> subsp. <i>denitrificans</i>	65 <i>Buchnera aphidicola</i>
10	<i>Acetobacterium woodi</i>	<i>Budvicia aquatica</i>
	<i>Acetobacter aceti</i>	<i>Burkholderia cepacia</i>
	<i>Acetobacter altoacetigenes</i>	<i>Burkholderia mallei</i>
	<i>Acetobacter polyoxogenes</i>	<i>Burkholderia pseudomallei</i>
	<i>Acholeplasma laidlawii</i>	70 <i>Buttiauxella agrestis</i>
15	<i>Acidothermus cellulolyticus</i>	<i>Butyrivibrio fibrisolvens</i>
	<i>Acidiphilum facilis</i>	<i>Campylobacter coli</i>
	<i>Acinetobacter baumannii</i>	<i>Campylobacter curvus</i>
	<i>Acinetobacter calcoaceticus</i>	<i>Campylobacter fetus</i> subsp. <i>fetus</i>
	<i>Acinetobacter lwoffii</i>	75 <i>Campylobacter fetus</i> subsp. <i>venerealis</i>
20	<i>Actinomyces meyeri</i>	<i>Campylobacter gracilis</i>
	<i>Aerococcus viridans</i>	<i>Campylobacter jejuni</i>
	<i>Aeromonas hydrophila</i>	<i>Campylobacter jejuni</i> subsp. <i>doylei</i>
	<i>Aeromonas salmonicida</i>	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i>
	<i>Agrobacterium radiobacter</i>	80 <i>Campylobacter lari</i>
25	<i>Agrobacterium tumefaciens</i>	<i>Campylobacter rectus</i>
	<i>Alcaligenes faecalis</i> subsp. <i>faecalis</i>	<i>Campylobacter sputorum</i> subsp. <i>sputorum</i>
	<i>Allochromatium vinosum</i>	<i>Campylobacter upsaliensis</i>
	<i>Anabaena variabilis</i>	<i>Cedecea davisae</i>
	<i>Anacystis nidulans</i>	85 <i>Cedecea lapagei</i>
30	<i>Anaerorhabdus furcosus</i>	<i>Cedecea neteri</i>
	<i>Aquifex aeolicus</i>	<i>Chlamydia pneumoniae</i>
	<i>Aquifex pyrophilus</i>	<i>Chlamydia psittaci</i>
	<i>Arcanobacterium haemolyticum</i>	<i>Chlamydia trachomatis</i>
	<i>Archaeoglobus fulgidus</i>	90 <i>Chlorobium vibrioforme</i>
35	<i>Azotobacter vinelandii</i>	<i>Chloroflexus aurantiacus</i>
	<i>Bacillus anthracis</i>	<i>Chryseobacterium meningosepticum</i>
	<i>Bacillus cereus</i>	<i>Citrobacter amalonaticus</i>
	<i>Bacillus firmus</i>	<i>Citrobacter braakii</i>
	<i>Bacillus halodurans</i>	95 <i>Citrobacter farmeri</i>
40	<i>Bacillus megaterium</i>	<i>Citrobacter freundii</i>
	<i>Bacillus mycoides</i>	<i>Citrobacter koseri</i>
	<i>Bacillus pseudomycoides</i>	<i>Citrobacter sedlakii</i>
	<i>Bacillus stearothermophilus</i>	<i>Citrobacter werkmanii</i>
	<i>Bacillus subtilis</i>	100 <i>Citrobacter youngae</i>
45	<i>Bacillus thuringiensis</i>	<i>Clostridium acetobutylicum</i>
	<i>Bacillus weihenstephanensis</i>	<i>Clostridium beijerinckii</i>
	<i>Bacteroides distasonis</i>	<i>Clostridium bifermentans</i>
	<i>Bacteroides fragilis</i>	<i>Clostridium botulinum</i>
	<i>Bacteroides forsythus</i>	105 <i>Clostridium difficile</i>
50	<i>Bacteroides ovatus</i>	<i>Clostridium innocuum</i>
	<i>Bacteroides vulgatus</i>	<i>Clostridium histolyticum</i>
	<i>Bartonella henselae</i>	<i>Clostridium novyi</i>
	<i>Bifidobacterium adolescentis</i>	<i>Clostridium septicum</i>
	<i>Bifidobacterium breve</i>	110 <i>Clostridium perfringens</i>
55	<i>Bifidobacterium dentium</i>	<i>Clostridium ramosum</i>
	<i>Bifidobacterium longum</i>	<i>Clostridium sordellii</i>
	<i>Blastochloris viridis</i>	<i>Clostridium tertium</i>
	<i>Borrelia burgdorferi</i>	<i>Clostridium tetani</i>
	<i>Bordetella pertussis</i>	115 <i>Comamonas acidovorans</i>
60	<i>Bordetella bronchiseptica</i>	<i>Corynebacterium accolens</i>
	<i>Brucella abortus</i>	<i>Corynebacterium bovis</i>
	<i>Brevibacterium linens</i>	<i>Corynebacterium cervicis</i>

Table 4. Example of microbial species for which *tuf* and/or *atpD* and/or *recA* nucleic acids and/or sequences are used in the present invention (continued).

Bacterial species (continued)	
5	<i>Corynebacterium diphtheriae</i>
	<i>Corynebacterium flavescens</i>
	<i>Corynebacterium genitalium</i>
	<i>Corynebacterium glutamicum</i>
10	<i>Corynebacterium jeikeium</i>
	<i>Corynebacterium kutscheri</i>
	<i>Corynebacterium minutissimum</i>
	<i>Corynebacterium mycetoides</i>
	<i>Corynebacterium pseudodiphtheriticum</i>
15	<i>Corynebacterium pseudogenitalium</i>
	<i>Corynebacterium pseudotuberculosis</i>
	<i>Corynebacterium renale</i>
	<i>Corynebacterium striatum</i>
	<i>Corynebacterium ulcerans</i>
20	<i>Corynebacterium urealyticum</i>
	<i>Corynebacterium xerosis</i>
	<i>Coxiella burnetii</i>
	<i>Cytophaga lytica</i>
	<i>Deinococcus radiodurans</i>
25	<i>Deinonema</i> sp.
	<i>Edwardsiella hoshinae</i>
	<i>Edwardsiella tarda</i>
	<i>Ehrlichia canis</i>
	<i>Ehrlichia risticii</i>
30	<i>Eikenella corrodens</i>
	<i>Enterobacter aerogenes</i>
	<i>Enterobacter agglomerans</i>
	<i>Enterobacter amnigenus</i>
	<i>Enterobacter asburiae</i>
35	<i>Enterobacter cancerogenus</i>
	<i>Enterobacter cloacae</i>
	<i>Enterobacter gergoviae</i>
	<i>Enterobacter hormaechei</i>
	<i>Enterobacter sakazakii</i>
40	<i>Enterococcus avium</i>
	<i>Enterococcus casseliflavus</i>
	<i>Enterococcus cecorum</i>
	<i>Enterococcus columbae</i>
	<i>Enterococcus dispar</i>
45	<i>Enterococcus durans</i>
	<i>Enterococcus faecalis</i>
	<i>Enterococcus faecium</i>
	<i>Enterococcus flavescens</i>
	<i>Enterococcus gallinarum</i>
50	<i>Enterococcus hirae</i>
	<i>Enterococcus malodoratus</i>
	<i>Enterococcus mundtii</i>
	<i>Enterococcus pseudoavium</i>
	<i>Enterococcus raffinosus</i>
55	<i>Enterococcus saccharolyticus</i>
	<i>Enterococcus solitarius</i>
	<i>Enterococcus sulfureus</i>
	<i>Erwinia amylovora</i>
	<i>Erwinia carotovora</i>
60	<i>Escherichia coli</i>
	<i>Escherichia fergusonii</i>
	<i>Escherichia hermannii</i>
	<i>Escherichia vulneris</i>
	<i>Eubacterium lentum</i>
65	<i>Eubacterium nodatum</i>
	<i>Ewingella americana</i>
	<i>Francisella tularensis</i>
	<i>Frankia alni</i>
	<i>Fervidobacterium islandicum</i>
70	<i>Fibrobacter succinogenes</i>
	<i>Flavobacterium ferrugineum</i>
	<i>Flexistipes sinusarabici</i>
	<i>Fusobacterium gonidiaformans</i>
	<i>Fusobacterium necrophorum</i> subsp. <i>necrophorum</i>
75	<i>Fusobacterium nucleatum</i> subsp. <i>polymorphum</i>
	<i>Gardnerella vaginalis</i>
	<i>Gemella haemolysans</i>
	<i>Gemella morbillorum</i>
	<i>Globicatella sanguis</i>
80	<i>Gloeobacter violaceus</i>
	<i>Gloeotheca</i> sp.
	<i>Gluconobacter oxydans</i>
	<i>Haemophilus actinomycetemcomitans</i>
	<i>Haemophilus aphrophilus</i>
85	<i>Haemophilus ducreyi</i>
	<i>Haemophilus haemolyticus</i>
	<i>Haemophilus influenzae</i>
	<i>Haemophilus parahaemolyticus</i>
	<i>Haemophilus parainfluenzae</i>
90	<i>Haemophilus paraphrophilus</i>
	<i>Haemophilus segnis</i>
	<i>Hafnia alvei</i>
	<i>Halobacterium marismortui</i>
	<i>Halobacterium salinarum</i>
95	<i>Haloferax volcanii</i>
	<i>Helicobacter pylori</i>
	<i>Herpetosiphon aurantiacus</i>
	<i>Kingella kingae</i>
	<i>Klebsiella ornithinolytica</i>
100	<i>Klebsiella oxytoca</i>
	<i>Klebsiella planticola</i>
	<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>
	<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>
	<i>Klebsiella pneumoniae</i> subsp.
105	<i>rhinoscleromatis</i>
	<i>Klebsiella terrigena</i>
	<i>Kluyvera ascorbata</i>
	<i>Kluyvera cryocrescens</i>
	<i>Kluyvera georgiana</i>
110	<i>Kocuria kristinae</i>
	<i>Lactobacillus acidophilus</i>
	<i>Lactobacillus garvieae</i>
	<i>Lactobacillus paracasei</i>
	<i>Lactobacillus casei</i> subsp. <i>casei</i>
115	<i>Lactococcus garvieae</i>
	<i>Lactococcus lactis</i>
	<i>Lactococcus lactis</i> subsp. <i>lactis</i>
	<i>Leclercia adecarboxylata</i>
	<i>Legionella micdadei</i>

Table 4. Example of microbial species for which *tuf* and/or *atpD* and/or *recA* nucleic acids and/or sequences are used in the present invention (continued).

5	Bacterial species (continued)	
	<i>Legionella pneumophila</i> subsp. <i>pneumophila</i>	<i>Neisseria gonorrhoeae</i>
	<i>Leminorella grimonii</i>	<i>Neisseria lactamica</i>
	<i>Leminorella richardii</i>	65 <i>Neisseria meningitidis</i>
10	<i>Leptospira biflexa</i>	<i>Neisseria mucosa</i>
	<i>Leptospira interrogans</i>	<i>Neisseria perflava</i>
	<i>Leuconostoc mesenteroides</i> subsp. <i>dextranicum</i>	<i>Neisseria pharyngis</i> var. <i>flava</i>
	<i>Listeria innocua</i>	70 <i>Neisseria polysaccharea</i>
15	<i>Listeria ivanovii</i>	<i>Neisseria sicca</i>
	<i>Listeria monocytogenes</i>	<i>Neisseria subflava</i>
	<i>Listeria seeligeri</i>	<i>Neisseria weaveri</i>
	<i>Macrococcus caseolyticus</i>	<i>Obesumbacterium proteus</i>
	<i>Magnetospirillum magnetotacticum</i>	75 <i>Ochrobactrum anthropi</i>
20	<i>Megamonas hypermegale</i>	<i>Pantoea agglomerans</i>
	<i>Methanobacterium thermoautotrophicum</i>	<i>Pantoea dispersa</i>
	<i>Methanococcus jannaschii</i>	<i>Paracoccus denitrificans</i>
	<i>Methanococcus vannielii</i>	<i>Pasteurella multocida</i>
	<i>Methanosarcina barkeri</i>	80 <i>Pectinatus frisingensis</i>
25	<i>Methanosarcina jannaschii</i>	<i>Peptococcus niger</i>
	<i>Methylobacillus flagellatum</i>	<i>Peptostreptococcus anaerobius</i>
	<i>Methylomonas clara</i>	<i>Peptostreptococcus asaccharolyticus</i>
	<i>Micrococcus luteus</i>	<i>Peptostreptococcus prevotii</i>
	<i>Micrococcus lylae</i>	85 <i>Phormidium ectocarpi</i>
30	<i>Mitsuokella multacidus</i>	<i>Pirellula marina</i>
	<i>Mobiluncus curtisii</i> subsp. <i>holmesii</i>	<i>Planobispora rosea</i>
	<i>Moellerella thermoacetica</i>	<i>Plesiomonas shigelloides</i>
	<i>Moellerella wisconsensis</i>	<i>Plectonema boryanum</i>
	<i>Moorella thermoacetica</i>	90 <i>Porphyromonas asaccharolytica</i>
35	<i>Moraxella catarrhalis</i>	<i>Porphyromonas gingivalis</i>
	<i>Moraxella osloensis</i>	<i>Pragia fontium</i>
	<i>Morganella morganii</i> subsp. <i>morganii</i>	<i>Prevotella buccalis</i>
	<i>Mycobacterium avium</i>	<i>Prevotella melaninogenica</i>
	<i>Mycobacterium bovis</i>	95 <i>Prevotella oralis</i>
40	<i>Mycobacterium gordonae</i>	<i>Prevotella ruminicola</i>
	<i>Mycobacterium kansasii</i>	<i>Prochlorothrix hollandica</i>
	<i>Mycobacterium leprae</i>	<i>Propionibacterium acnes</i>
	<i>Mycobacterium terrae</i>	<i>Propionigenium modestum</i>
	<i>Mycobacterium tuberculosis</i>	100 <i>Proteus mirabilis</i>
45	<i>Mycoplasma capricolum</i>	<i>Proteus penneri</i>
	<i>Mycoplasma gallisepticum</i>	<i>Proteus vulgaris</i>
	<i>Mycoplasma genitalium</i>	<i>Providencia alcalifaciens</i>
	<i>Mycoplasma hominis</i>	<i>Providencia rettgeri</i>
	<i>Mycoplasma pirum</i>	105 <i>Providencia rustigianii</i>
50	<i>Mycoplasma mycoides</i>	<i>Providencia stuartii</i>
	<i>Mycoplasma pneumoniae</i>	<i>Pseudomonas aeruginosa</i>
	<i>Mycoplasma pulmonis</i>	<i>Pseudomonas fluorescens</i>
	<i>Mycoplasma salivarium</i>	<i>Pseudomonas putida</i>
	<i>Myxococcus xanthus</i>	110 <i>Pseudomonas stutzeri</i>
55	<i>Neisseria animalis</i>	<i>Psychrobacter phenylpyruvicum</i>
	<i>Neisseria canis</i>	<i>Pyrococcus abyssi</i>
	<i>Neisseria cinerea</i>	<i>Rahnella aquatilis</i>
	<i>Neisseria cuniculi</i>	<i>Rickettsia prowazekii</i>
	<i>Neisseria elongata</i> subsp. <i>elongata</i>	115 <i>Rhizobium leguminosarum</i>
60	<i>Neisseria elongata</i> subsp. <i>intermedia</i>	<i>Rhizobium phaseoli</i>
	<i>Neisseria flava</i>	<i>Rhodobacter capsulatus</i>
	<i>Neisseria flavescens</i>	<i>Rhodobacter sphaeroides</i>

Table 4. Example of microbial species for which *tuf* and/or *atpD* and/or *recA* nucleic acids and/or sequences are used in the present invention (continued).

5	Bacterial species (continued)	
10	<i>Rhodopseudomonas palustris</i> <i>Rhodospirillum rubrum</i> <i>Ruminococcus albus</i> <i>Ruminococcus bromii</i> <i>Salmonella bongori</i> <i>Salmonella choleraesuis</i> subsp. <i>arizonae</i> <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> <i>Salmonella choleraesuis</i> subsp. <i>diarizonae</i> <i>Salmonella choleraesuis</i> subsp. <i>houtenae</i> <i>Salmonella choleraesuis</i> subsp. <i>indica</i> <i>Salmonella choleraesuis</i> subsp. <i>salamae</i> <i>Serpulina hyodysenteriae</i> <i>Serratia ficaria</i> <i>Serratia fonticola</i> <i>Serratia grimesii</i> <i>Serratia liquefaciens</i> <i>Serratia marcescens</i> <i>Serratia odorifera</i> <i>Serratia plymuthica</i> <i>Serratia rubidaea</i> <i>Shewanella putrefaciens</i> <i>Shigella boydii</i> <i>Shigella dysenteriae</i> <i>Shigella flexneri</i> <i>Shigella sonnei</i> <i>Sinorhizobium meliloti</i> <i>Spirochaeta aurantia</i> <i>Staphylococcus aureus</i> <i>Staphylococcus aureus</i> subsp. <i>aureus</i> <i>Staphylococcus auricularis</i> <i>Staphylococcus capitis</i> subsp. <i>capitis</i> <i>Staphylococcus cohnii</i> subsp. <i>cohnii</i> <i>Staphylococcus epidermidis</i> <i>Staphylococcus haemolyticus</i> <i>Staphylococcus hominis</i> <i>Staphylococcus hominis</i> subsp. <i>hominis</i> <i>Staphylococcus lugdunensis</i> <i>Staphylococcus saprophyticus</i> <i>Staphylococcus sciuri</i> subsp. <i>sciuri</i> <i>Staphylococcus simulans</i> <i>Staphylococcus warneri</i> <i>Stigmatella aurantiaca</i> <i>Stenotrophomonas maltophilia</i> <i>Streptococcus acidominimus</i> <i>Streptococcus agalactiae</i> <i>Streptococcus anginosus</i> <i>Streptococcus bovis</i> <i>Streptococcus cricetus</i> <i>Streptococcus cristatus</i> <i>Streptococcus downei</i> <i>Streptococcus dysgalactiae</i> <i>Streptococcus equi</i> subsp. <i>equi</i> <i>Streptococcus ferus</i>	65 <i>Streptococcus gordonii</i> <i>Streptococcus macacae</i> <i>Streptococcus mitis</i> <i>Streptococcus mutans</i> <i>Streptococcus oralis</i> <i>Streptococcus parasanguinis</i> 70 <i>Streptococcus pneumoniae</i> <i>Streptococcus pyogenes</i> <i>Streptococcus rattii</i> <i>Streptococcus salivarius</i> <i>Streptococcus salivarius</i> subsp. <i>thermophilus</i> 75 <i>Streptococcus sanguinis</i> <i>Streptococcus sobrinus</i> <i>Streptococcus suis</i> <i>Streptococcus uberis</i> <i>Streptococcus vestibularis</i> 80 <i>Streptomyces anofaciens</i> <i>Streptomyces aureofaciens</i> <i>Streptomyces cinnamomeus</i> <i>Streptomyces coelicolor</i> <i>Streptomyces collinus</i> 85 <i>Streptomyces lividans</i> <i>Streptomyces netropsis</i> <i>Streptomyces ramocissimus</i> <i>Streptomyces rimosus</i> <i>Streptomyces venezuelae</i> 90 <i>Succinivibrio dextrinosolvens</i> <i>Synechococcus</i> sp. <i>Synechocystis</i> sp. <i>Tatumella ptyseos</i> <i>Taxobacter occealus</i> 95 <i>Tetragenococcus halophilus</i> <i>Thermoplasma acidophilum</i> <i>Thermotoga maritima</i> <i>Thermus aquaticus</i> <i>Thermus thermophilus</i> 100 <i>Thiobacillus ferrooxidans</i> <i>Thiomonas cuprina</i> <i>Trabulsiella guamensis</i> <i>Treponema pallidum</i> <i>Ureaplasma urealyticum</i> 105 <i>Veillonella parvula</i> <i>Vibrio alginolyticus</i> <i>Vibrio anguillarum</i> <i>Vibrio cholerae</i> <i>Vibrio mimicus</i> 110 <i>Wolinella succinogenes</i> <i>Xanthomonas citri</i> <i>Xanthomonas oryzae</i> <i>Xenorhabdus bovienii</i> <i>Xenorhabdus nematophilus</i> 115 <i>Yersinia bercovieri</i> <i>Yersinia enterocolitica</i> <i>Yersinia frederiksenii</i> <i>Yersinia intermedia</i> <i>Yersinia pestis</i>

Table 4. **Example of microbial species for which *tuf* and/or *atpD* and/or *recA* nucleic acids and/or sequences are used in the present invention (continued).**

5	Bacterial species (continued)
	<i>Yersinia pseudotuberculosis</i>
	<i>Yersinia rohdei</i>
	<i>Yokenella regensburgei</i>
10	<i>Zoogloea ramigera</i>

Table 4. Example of microbial species for which *tuf* and/or *atpD* and/or *recA* nucleic acids and/or sequences are used in the present invention (continued).

5	Fungal species
<i>Absidia corymbifera</i>	<i>Fusarium moniliforme</i>
<i>Absidia glauca</i>	<i>Fusarium oxysporum</i>
<i>Alternaria alternata</i>	65 <i>Fusarium solani</i>
10 <i>Arxula adeninivorans</i>	<i>Geotrichum</i> sp.
<i>Aspergillus flavus</i>	<i>Histoplasma capsulatum</i>
<i>Aspergillus fumigatus</i>	<i>Hortaea werneckii</i>
<i>Aspergillus nidulans</i>	<i>Issatchenkia orientalis</i> Kudrjanzev
<i>Aspergillus niger</i>	70 <i>Kluyveromyces lactis</i>
15 <i>Aspergillus oryzae</i>	<i>Malassezia furfur</i>
<i>Aspergillus terreus</i>	<i>Malassezia pachydermatis</i>
<i>Aspergillus versicolor</i>	<i>Malbranchea filamentosa</i>
<i>Aureobasidium pullulans</i>	<i>Metschnikowia pulcherrima</i>
<i>Basidiobolus ranarum</i>	75 <i>Microsporum audouinii</i>
20 <i>Bipolaris hawaiiensis</i>	<i>Microsporum canis</i>
<i>Bilophila wadsworthia</i>	<i>Mucor circinelloides</i>
<i>Blastoschizomyces capitatus</i>	<i>Neurospora crassa</i>
<i>Blastomyces dermatitidis</i>	<i>Paecilomyces lilacinus</i>
<i>Candida albicans</i>	80 <i>Paracoccidioides brasiliensis</i>
25 <i>Candida catenulata</i>	<i>Penicillium marneffeii</i>
<i>Candida dubliniensis</i>	<i>Phialophora verrucosa</i>
<i>Candida famata</i>	<i>Pichia anomala</i>
<i>Candida glabrata</i>	<i>Piedraia hortai</i>
<i>Candida guilliermondii</i>	85 <i>Podospora anserina</i>
30 <i>Candida haemulonii</i>	<i>Podospora curvicolla</i>
<i>Candida inconspicua</i>	<i>Puccinia graminis</i>
<i>Candida kefyr</i>	<i>Pseudallescheria boydii</i>
<i>Candida krusei</i>	<i>Reclinomonas americana</i>
<i>Candida lambica</i>	90 <i>Rhizomucor racemosus</i>
35 <i>Candida lusitanae</i>	<i>Rhizopus oryzae</i>
<i>Candida norvegica</i>	<i>Rhodotorula minuta</i>
<i>Candida norvegensis</i>	<i>Rhodotorula mucilaginosa</i>
<i>Candida parapsilosis</i>	<i>Saccharomyces cerevisiae</i>
<i>Candida rugosa</i>	95 <i>Saksenaea vasiformis</i>
40 <i>Candida sphaerica</i>	<i>Schizosaccharomyces pombe</i>
<i>Candida tropicalis</i>	<i>Scopulariopsis koningii</i>
<i>Candida utilis</i>	<i>Sordaria macrospora</i>
<i>Candida viswanathii</i>	<i>Sporobolomyces salmonicolor</i>
<i>Candida zeylanoides</i>	100 <i>Sporothrix schenckii</i>
45 <i>Cladophialophora carrionii</i>	<i>Stephanoascus ciferrii</i>
<i>Coccidioides immitis</i>	<i>Syncephalastrum racemosum</i>
<i>Coprinus cinereus</i>	<i>Trichoderma reesei</i>
<i>Cryptococcus albidus</i>	<i>Trichophyton mentagrophytes</i>
<i>Cryptococcus humicolus</i>	105 <i>Trichophyton rubrum</i>
50 <i>Cryptococcus laurentii</i>	<i>Trichophyton tonsurans</i>
<i>Cryptococcus neoformans</i>	<i>Trichosporon cutaneum</i>
<i>Cunninghamella bertholletiae</i>	<i>Ustilago maydis</i>
<i>Curvularia lunata</i>	<i>Wangiella dermatitidis</i>
<i>Emericella nidulans</i>	110 <i>Yarrowia lipolytica</i>
55 <i>Emmonsia parva</i>	
<i>Eremothecium gossypii</i>	
<i>Exophiala dermatitidis</i>	
<i>Exophiala jeanselmei</i>	
<i>Exophiala moniliae</i>	
60 <i>Exserohilum rostratum</i>	
<i>Eremothecium gossypii</i>	
<i>Fonsecaea pedrosoi</i>	

Table 4. Example of microbial species for which *tuf* and/or *atpD* and/or *recA* nucleic acids and/or sequences are used in the present invention (continued).

Parasitical species	
5	<i>Babesia bigemina</i>
	<i>Babesia bovis</i>
	<i>Babesia microti</i>
	<i>Blastocystis hominis</i>
10	<i>Crithidia fasciculata</i>
	<i>Cryptosporidium parvum</i>
	<i>Entamoeba histolytica</i>
	<i>Giardia lamblia</i>
	<i>Kentrophoros sp.</i>
15	<i>Leishmania aethiopica</i>
	<i>Leishmania amazonensis</i>
	<i>Leishmania braziliensis</i>
	<i>Leishmania donovani</i>
	<i>Leishmania infantum</i>
20	<i>Leishmania enriettii</i>
	<i>Leishmania gerbilli</i>
	<i>Leishmania guyanensis</i>
	<i>Leishmania hertigi</i>
	<i>Leishmania major</i>
25	<i>Leishmania mexicana</i>
	<i>Leishmania panamensis</i>
	<i>Leishmania tarentolae</i>
	<i>Leishmania tropica</i>
	<i>Neospora caninum</i>
30	<i>Onchocerca volvulus</i>
	<i>Plasmodium berghei</i>
	<i>Plasmodium falciparum</i>
	<i>Plasmodium knowlesi</i>
	<i>Porphyra purpurea</i>
35	<i>Toxoplasma gondii</i>
	<i>Treponema pallidum</i>
	<i>Trichomonas tenax</i>
	<i>Trichomonas vaginalis</i>
	<i>Trypanosoma brucei</i>
40	<i>Trypanosoma brucei</i> subsp. <i>brucei</i>
	<i>Trypanosoma congolense</i>
	<i>Trypanosoma cruzi</i>

Table 5. Antimicrobial agents resistance genes selected for diagnostic purposes.

	Gene	Antimicrobial agent	Bacteria ¹	ACCESSION NO.	SEQ ID NO.
5	<i>aac(3)-Ib</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> <i>Pseudomonads</i>	L06157	
	<i>aac(3)-IIb</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	M97172	
	<i>aac(3)-IVa</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i>	X01385	
10	<i>aac(3)-VIa</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	M88012	
	<i>aac(2')-Ia</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	X04555	
	<i>aac(6')-aph(2'')</i> ²	Aminoglycosides	<i>Enterococcus</i> sp., <i>Staphylococcus</i> sp.		83-86 ³
15	<i>aac(6')-Ia</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	M18967	
	<i>aac(6')-Ic</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	M94066	
20	<i>aac(6')-IIa</i> ²	Aminoglycosides	<i>Pseudomonads</i>		112 ⁴
	<i>aadB</i> [<i>ant(2'')-Ia</i> ²]	Aminoglycosides	<i>Enterobacteriaceae</i>		53-54 ³
	<i>aacCI</i> [<i>aac(3)-Ia</i> ²]	Aminoglycosides	<i>Pseudomonads</i>		55-56 ³
	<i>aacC2</i> [<i>aac(3)-IIa</i> ²]	Aminoglycosides	<i>Pseudomonads</i>		57-58 ³
	<i>aacC3</i> [<i>aac(3)-III</i> ²]	Aminoglycosides	<i>Pseudomonads</i>		59-60 ³
25	<i>aacA4</i> [<i>aac(6')-Ib</i> ²]	Aminoglycosides	<i>Pseudomonads</i>		65-66 ³
	<i>ant(3'')-Ia</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Enterococcus</i> sp., <i>Staphylococcus</i> sp.	X02340 M10241	
	<i>ant(4')-Ia</i> ²	Aminoglycosides	<i>Staphylococcus</i> sp.	V01282	
30	<i>aph(3')-Ia</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	J01839	
	<i>aph(3')-IIa</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	V00618	
	<i>aph(3')-IIIa</i> ²	Aminoglycosides	<i>Enterococcus</i> sp., <i>Staphylococcus</i> sp.	V01547	
35	<i>aph(3')-VIa</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	X07753	
	<i>rpsL</i> ²	Streptomycin	<i>M. tuberculosis</i> , <i>M. avium</i> complex	X80120 U14749 X70995 L08011	
40					
	<i>bla_{OXA}</i> ^{5,6}	β -lactams	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	Y10693 AJ238349 AJ009819 X06046 X03037 X07260 U13880 X75562 AF034958 J03427 Z22590 U59183 L38523 U63835 AF043100 AF060206 U85514 AF043381 AF024602 AF064820	110 ⁴
45					
50					
55					
60					
	<i>bla_{ROB}</i> ⁵	β -lactams	<i>Haemophilus</i> sp. <i>Pasteurella</i> sp.		45-48 ³
65					

Table 5. Antimicrobial agents resistance genes selected for diagnostic purposes (continued).

	Gene	Antimicrobial agent	Bacteria ¹	ACCESSION NO.	SEQ ID NO.
5	<i>bla_{SHV}</i> ^{5,6}	β -lactams	<i>Enterobacteriaceae</i> , <i>Pseudomonas aeruginosa</i>	AF124984	41-44 ³
				AF148850	
				M59181	
				X98099	
10				M33655	
				AF148851	
				X53433	
				L47119	
				AF074954	
15				X53817	
				AF096930	
				X55640	
				Y11069	
20				U20270	
				U92041	
				S82452	
				X98101	
				X98105	
25				AF164577	
				AJ011428	
				AF116855	
				AB023477	
				AF293345	
30				AF227204	
				AF208796	
				AF132290	
	<i>bla_{TEM}</i> ^{5,6}	β -lactams	<i>Enterobacteriaceae</i> , <i>Neisseria</i> sp., <i>Haemophilus</i> sp.	AF012911	37-40 ³
				U48775	
35				AF093512	
				AF052748	
				X64523	
				Y13612	
				X57972	
40				AF157413	
				U31280	
				U36911	
				U48775	
				V00613	
				X97254	
45				AJ012256	
				X04515	
				AF126482	
				U09188	
50				M88143	
				Y14574	
				AF188200	
				AJ251946	
				Y17581	
55				Y17582	
				Y17583	
				M88143	
				U37195	
				Y17584	
60				X64523	
				U95363	
				Y10279	
				Y10280	
				Y10281	
65				AF027199	
				AF104441	
				AF104442	
				AF062386	
				X57972	
70				AF047171	
				AF188199	
				AF157553	
				AF190694	
				AF190695	
75				AF190693	
				AF190692	

Table 5. Antimicrobial agents resistance genes selected for diagnostic purposes (continued).

	Gene	Antimicrobial agent	Bacteria ¹	ACCESSION NO.	SEQ ID NO.
5	<i>bla_{CARB}</i> ⁵	β-lactams	<i>Pseudomonas</i> sp., <i>Enterobacteriaceae</i>	J05162 S46063 M69058 U14749	
10				D86225 D13210 Z18955 AF071555 AF153200 AF030945	
15	<i>bla_{CTX-M-1}</i> ⁵	β-lactams	<i>Enterobacteriaceae</i>	X92506	
	<i>bla_{CTX-M-2}</i> ⁵	β-lactams	<i>Enterobacteriaceae</i>	X92507	
	<i>bla_{CMY-2}</i> ⁷	β-lactams	<i>Enterobacteriaceae</i>	X91840	
20				AJ007826 AJ011293 AJ011291 Y17716 Y16783 Y16781 Y15130 U77414 S83226 Y15412 X78117	
25					
30	<i>bla_{IMP}</i> ⁵	β-lactams	<i>Enterobacteriaceae</i> , <i>Pseudomonas aeruginosa</i>	AJ223604 S71932 D50438 D29636 X98393 AB010417 D78375	
35	<i>bla_{PER-1}</i> ⁵	β-lactams	<i>Enterobacteriaceae</i> , <i>Pseudomonadaceae</i>	Z21957	
40	<i>bla_{PER-2}</i> ⁷	β-lactams	<i>Enterobacteriaceae</i>	X93314	
	<i>bla_Z</i> ¹²	β-lactams	<i>Enterococcus</i> sp., <i>Staphylococcus</i> sp.		111 ⁴
	<i>mecA</i> ¹²	β-lactams	<i>Staphylococcus</i> sp.		97-98 ³

Table 5. Antimicrobial agents resistance genes selected for diagnostic purposes (continued).

Gene	Antimicrobial agent	Bacteria ¹	ACCESSION NO.	SEQ ID NO.
5 <i>pbp1a</i> ¹³	β -lactams	<i>Streptococcus pneumoniae</i>	M90527	1004-1018, 1648,2056-2064, 2273-2276
			X67872	
			AB006868	
			AB006874	
			X67873	
			AB006878	
			AB006875	
			AB006877	
			AB006879	
			AF046237	
			AF046235	
			AF026431	
			AF046232	
			AF046233	
			AF046236	
			X67871	
			Z49095	
			AF046234	
			AB006873	
			X67866	
			X67868	
			AB006870	
			AB006869	
			AB006872	
			X67870	
			AB006871	
			X67867	
			X67869	
			AB006876	
			AF046230	
			AF046238	
			Z49094	
40 <i>pbp2b</i> ¹³	β -lactams	<i>Streptococcus pneumoniae</i>	X16022	1019-1033
			M25516	
			M25518	
			M25515	
			U20071	
			U20084	
			U20082	
			U20067	
			U20079	
			Z22185	
			U20072	
			U20083	
			U20081	
50 <i>pbp2b</i> ¹³	β -lactams	<i>Streptococcus pneumoniae</i>	M25522	
			U20075	
			U20070	
			U20077	
			U20068	
			Z22184	
			U20069	
			U20078	
			M25521	
			M25525	
			M25519	
			Z21981	
			M25523	
60 65 70 75			M25526	
			U20076	
			U20074	
			M25520	
			M25517	
			M25524	
			Z22230	
			U20073	
			U20080	

Table 5. Antimicrobial agents resistance genes selected for diagnostic purposes (continued).

	Gene	Antimicrobial agent	Bacteria ¹	ACCESSION NO.	SEQ ID NO.
5	<i>pbp2x</i> ¹³	β -lactams	<i>Streptococcus pneumoniae</i>	X16367 X65135 AB011204 AB011209 AB011199 AB011200 AB011201 AB011202 AB011198 AB011208 AB011205 AB015852 AB011210 AB015849 AB015850 AB015851 AB015847 AB015846 AB011207 AB015848 Z49096	1034-1048
10					
15					
20					
25					
	<i>int</i>	-lactams, trimethoprim	<i>Enterobacteriaceae</i> ,		99-102 ³
30	<i>sul</i>	aminoglycosides, antiseptic, chloramphenicol	<i>Pseudomonads</i>		103-106 ³
	<i>ermA</i> ¹⁴	Macrolides, lincosamides, streptogramin B	<i>Staphylococcus</i> sp.		113 ⁴
35	<i>ermB</i> ¹⁴	Macrolides, lincosamides, streptogramin B	<i>Enterobacteriaceae</i> , <i>Staphylococcus</i> sp. <i>Enterococcus</i> sp.		114 ⁴
40	<i>ermC</i> ¹⁴	Macrolides, lincosamides, streptogramin B	<i>Streptococcus</i> sp. <i>Enterobacteriaceae</i> , <i>Staphylococcus</i> sp.		115 ⁴
45	<i>ereA</i> ¹²	Macrolides	<i>Enterobacteriaceae</i> , <i>Staphylococcus</i> sp.	M11277 E01199 AF099140 A15097 X03988	
	<i>ereB</i> ¹²	Macrolides	<i>Enterobacteriaceae</i> <i>Staphylococcus</i> sp.		
50	<i>msrA</i> ¹²	Macrolides	<i>Staphylococcus</i> sp.		77-80 ³
	<i>mefA</i> , <i>mefE</i> ⁸	Macrolides	<i>Streptococcus</i> sp.	U70055 U83667 D16251 U34344 U36578 J03947 M14039 A15070 E01245 AF110130 AJ238249	
55	<i>mphA</i> ⁸	Macrolides	<i>Enterobacteriaceae</i> , <i>Staphylococcus</i> sp.		
	<i>linA/linA'</i> ⁹	Lincosamides	<i>Staphylococcus</i> sp.		
60	<i>linB</i> ¹⁰	Lincosamides	<i>Enterococcus faecium</i>		
	<i>vga</i> ¹⁵	Streptogramin	<i>Staphylococcus</i> sp.	M90056 U82085 M36022 M20219 AF015628	89-90 ³
65	<i>vgb</i> ¹⁵	Streptogramin	<i>Staphylococcus</i> sp.		

Table 5. Antimicrobial agents resistance genes selected for diagnostic purposes (continued).

	Gene	Antimicrobial agent	Bacteria ¹	ACCESSION NO.	SEQ ID NO.
5	<i>vat</i> ¹⁵ <i>vatB</i> ¹⁵	Streptogramin Streptogramin	<i>Staphylococcus</i> sp. <i>Staphylococcus</i> sp.	L07778 U19459 L38809	87-88 ³
10	<i>satA</i> ¹⁵ <i>mupA</i> ¹²	Streptogramin Mupirocin	<i>Enterococcus faecium</i> <i>Staphylococcus aureus</i>	L12033 X75439 X59478 X59477	81-82 ³
15	<i>gyrA</i> ¹⁶	Quinolones	Gram-positive and gram-negative bacteria	X95718 X06744 X57174 X16817 X71437 AF065152 AF060881 D32252	1255, 1607-1608, 1764-1776, 2013-2014, 2277-2280
20	<i>parC/grlA</i> ¹⁶	Quinolones	Gram-positive and gram-negative bacteria	AB005036 AF056287 X95717 AF129764 AB017811 AF065152	1777-1785
25	<i>parE/grlB</i> ¹⁶	Quinolones	Gram-positive bacteria	X95717 AF065153 AF058920	
30	<i>norA</i> ¹⁶	Quinolones	<i>Staphylococcus</i> sp.	D90119 M80252 M97169	
35	<i>mexR (nalB)</i> ¹⁶ <i>nfxB</i> ¹⁶ <i>cat</i> ¹²	Quinolones Quinolones Chloramphenicol	<i>Pseudomonas aeruginosa</i> <i>Pseudomonas aeruginosa</i> Gram-positive and gram-negative bacteria	U23763 X65646 M55620 X15100 A24651 M28717 A00568 A00569 X74948 Y00723 A24362 A00569 M93113 M62822 M58516 V01277 X02166 M77169 X53796 J01841 X07848	
40					
45					
50					
55	<i>ppflo</i> -like <i>embB</i> ¹⁷ <i>pncA</i> ¹⁷	Chloramphenicol Ethambutol Pyrazinamide	<i>Mycobacterium tuberculosis</i> <i>Mycobacterium tuberculosis</i>	AF071555 U68480 U59967	
60	<i>rpoB</i> ¹⁷	Rifampin	<i>Mycobacterium tuberculosis</i>	AF055891 AF055892 S71246 L27989 AF055893 AF106077 U02492	
65	<i>inhA</i> ¹⁷	Isoniazid	<i>Mycobacterium tuberculosis</i>		

Table 5. Antimicrobial agents resistance genes selected for diagnostic purposes (continued).

	Gene	Antimicrobial agent	Bacteria ¹	ACCESSION NO.	SEQ ID NO.
5	<i>vanA</i> ¹²	Vancomycin	<i>Enterococcus</i> sp.		67-70 ³
	<i>vanB</i> ¹²	Vancomycin	<i>Enterococcus</i> sp.		1049-1057
	<i>vanC1</i> ¹²	Vancomycin	<i>Enterococcus gallinarum</i>		116 ⁴
10	<i>vanC2</i> ¹²	Vancomycin	<i>Enterococcus casseliflavus</i>		117 ⁴
				U94521	1058-1059
				U94522	1060-1063
				U94523	
15				U94524	
				U94525	
				L29638	
	<i>vanC3</i> ¹²	Vancomycin	<i>Enterococcus flavescens</i>		1064-1066
				L29639	
20	<i>vanD</i> ¹⁸	Vancomycin	<i>Enterococcus faecium</i>	U72706	
	<i>vanE</i> ¹²	Vancomycin	<i>Enterococcus faecium</i>	AF130997	
	<i>tetB</i> ¹⁹	Tetracycline	Gram-negative bacteria	AF136925	
				J01830	
25				AF162223	
				AP000342	
				S83213	
				U81141	
				V00611	
30	<i>tetM</i> ¹⁹	Tetracycline	Gram-negative and Gram-positive bacteria	X52632	
				AF116348	
				U50983	
				X92947	
				M211136	
				U08812	
35	<i>sul II</i> ²⁰	Sulfonamides	Gram-negative bacteria	X04388	
				M36657	
				AF017389	
				AF017391	
40	<i>dhfrIa</i> ²⁰	Trimethoprim	Gram-negative bacteria	AJ238350	
				X17477	
				K00052	
				U09476	
				X00926	
45	<i>dhfrIb</i> ²⁰	Trimethoprim	Gram-negative bacteria	Z50805	
	<i>dhfrV</i> ²⁰	Trimethoprim	Gram-negative bacteria	Z50804	
	<i>dhfrVI</i> ²⁰	Trimethoprim	Gram-negative bacteria	X12868	
	<i>dhfrVII</i> ²⁰	Trimethoprim	Gram-negative bacteria	Z86002	
				U31119	
				AF139109	
50	<i>dhfrVIII</i> ²⁰	Trimethoprim	Gram-negative bacteria	X58425	
				U10186	
				U09273	
	<i>dhfrIX</i> ²⁰	Trimethoprim	Gram-negative bacteria	X57730	
	<i>dhfrXII</i> ²⁰	Trimethoprim	Gram-negative bacteria	Z21672	
55				AF175203	
				AF180731	
				M84522	
	<i>dhfrXIII</i> ²⁰	Trimethoprim	Gram-negative bacteria	Z50802	
	<i>dhfrXV</i> ²⁰	Trimethoprim	Gram-negative bacteria	Z83331	
60	<i>dhfrXVII</i> ²⁰	Trimethoprim	Gram-negative bacteria	AF170088	
				AF180469	
				AF169041	

Table 5. Antimicrobial agents resistance genes selected for diagnostic purposes (continued).

Gene	Antimicrobial agent	Bacteria ¹	ACCESSION NO.	SEQ ID NO.
5 <i>dfra</i> 20	Trimethoprim	<i>Staphylococcus</i> sp.	AF045472 U40259 AF051916 X13290 Y07536 Z16422 Z48233	
15				
1	Bacteria having high incidence for the specified antibiotic resistance gene. The presence of the antibiotic resistance genes in other bacteria is not excluded.			
2	Shaw, K. J., P. N. Rather, R. S. Hare, and G. H. Miller. 1993. Molecular genetics of aminoglycoside resistance genes and familial relationships of the aminoglycoside-modifying enzymes. Microbiol. Rev. 57:138-163.			
20	3 Antibiotic resistance genes from our assigned US patent no. 6,001,564 for which we have selected PCR primer pairs.			
4	These SEQ ID NOs. refer to a previous patent (publication WO98/20157).			
5	Bush, K., G.A. Jacoby and A. Medeiros. 1995. A functional classification scheme for β -lactamase and its correlation with molecular structure. Antimicrob. Agents. Chemother. 39:1211-1233.			
25	6 Nucleotide mutations in bla _{SHV} , bla _{TEM} , and bla _{OXA} , are associated with extended-spectrum β -lactamase or inhibitor-resistant β -lactamase.			
7	Bauerfeind, A., Y. Chong, and K. Lee. 1998. Plasmid-encoded AmpC beta-lactamases: how far have we gone 10 ears after discovery? Yonsei Med. J. 39:520-525.			
30	8 Sutcliffe, J., T. Grebe, A. Tait-Kamradt, and L. Wondrack. 1996. Detection of erythromycin-resistant determinants by PCR. Antimicrob. Agent Chemother. 40:2562-2566.			
9	Leclerc, R., A., Brisson-Noël, J. Duval, and P. Courvalin. 1991. Phenotypic expression and genetic heterogeneity of lincosamide inactivation in <i>Staphylococcus</i> sp. Antimicrob. Agents. Chemother. 31:1887-1891.			
35	10 Bozdogan, B., L. Berrezouga, M.-S. Kuo, D. A. Yurek, K. A. Farley, B. J. Stockman, and R. Leclercq. 1999. A new gene, linB, conferring resistance to lincosamides by nucleotidylation in <i>Enterococcus faecium</i> HM1025. Antimicrob. Agents. Chemother. 43:925-929.			
11	Cockerill III, F.R. 1999. Genetic methods for assessing antimicrobial resistance. Antimicrob. Agents. Chemother. 43:199-212.			
40	12 Tenover, F. C., T. Popovic, and O. Olsvik. 1996. Genetic methods for detecting antibacterial resistance genes. pp. 1368-1378. In Murray, P. R., E. J. Baron, M. A. Pfaller, F. C. Tenover, R. H. Tenover (eds). Manual of clinical microbiology. 6th ed., ASM Press, Washington, D.C. USA			
13	Dowson, C. G., T. J. Tracey, and B. G. Spratt. 1994. Origin and molecular epidemiology of penicillin-binding-protein-mediated resistance to β -lactam antibiotics. Trends Molec. Microbiol. 2: 361-366.			
45	14 Jensen, L. B., N. Frimodt-Moller, F. M. Aarestrup. 1999. Presence of erm gene classes in Gram-positive bacteria of animal and human origin in Denmark. FEMS Microbiol. 170:151-158.			
15	Thal, L. A., and M. J. Zervos. 1999. Occurrence and epidemiology of resistance to virginimycin and streptogramins. J. Antimicrob. Chemother. 43:171-176.			
50	16 Martinez J. L., A. Alonso, J. M. Gomez-Gomez, and F. Baquero. 1998. Quinolone resistance by mutations in chromosomal gyrase genes. Just the tip of the iceberg? J. Antimicrob. Chemother. 42:683-688			
17	Cockerill III, F.R. 1999. Genetic methods for assessing antimicrobial resistance. Antimicrob. Agents. Chemother. 43:199-212.			
55	18 Casadewall, B. and P. Courvalin. 1999 Characterization of the vanD glycopeptide resistance gene cluster from <i>Enterococcus faecium</i> BM 4339. J. Bacteriol. 181:3644-3648.			
19	Roberts, M.C. 1999. Genetic mobility and distribution of tetracycline resistance determinants. Ciba Found. Symp. 207:206-222.			
60	20 Huovinen, P., L. Sundström, G. Swedberg, and O. Sköld. 1995. Trimethoprim and sulfonamide resistance. Antimicrob. Agent Chemother. 39:279-289.			

Table 6. List of bacterial toxins selected for diagnostic purposes.

	Organism	Toxin	Accession number
5	<i>Actinobacillus actinomycetemcomitans</i>	Cytolethal distending toxin (<i>cdtA</i> , <i>cdtB</i> , <i>cdtC</i>)	AF006830
		Leukotoxin (<i>ltxA</i>)	M27399
	<i>Actinomyces pyogenes</i>	Hemolysin (pyolysin)	U84782
10	<i>Aeromonas hydrophila</i>	Aerolysin (<i>aerA</i>)	M16495
		Haemolysin (<i>hlyA</i>)	U81555
		Cytotoxic enterotoxin (<i>alt</i>)	L77573
15	<i>Bacillus anthracis</i>	Anthrax toxin (<i>cya</i>)	M23179
	<i>Bacillus cereus</i>	Enterotoxin (<i>bceT</i>)	D17312
			AF192766, AF192767
		Enterotoxic hemolysin BL	AJ237785
20	<i>Bacillus mycoides</i>	Non-haemolytic enterotoxins A,B and C (<i>nhe</i>)	Y19005
	<i>Bacillus pseudomycoides</i>	Hemolytic enterotoxin HBL	AJ243150 to AJ243153
	<i>Bacteroides fragilis</i>	Hemolytic enterotoxin HBL	AJ243154 to AJ243156
		Enterotoxin (<i>bftP</i>)	U67735
25		Matrix metalloprotease/enterotoxin (fragilysin)	S75941, AF038459
		Metalloprotease toxin-2	U90931
			AF081785
30	<i>Bordetella bronchiseptica</i>	Metalloprotease toxin-3	AF056297
		Adenylate cyclase hemolysin (<i>cyaA</i>)	Z37112, U22953
		Dermonecrotic toxin (<i>dnt</i>)	U59687
35	<i>Bordetella pertussis</i>	Pertussis toxin (S1 subunit, <i>tox</i>)	AB020025
			AJ006151
			AJ006153
			AJ006155
			AJ006157
			AJ006159
40			AJ007363
			M14378, M16494
			AJ007364
			M13223
			X16347
45		Adenyl cyclase (<i>cya</i>)	18323
		Dermonecrotic toxin (<i>dnt</i>)	U10527
50	<i>Campylobacter jejuni</i>	Cytolethal distending toxin (<i>cdtA</i> , <i>cdtB</i> , <i>cdtC</i>)	U51121
	<i>Citrobacter freundii</i>	Shiga-like toxin (<i>slt-IIcA</i>)	X67514, S53206
	<i>Clostridium botulinum</i>	Botulism toxin (BoNT) (A,B,E and F serotypes are neurotoxic for humans; the other serotypes have not been considered)	X52066, X52088
			X73423
			M30196
55			X70814
			X70819
			X71343
			Z11934
			X70817
			M81186
60			X70818
			X70815
			X62089
			X62683
			S76749
65			X81714
			X70816

Table 6. List of bacterial toxins selected for diagnostic purposes (continued).

	Organism	Toxin	Accession number
5	<i>Clostridium botulinum</i> (continued)		X70820 X70281 L35496 M92906
10	<i>Clostridium difficile</i>	A toxin (enterotoxin) (<i>tcdA</i>) (<i>cdtA</i>)	AB012304 AF053400 Y12616 X51797 X17194 M30307
15		B toxin (cytotoxin) (<i>toxB</i>) (<i>cdtB</i>)	Z23277 X53138
20	<i>Clostridium perfringens</i>	Alpha (phospholipase C) (<i>cpa</i>)	L43545 L43546 L43547 L43548 X13608 X17300 D10248
25		Beta (dermonecrotic protein) (<i>cpb</i>)	L13198 X83275 L77965
30		Enterotoxin (<i>cpe</i>)	AJ000766 M98037 X81849 X71844 Y16009
35		Enterotoxin pseudogene (not expressed)	AF037328 AF037329 AF037330
40		Epsilon toxin (<i>etxD</i>)	M80837 M95206 X60694
45		Iota (Ia and Ib)	X73562
		Lambda (metalloprotease)	D45904
50	<i>Clostridium sordellii</i> <i>Clostridium tetani</i>	Theta (perfringolysin O) Cytotoxin L Tetanos toxin	M36704 X82638 X06214 X04436
	<i>Corynebacterium diphtheriae</i>	Diphtheriae toxin	X00703
	<i>Corynebacterium pseudotuberculosis</i>	Phospholipase C	A21336
55	<i>Eikenella corrodens</i> <i>Enterobacter cloacae</i> <i>Enterococcus faecalis</i> <i>Escherichia coli</i> (EHEC)	lysine decarboxylase (<i>cadA</i>) Shiga-like toxin II Cytolysin B (<i>cylB</i>) Hemolysin toxin (<i>hlyA</i> and <i>ehxA</i>)	U89166 Z50754, U33502 M38052 AF043471
60			X94129 X79839 X86087 AB011549 AF074613

Table 6. List of bacterial toxins selected for diagnostic purposes (continued).

	Organism	Toxin	Accession number
5	<i>Escherichia coli</i> (EHEC)	Shiga-like (Vero cytotoxin) (<i>stx</i>)	X81418, M36727 M14107, E03962 M10133, E03959 M12863, X07865 X81417, Y10775
10			X81416, Z50754 X81415, X67515 Z36900, AF043627 L11078, M19473 L04539, M17358
15			L11079, M19437 X65949, M24352 M21534, X07903 M29153, Z36899 Z37725
20			Z36901 X61283 AB017524 U72191 X61283
25	<i>Escherichia coli</i> (ETEC)	Enterotoxin (heat-labile) (<i>eltB</i>)	M17874 M17873 J01605 AB011677
30		Enterotoxin (heat-stable) (<i>astA</i>) (<i>estA1</i>)	L11241 M58746 M29255 V00612 J01831
35	<i>Escherichia coli</i> (other)	Cytolethal-distending toxin (<i>cdt</i>) (3 genes)	U03293 U04208 U89305
40		Cytotoxic necrotizing factor 1 (<i>cnf1</i>)	U42629
45	<i>Haemophilus ducreyi</i> <i>Helicobacter pylori</i>	Microcin 24 (<i>mtfS</i>) Autotransporter enterotoxin (<i>Pet</i>) (cytotoxin) Cytolethal distending toxin (<i>cdtA</i> , <i>cdtB</i> , <i>cdtC</i>) Vacuolating toxin (<i>vacA</i>)	U47048 AF056581 U53215 U07145 U80067 U80068 AF077938 AF077939 AF077940 AF077941 AF057703
50	<i>Legionella pneumophila</i> <i>Listeria monocytogenes</i>	Structural toxin protein (<i>rtxA</i>) Listeriolysin O (<i>lisA</i> , <i>hlyA</i>)	X15127 M24199 X60035
55			U25452 U25443 U25446 U25449
60	<i>Pasteurella multocida</i>	Mitogenic toxin (dermonecrotic toxin)	X57775, Z28388 X51512 X52478
65	<i>Proteus mirabilis</i> <i>Pseudomonas aeruginosa</i> <i>Salmonella typhimurium</i>	Hemolysin (<i>hpmA</i>) Cytotoxin (Enterotoxin A) Calmodulin-sensitive adenylate cyclase toxin (<i>cya</i>)	M30186 X14956 AF060869
		Cytolysin (salmolysin) (<i>shyA</i>)	U03842
		Enterotoxin (<i>stn</i>)	L16014

Table 6. List of bacterial toxins selected for diagnostic purposes (continued).

	Organism	Toxin	Accession number
5	<i>Serratia marcescens</i>	Hemolysin (<i>shlA</i>)	M22618
	<i>Shigella dysenteriae</i> type 1	Shiga toxin (<i>stxA</i> and <i>stxB</i>)	X07903, M32511
			M19437
			M24352, M21947
10	<i>Shigella flexneri</i>	ShET2 enterotoxin (<i>senA</i>)	Z54211
			Z47381
15	<i>Shigella sonnei</i> <i>Sphingomonas paucimobilis</i> <i>Staphylococcus aureus</i>	Enterotoxin 1 (<i>set1A</i> and <i>set1B</i>)	U35656
		Hemolysin E (<i>hlyE</i> , <i>ctyA</i> , <i>sheA</i>)	AF200955
		Shiga toxin (<i>stxA</i> and <i>stxB</i>)	AJ132761
		Beta-hemolysin (<i>hlyA</i>)	L01270
20		Gamma-hemolysin (<i>hlg2</i>)	D42143
			L01055
		Enterotoxin	U93688
25		Enterotoxin A (<i>sea</i>)	L22565, L22566
			M18970
		Enterotoxin B	M11118
30		Enterotoxin C1 (<i>entC1</i>)	X05815
		Enterotoxin C2 (<i>entC2</i>)	P34071
		Enterotoxin C3 (<i>entC3</i>)	X51661
		Enterotoxin D (<i>sed</i>)	M94872
35		Enterotoxin E	M21319
		Enterotoxin G (<i>seg</i>)	AF064773
		Enterotoxin H (<i>seh</i>)	U11702
40		Enterotoxin I (<i>sei</i>)	AF064774
		Enterotoxin J	AF053140
45		Exfoliative toxin A (ETA, Epidermolytic toxin A)	M17347
			M17357
			L25372, M20371
50		Exfoliative toxin B (ETB)	M17348, M13775
		Leukocidin R (F and S component, <i>lukF</i> and <i>lukS</i> ; Hemolysin B and C)	X64389, S53213
			X72700
55			L01055
		Toxic shock syndrome toxin 1 (TSST-1, alpha toxin, alpha hemolysin)	X01645
			M90536
			J02615
60	<i>Staphylococcus epidermidis</i> <i>Staphylococcus intermedius</i>	Delta toxin (<i>hld</i>)	U93688
		Enterotoxin 1	AF068634
			U91526
		Leukocidin R (F and S component, <i>lukF</i> and <i>lukS</i> ; synergohymenotropic toxin)	X79188
65	<i>Streptococcus pneumoniae</i>	Pneumolysin	X52474

Table 6. List of bacterial toxins selected for diagnostic purposes (continued).

	Organism	Toxin	Accession number
5	<i>Streptococcus pyogenes</i>	<i>Streptococcus</i> pyrogenic exotoxin A (<i>speA</i>)	X61553 to X61573 X03929 U40453, M19350
		Pyrogenic exotoxin B (<i>speB</i>) M86905, M35110	U63134
10	<i>Vibrio cholerae</i>	Cholerae toxin (<i>ctxA</i> and <i>ctxB</i> subunits)	X00171 X76390 X58786 X58785, S55782 D30052 D30053 K02679 AF175708
15			
20		Accessory cholera enterotoxin (<i>ace</i>)	Z22569, AF175708
		Heat-stable enterotoxin (<i>sto</i>)	X74108, M85198 M97591, L03220
		<i>Zonula occludens</i> toxin (<i>zot</i>)	M83563, AF175708
25	<i>Vibrio parahaemolyticus</i>	Thermostable direct hemolysin (<i>tdh</i>)	S67841
	<i>Vibrio vulnificus</i>	Cytolysin (<i>vvhA</i>)	M34670
	<i>Yersinia enterocolitica</i>	Heat-stable enterotoxin (<i>yst</i>)	U09235, X65999
30		Heat-stable enterotoxin type B (<i>ystB</i>)	D88145
		Heat-stable enterotoxin type C (<i>ystC</i>)	D63578
	<i>Yersinia kristensenii</i>	Enterotoxin	X69218
	<i>Yersinia pestis</i>	Toxin	X92727
35			

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing.

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source Gene*
5	1	<i>Acinetobacter baumannii</i>	This patent
	2	<i>Actinomyces meyeri</i>	This patent
	3	<i>Aerococcus viridans</i>	This patent
	4	<i>Achromobacter xylosoxidans</i> subsp. <i>denitrificans</i>	This patent
	5	<i>Anaerorhabdus furcosus</i>	This patent
10	6	<i>Bacillus anthracis</i>	This patent
	7	<i>Bacillus cereus</i>	This patent
	8	<i>Bacteroides distasonis</i>	This patent
	9	<i>Enterococcus casseliflavus</i>	This patent
15	10	<i>Staphylococcus saprophyticus</i>	This patent
	11	<i>Bacteroides ovatus</i>	This patent
	12	<i>Bartonella henselae</i>	This patent
	13	<i>Bifidobacterium adolescentis</i>	This patent
	14	<i>Bifidobacterium dentium</i>	This patent
20	15	<i>Brucella abortus</i>	This patent
	16	<i>Burkholderia cepacia</i>	This patent
	17	<i>Cedecea davisae</i>	This patent
	18	<i>Cedecea neteri</i>	This patent
	19	<i>Cedecea lapagei</i>	This patent
25	20	<i>Chlamydia pneumoniae</i>	This patent
	21	<i>Chlamydia psittaci</i>	This patent
	22	<i>Chlamydia trachomatis</i>	This patent
	23	<i>Chryseobacterium meningosepticum</i>	This patent
	24	<i>Citrobacter amalonaticus</i>	This patent
30	25	<i>Citrobacter braakii</i>	This patent
	26	<i>Citrobacter koseri</i>	This patent
	27	<i>Citrobacter farmeri</i>	This patent
	28	<i>Citrobacter freundii</i>	This patent
	29	<i>Citrobacter sedlakii</i>	This patent
35	30	<i>Citrobacter werkmanii</i>	This patent
	31	<i>Citrobacter youngae</i>	This patent
	32	<i>Clostridium perfringens</i>	This patent
	33	<i>Comamonas acidovorans</i>	This patent
	34	<i>Corynebacterium bovis</i>	This patent
40	35	<i>Corynebacterium cervicis</i>	This patent
	36	<i>Corynebacterium flavesens</i>	This patent
	37	<i>Corynebacterium kutscheri</i>	This patent
	38	<i>Corynebacterium minutissimum</i>	This patent
	39	<i>Corynebacterium mycetoides</i>	This patent
45	40	<i>Corynebacterium pseudogenitalium</i>	This patent
	41	<i>Corynebacterium renale</i>	This patent
	42	<i>Corynebacterium ulcerans</i>	This patent
	43	<i>Corynebacterium urealyticum</i>	This patent
	44	<i>Corynebacterium xerosis</i>	This patent
50	45	<i>Coxiella burnetii</i>	This patent
	46	<i>Edwardsiella hoshinae</i>	This patent
	47	<i>Edwardsiella tarda</i>	This patent
	48	<i>Eikenella corrodens</i>	This patent
	49	<i>Enterobacter aerogenes</i>	This patent
55	50	<i>Enterobacter agglomerans</i>	This patent
	51	<i>Enterobacter amnigenus</i>	This patent
	52	<i>Enterobacter asburiae</i>	This patent
	53	<i>Enterobacter cancerogenus</i>	This patent
	54	<i>Enterobacter cloacae</i>	This patent
60	55	<i>Enterobacter gergoviae</i>	This patent
	56	<i>Enterobacter hormaechei</i>	This patent
	57	<i>Enterobacter sakazakii</i>	This patent
	58	<i>Enterococcus casseliflavus</i>	This patent
	59	<i>Enterococcus cecorum</i>	This patent
65	60	<i>Enterococcus dispar</i>	This patent
	61	<i>Enterococcus durans</i>	This patent

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	62	<i>Enterococcus faecalis</i>	This patent	<i>tuf</i>
	63	<i>Enterococcus faecalis</i>	This patent	<i>tuf</i>
	64	<i>Enterococcus faecium</i>	This patent	<i>tuf</i>
	65	<i>Enterococcus flavescens</i>	This patent	<i>tuf</i>
	66	<i>Enterococcus gallinarum</i>	This patent	<i>tuf</i>
10	67	<i>Enterococcus hirae</i>	This patent	<i>tuf</i>
	68	<i>Enterococcus mundtii</i>	This patent	<i>tuf</i>
	69	<i>Enterococcus pseudoavium</i>	This patent	<i>tuf</i>
	70	<i>Enterococcus raffinosus</i>	This patent	<i>tuf</i>
	71	<i>Enterococcus saccharolyticus</i>	This patent	<i>tuf</i>
15	72	<i>Enterococcus solitarius</i>	This patent	<i>tuf</i>
	73	<i>Enterococcus casseliflavus</i>	This patent	<i>tuf</i> (C)
	74	<i>Staphylococcus saprophyticus</i>	This patent	unknown
	75	<i>Enterococcus flavescens</i>	This patent	<i>tuf</i> (C)
	76	<i>Enterococcus gallinarum</i>	This patent	<i>tuf</i> (C)
20	77	<i>Ehrlichia canis</i>	This patent	<i>tuf</i>
	78	<i>Escherichia coli</i>	This patent	<i>tuf</i>
	79	<i>Escherichia fergusonii</i>	This patent	<i>tuf</i>
	80	<i>Escherichia hermannii</i>	This patent	<i>tuf</i>
	81	<i>Escherichia vulneris</i>	This patent	<i>tuf</i>
25	82	<i>Eubacterium lentum</i>	This patent	<i>tuf</i>
	83	<i>Eubacterium nodatum</i>	This patent	<i>tuf</i>
	84	<i>Ewingella americana</i>	This patent	<i>tuf</i>
	85	<i>Francisella tularensis</i>	This patent	<i>tuf</i>
	86	<i>Fusobacterium nucleatum</i> subsp. <i>polymorphum</i>	This patent	<i>tuf</i>
30	87	<i>Gemella haemolysans</i>	This patent	<i>tuf</i>
	88	<i>Gemella morbillorum</i>	This patent	<i>tuf</i>
	89	<i>Haemophilus actinomycetemcomitans</i>	This patent	<i>tuf</i>
	90	<i>Haemophilus aphrophilus</i>	This patent	<i>tuf</i>
	91	<i>Haemophilus ducreyi</i>	This patent	<i>tuf</i>
35	92	<i>Haemophilus haemolyticus</i>	This patent	<i>tuf</i>
	93	<i>Haemophilus parahaemolyticus</i>	This patent	<i>tuf</i>
	94	<i>Haemophilus parainfluenzae</i>	This patent	<i>tuf</i>
	95	<i>Haemophilus paraphrophilus</i>	This patent	<i>tuf</i>
	96	<i>Haemophilus segnis</i>	This patent	<i>tuf</i>
40	97	<i>Hafnia alvei</i>	This patent	<i>tuf</i>
	98	<i>Kingella kingae</i>	This patent	<i>tuf</i>
	99	<i>Klebsiella ornithinolytica</i>	This patent	<i>tuf</i>
	100	<i>Klebsiella oxytoca</i>	This patent	<i>tuf</i>
	101	<i>Klebsiella planticola</i>	This patent	<i>tuf</i>
45	102	<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	This patent	<i>tuf</i>
	103	<i>Klebsiella pneumoniae pneumoniae</i>	This patent	<i>tuf</i>
	104	<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	This patent	<i>tuf</i>
	105	<i>Kluyvera ascorbata</i>	This patent	<i>tuf</i>
	106	<i>Kluyvera cryocrescens</i>	This patent	<i>tuf</i>
50	107	<i>Kluyvera georgiana</i>	This patent	<i>tuf</i>
	108	<i>Lactobacillus casei</i> subsp. <i>casei</i>	This patent	<i>tuf</i>
	109	<i>Lactococcus lactis</i> subsp. <i>lactis</i>	This patent	<i>tuf</i>
	110	<i>Leclercia adecarboxylata</i>	This patent	<i>tuf</i>
	111	<i>Legionella micdadei</i>	This patent	<i>tuf</i>
55	112	<i>Legionella pneumophila</i> subsp. <i>pneumophila</i>	This patent	<i>tuf</i>
	113	<i>Leminorella grimonii</i>	This patent	<i>tuf</i>
	114	<i>Leminorella richardii</i>	This patent	<i>tuf</i>
	115	<i>Leptospira interrogans</i>	This patent	<i>tuf</i>
	116	<i>Megamonas hypermegale</i>	This patent	<i>tuf</i>
60	117	<i>Mitsuokella multacidus</i>	This patent	<i>tuf</i>
	118	<i>Mobiluncus curtisii</i> subsp. <i>holmesii</i>	This patent	<i>tuf</i>
	119	<i>Moellerella wisconsensis</i>	This patent	<i>tuf</i>
	120	<i>Moraxella catarrhalis</i>	This patent	<i>tuf</i>
	121	<i>Morganella morganii</i> subsp. <i>morganii</i>	This patent	<i>tuf</i>
65	122	<i>Mycobacterium tuberculosis</i>	This patent	<i>tuf</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	123	<i>Neisseria cinerea</i>	This patent	tuf
	124	<i>Neisseria elongata</i> subsp. <i>elongata</i>	This patent	tuf
	125	<i>Neisseria flavescens</i>	This patent	tuf
	126	<i>Neisseria gonorrhoeae</i>	This patent	tuf
	127	<i>Neisseria lactamica</i>	This patent	tuf
10	128	<i>Neisseria meningitidis</i>	This patent	tuf
	129	<i>Neisseria mucosa</i>	This patent	tuf
	130	<i>Neisseria sicca</i>	This patent	tuf
	131	<i>Neisseria subflava</i>	This patent	tuf
	132	<i>Neisseria weaveri</i>	This patent	tuf
15	133	<i>Ochrobactrum anthropi</i>	This patent	tuf
	134	<i>Pantoea agglomerans</i>	This patent	tuf
	135	<i>Pantoea dispersa</i>	This patent	tuf
	136	<i>Pasteurella multocida</i>	This patent	tuf
	137	<i>Peptostreptococcus anaerobius</i>	This patent	tuf
20	138	<i>Peptostreptococcus asaccharolyticus</i>	This patent	tuf
	139	<i>Peptostreptococcus prevotii</i>	This patent	tuf
	140	<i>Porphyromonas asaccharolytica</i>	This patent	tuf
	141	<i>Porphyromonas gingivalis</i>	This patent	tuf
	142	<i>Pragia fontium</i>	This patent	tuf
25	143	<i>Prevotella melaninogenica</i>	This patent	tuf
	144	<i>Prevotella oralis</i>	This patent	tuf
	145	<i>Propionibacterium acnes</i>	This patent	tuf
	146	<i>Proteus mirabilis</i>	This patent	tuf
	147	<i>Proteus penneri</i>	This patent	tuf
30	148	<i>Proteus vulgaris</i>	This patent	tuf
	149	<i>Providencia alcalifaciens</i>	This patent	tuf
	150	<i>Providencia rettgeri</i>	This patent	tuf
	151	<i>Providencia rustigianii</i>	This patent	tuf
	152	<i>Providencia stuartii</i>	This patent	tuf
35	153	<i>Pseudomonas aeruginosa</i>	This patent	tuf
	154	<i>Pseudomonas fluorescens</i>	This patent	tuf
	155	<i>Pseudomonas stutzeri</i>	This patent	tuf
	156	<i>Psychrobacter phenylpyruvicum</i>	This patent	tuf
	157	<i>Rahnella aquatilis</i>	This patent	tuf
40	158	<i>Salmonella choleraesuis</i> subsp. <i>arizonae</i>	This patent	tuf
	159	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	This patent	tuf
		serotype Choleraesuis		
	160	<i>Salmonella choleraesuis</i> subsp. <i>diarizonae</i>	This patent	tuf
	161	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	This patent	tuf
45		serotype Heidelberg		
	162	<i>Salmonella choleraesuis</i> subsp. <i>houtenae</i>	This patent	tuf
	163	<i>Salmonella choleraesuis</i> subsp. <i>indica</i>	This patent	tuf
	164	<i>Salmonella choleraesuis</i> subsp. <i>salamae</i>	This patent	tuf
	165	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Typhi	This patent	tuf
50	166	<i>Serratia fonticola</i>	This patent	tuf
	167	<i>Serratia liquefaciens</i>	This patent	tuf
	168	<i>Serratia marcescens</i>	This patent	tuf
	169	<i>Serratia odorifera</i>	This patent	tuf
	170	<i>Serratia plymuthica</i>	This patent	tuf
55	171	<i>Serratia rubidaea</i>	This patent	tuf
	172	<i>Shigella boydii</i>	This patent	tuf
	173	<i>Shigella dysenteriae</i>	This patent	tuf
	174	<i>Shigella flexneri</i>	This patent	tuf
	175	<i>Shigella sonnei</i>	This patent	tuf
60	176	<i>Staphylococcus aureus</i>	This patent	tuf
	177	<i>Staphylococcus aureus</i>	This patent	tuf
	178	<i>Staphylococcus aureus</i>	This patent	tuf
	179	<i>Staphylococcus aureus</i>	This patent	tuf
	180	<i>Staphylococcus aureus</i> subsp. <i>aureus</i>	This patent	tuf
65	181	<i>Staphylococcus auricularis</i>	This patent	tuf
	182	<i>Staphylococcus capitis</i> subsp. <i>capitis</i>	This patent	tuf

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	183	<i>Macrococcus caseolyticus</i>	This patent	<i>tuf</i>
	184	<i>Staphylococcus cohnii</i> subsp. <i>cohnii</i>	This patent	<i>tuf</i>
	185	<i>Staphylococcus epidermidis</i>	This patent	<i>tuf</i>
	186	<i>Staphylococcus haemolyticus</i>	This patent	<i>tuf</i>
	187	<i>Staphylococcus warneri</i>	This patent	<i>tuf</i>
10	188	<i>Staphylococcus haemolyticus</i>	This patent	<i>tuf</i>
	189	<i>Staphylococcus haemolyticus</i>	This patent	<i>tuf</i>
	190	<i>Staphylococcus haemolyticus</i>	This patent	<i>tuf</i>
	191	<i>Staphylococcus hominis</i> subsp. <i>hominis</i>	This patent	<i>tuf</i>
	192	<i>Staphylococcus warneri</i>	This patent	<i>tuf</i>
15	193	<i>Staphylococcus hominis</i>	This patent	<i>tuf</i>
	194	<i>Staphylococcus hominis</i>	This patent	<i>tuf</i>
	195	<i>Staphylococcus hominis</i>	This patent	<i>tuf</i>
	196	<i>Staphylococcus hominis</i>	This patent	<i>tuf</i>
	197	<i>Staphylococcus lugdunensis</i>	This patent	<i>tuf</i>
20	198	<i>Staphylococcus saprophyticus</i>	This patent	<i>tuf</i>
	199	<i>Staphylococcus saprophyticus</i>	This patent	<i>tuf</i>
	200	<i>Staphylococcus saprophyticus</i>	This patent	<i>tuf</i>
	201	<i>Staphylococcus sciuri</i> subsp. <i>sciuri</i>	This patent	<i>tuf</i>
	202	<i>Staphylococcus warneri</i>	This patent	<i>tuf</i>
25	203	<i>Staphylococcus warneri</i>	This patent	<i>tuf</i>
	204	<i>Bifidobacterium longum</i>	This patent	<i>tuf</i>
	205	<i>Stenotrophomonas maltophilia</i>	This patent	<i>tuf</i>
	206	<i>Streptococcus acidominimus</i>	This patent	<i>tuf</i>
	207	<i>Streptococcus agalactiae</i>	This patent	<i>tuf</i>
30	208	<i>Streptococcus agalactiae</i>	This patent	<i>tuf</i>
	209	<i>Streptococcus agalactiae</i>	This patent	<i>tuf</i>
	210	<i>Streptococcus agalactiae</i>	This patent	<i>tuf</i>
	211	<i>Streptococcus anginosus</i>	This patent	<i>tuf</i>
	212	<i>Streptococcus bovis</i>	This patent	<i>tuf</i>
35	213	<i>Streptococcus anginosus</i>	This patent	<i>tuf</i>
	214	<i>Streptococcus cricetus</i>	This patent	<i>tuf</i>
	215	<i>Streptococcus cristatus</i>	This patent	<i>tuf</i>
	216	<i>Streptococcus downei</i>	This patent	<i>tuf</i>
	217	<i>Streptococcus dysgalactiae</i>	This patent	<i>tuf</i>
40	218	<i>Streptococcus equi</i> subsp. <i>equi</i>	This patent	<i>tuf</i>
	219	<i>Streptococcus ferus</i>	This patent	<i>tuf</i>
	220	<i>Streptococcus gordonii</i>	This patent	<i>tuf</i>
	221	<i>Streptococcus anginosus</i>	This patent	<i>tuf</i>
	222	<i>Streptococcus macacae</i>	This patent	<i>tuf</i>
45	223	<i>Streptococcus gordonii</i>	This patent	<i>tuf</i>
	224	<i>Streptococcus mutans</i>	This patent	<i>tuf</i>
	225	<i>Streptococcus parasanguinis</i>	This patent	<i>tuf</i>
	226	<i>Streptococcus rattii</i>	This patent	<i>tuf</i>
	227	<i>Streptococcus sanguinis</i>	This patent	<i>tuf</i>
50	228	<i>Streptococcus sobrinus</i>	This patent	<i>tuf</i>
	229	<i>Streptococcus suis</i>	This patent	<i>tuf</i>
	230	<i>Streptococcus uberis</i>	This patent	<i>tuf</i>
	231	<i>Streptococcus vestibularis</i>	This patent	<i>tuf</i>
	232	<i>Tatumella tyseos</i>	This patent	<i>tuf</i>
55	233	<i>Trabulsiella guamensis</i>	This patent	<i>tuf</i>
	234	<i>Veillonella parvula</i>	This patent	<i>tuf</i>
	235	<i>Yersinia enterocolitica</i>	This patent	<i>tuf</i>
	236	<i>Yersinia frederiksenii</i>	This patent	<i>tuf</i>
	237	<i>Yersinia intermedia</i>	This patent	<i>tuf</i>
60	238	<i>Yersinia pestis</i>	This patent	<i>tuf</i>
	239	<i>Yersinia pseudotuberculosis</i>	This patent	<i>tuf</i>
	240	<i>Yersinia rohdei</i>	This patent	<i>tuf</i>
	241	<i>Yokenella regensburgei</i>	This patent	<i>tuf</i>
	242	<i>Achromobacter xylosoxidans</i> subsp. <i>denitrificans</i>	This patent	<i>atpD</i>
65	243	<i>Acinetobacter baumannii</i>	This patent	<i>atpD</i>
	244	<i>Acinetobacter lwoffii</i>	This patent	<i>atpD</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	245	<i>Staphylococcus saprophyticus</i>	This patent	<i>atpD</i>
	246	<i>Alcaligenes faecalis</i> subsp. <i>faecalis</i>	This patent	<i>atpD</i>
	247	<i>Bacillus anthracis</i>	This patent	<i>atpD</i>
	248	<i>Bacillus cereus</i>	This patent	<i>atpD</i>
	249	<i>Bacteroides distasonis</i>	This patent	<i>atpD</i>
10	250	<i>Bacteroides ovatus</i>	This patent	<i>atpD</i>
	251	<i>Lectercia adecarboxylata</i>	This patent	<i>atpD</i>
	252	<i>Stenotrophomonas maltophilia</i>	This patent	<i>atpD</i>
	253	<i>Bartonella henselae</i>	This patent	<i>atpD</i>
	254	<i>Bifidobacterium adolescentis</i>	This patent	<i>atpD</i>
15	255	<i>Brucella abortus</i>	This patent	<i>atpD</i>
	256	<i>Cedecea davisae</i>	This patent	<i>atpD</i>
	257	<i>Cedecea lapagei</i>	This patent	<i>atpD</i>
	258	<i>Cedecea neteri</i>	This patent	<i>atpD</i>
	259	<i>Chryseobacterium meningosepticum</i>	This patent	<i>atpD</i>
20	260	<i>Citrobacter amalonaticus</i>	This patent	<i>atpD</i>
	261	<i>Citrobacter braakii</i>	This patent	<i>atpD</i>
	262	<i>Citrobacter koseri</i>	This patent	<i>atpD</i>
	263	<i>Citrobacter farmeri</i>	This patent	<i>atpD</i>
	264	<i>Citrobacter freundii</i>	This patent	<i>atpD</i>
25	265	<i>Citrobacter koseri</i>	This patent	<i>atpD</i>
	266	<i>Citrobacter sedlakii</i>	This patent	<i>atpD</i>
	267	<i>Citrobacter werkmanii</i>	This patent	<i>atpD</i>
	268	<i>Citrobacter youngae</i>	This patent	<i>atpD</i>
	269	<i>Clostridium innocuum</i>	This patent	<i>atpD</i>
30	270	<i>Clostridium perfringens</i>	This patent	<i>atpD</i>
	272	<i>Corynebacterium diphtheriae</i>	This patent	<i>atpD</i>
	273	<i>Corynebacterium pseudodiphtheriticum</i>	This patent	<i>atpD</i>
	274	<i>Corynebacterium ulcerans</i>	This patent	<i>atpD</i>
	275	<i>Corynebacterium urealyticum</i>	This patent	<i>atpD</i>
35	276	<i>Coxiella burnetii</i>	This patent	<i>atpD</i>
	277	<i>Edwardsiella hoshinae</i>	This patent	<i>atpD</i>
	278	<i>Edwardsiella tarda</i>	This patent	<i>atpD</i>
	279	<i>Eikenella corrodens</i>	This patent	<i>atpD</i>
	280	<i>Enterobacter agglomerans</i>	This patent	<i>atpD</i>
40	281	<i>Enterobacter amnigenus</i>	This patent	<i>atpD</i>
	282	<i>Enterobacter asburiae</i>	This patent	<i>atpD</i>
	283	<i>Enterobacter cancerogenus</i>	This patent	<i>atpD</i>
	284	<i>Enterobacter cloacae</i>	This patent	<i>atpD</i>
	285	<i>Enterobacter gergoviae</i>	This patent	<i>atpD</i>
45	286	<i>Enterobacter hormaechei</i>	This patent	<i>atpD</i>
	287	<i>Enterobacter sakazakii</i>	This patent	<i>atpD</i>
	288	<i>Enterococcus avium</i>	This patent	<i>atpD</i>
	289	<i>Enterococcus casseliflavus</i>	This patent	<i>atpD</i>
	290	<i>Enterococcus durans</i>	This patent	<i>atpD</i>
50	291	<i>Enterococcus faecalis</i>	This patent	<i>atpD</i>
	292	<i>Enterococcus faecium</i>	This patent	<i>atpD</i>
	293	<i>Enterococcus gallinarum</i>	This patent	<i>atpD</i>
	294	<i>Enterococcus saccharolyticus</i>	This patent	<i>atpD</i>
	295	<i>Escherichia fergusonii</i>	This patent	<i>atpD</i>
55	296	<i>Escherichia hermannii</i>	This patent	<i>atpD</i>
	297	<i>Escherichia vulneris</i>	This patent	<i>atpD</i>
	298	<i>Eubacterium lentum</i>	This patent	<i>atpD</i>
	299	<i>Ewingella americana</i>	This patent	<i>atpD</i>
	300	<i>Francisella tularensis</i>	This patent	<i>atpD</i>
60	301	<i>Fusobacterium gonidiaformans</i>	This patent	<i>atpD</i>
	302	<i>Fusobacterium necrophorum</i> subsp. <i>necrophorum</i>	This patent	<i>atpD</i>
	303	<i>Fusobacterium nucleatum</i> subsp. <i>polymorphum</i>	This patent	<i>atpD</i>
	304	<i>Gardnerella vaginalis</i>	This patent	<i>atpD</i>
	305	<i>Gemella haemolysans</i>	This patent	<i>atpD</i>
65	306	<i>Gemella morbillorum</i>	This patent	<i>atpD</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	307	<i>Haemophilus ducreyi</i>	This patent	<i>atpD</i>
	308	<i>Haemophilus haemolyticus</i>	This patent	<i>atpD</i>
	309	<i>Haemophilus parahaemolyticus</i>	This patent	<i>atpD</i>
	310	<i>Haemophilus parainfluenzae</i>	This patent	<i>atpD</i>
	311	<i>Hafnia alvei</i>	This patent	<i>atpD</i>
10	312	<i>Kingella kingae</i>	This patent	<i>atpD</i>
	313	<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	This patent	<i>atpD</i>
	314	<i>Klebsiella ornithinolytica</i>	This patent	<i>atpD</i>
	315	<i>Klebsiella oxytoca</i>	This patent	<i>atpD</i>
	316	<i>Klebsiella planticola</i>	This patent	<i>atpD</i>
15	317	<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	This patent	<i>atpD</i>
	318	<i>Kluyvera ascorbata</i>	This patent	<i>atpD</i>
	319	<i>Kluyvera cryocrescens</i>	This patent	<i>atpD</i>
	320	<i>Kluyvera georgiana</i>	This patent	<i>atpD</i>
	321	<i>Lactobacillus acidophilus</i>	This patent	<i>atpD</i>
20	322	<i>Legionella pneumophila</i> subsp. <i>pneumophila</i>	This patent	<i>atpD</i>
	323	<i>Leminorella grimonii</i>	This patent	<i>atpD</i>
	324	<i>Listeria monocytogenes</i>	This patent	<i>atpD</i>
	325	<i>Micrococcus lylae</i>	This patent	<i>atpD</i>
	326	<i>Moellerella wisconsensis</i>	This patent	<i>atpD</i>
25	327	<i>Moraxella catarrhalis</i>	This patent	<i>atpD</i>
	328	<i>Moraxella osloensis</i>	This patent	<i>atpD</i>
	329	<i>Morganella morganii</i> subsp. <i>morganii</i>	This patent	<i>atpD</i>
	330	<i>Pantoea agglomerans</i>	This patent	<i>atpD</i>
	331	<i>Pantoea dispersa</i>	This patent	<i>atpD</i>
30	332	<i>Pasteurella multocida</i>	This patent	<i>atpD</i>
	333	<i>Pragia fontium</i>	This patent	<i>atpD</i>
	334	<i>Proteus mirabilis</i>	This patent	<i>atpD</i>
	335	<i>Proteus vulgaris</i>	This patent	<i>atpD</i>
	336	<i>Providencia alcalifaciens</i>	This patent	<i>atpD</i>
35	337	<i>Providencia rettgeri</i>	This patent	<i>atpD</i>
	338	<i>Providencia rustigianii</i>	This patent	<i>atpD</i>
	339	<i>Providencia stuartii</i>	This patent	<i>atpD</i>
	340	<i>Psychrobacter phenylpyruvicum</i>	This patent	<i>atpD</i>
	341	<i>Rahnella aquatilis</i>	This patent	<i>atpD</i>
40	342	<i>Salmonella choleraesuis</i> subsp. <i>arizonae</i>	This patent	<i>atpD</i>
	343	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	This patent	<i>atpD</i>
		serotype Choleraesuis		
	344	<i>Salmonella choleraesuis</i> subsp. <i>diarizonae</i>	This patent	<i>atpD</i>
	345	<i>Salmonella choleraesuis</i> subsp. <i>houtenae</i>	This patent	<i>atpD</i>
45	346	<i>Salmonella choleraesuis</i> subsp. <i>indica</i>	This patent	<i>atpD</i>
	347	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	This patent	<i>atpD</i>
		serotype Paratyphi A		
	348	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	This patent	<i>atpD</i>
		serotype Paratyphi B		
50	349	<i>Salmonella choleraesuis</i> subsp. <i>salamae</i>	This patent	<i>atpD</i>
	350	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Typhi	This patent	<i>atpD</i>
	351	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	This patent	<i>atpD</i>
		serotype Typhimurium		
	352	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	This patent	<i>atpD</i>
55		serotype Virchow		
	353	<i>Serratia ficaria</i>	This patent	<i>atpD</i>
	354	<i>Serratia fonticola</i>	This patent	<i>atpD</i>
	355	<i>Serratia grimesii</i>	This patent	<i>atpD</i>
	356	<i>Serratia liquefaciens</i>	This patent	<i>atpD</i>
60	357	<i>Serratia marcescens</i>	This patent	<i>atpD</i>
	358	<i>Serratia odorifera</i>	This patent	<i>atpD</i>
	359	<i>Serratia plymuthica</i>	This patent	<i>atpD</i>
	360	<i>Serratia rubidaea</i>	This patent	<i>atpD</i>
	361	<i>Pseudomonas putida</i>	This patent	<i>atpD</i>
65	362	<i>Shigella boydii</i>	This patent	<i>atpD</i>
	363	<i>Shigella dysenteriae</i>	This patent	<i>atpD</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source Gene*
5	364	<i>Shigella flexneri</i>	This patent
	365	<i>Shigella sonnei</i>	This patent
	366	<i>Staphylococcus aureus</i>	This patent
	367	<i>Staphylococcus auricularis</i>	This patent
	368	<i>Staphylococcus capitis</i> subsp. <i>capitis</i>	This patent
10	369	<i>Staphylococcus cohnii</i> subsp. <i>cohnii</i>	This patent
	370	<i>Staphylococcus epidermidis</i>	This patent
	371	<i>Staphylococcus haemolyticus</i>	This patent
	372	<i>Staphylococcus hominis</i> subsp. <i>hominis</i>	This patent
	373	<i>Staphylococcus hominis</i>	This patent
15	374	<i>Staphylococcus lugdunensis</i>	This patent
	375	<i>Staphylococcus saprophyticus</i>	This patent
	376	<i>Staphylococcus simulans</i>	This patent
	377	<i>Staphylococcus warneri</i>	This patent
	378	<i>Streptococcus acidominimus</i>	This patent
20	379	<i>Streptococcus agalactiae</i>	This patent
	380	<i>Streptococcus agalactiae</i>	This patent
	381	<i>Streptococcus agalactiae</i>	This patent
	382	<i>Streptococcus agalactiae</i>	This patent
	383	<i>Streptococcus agalactiae</i>	This patent
25	384	<i>Streptococcus dysgalactiae</i>	This patent
	385	<i>Streptococcus equi</i> subsp. <i>equi</i>	This patent
	386	<i>Streptococcus anginosus</i>	This patent
	387	<i>Streptococcus salivarius</i>	This patent
	388	<i>Streptococcus suis</i>	This patent
30	389	<i>Streptococcus uberis</i>	This patent
	390	<i>Tatumella ptyseos</i>	This patent
	391	<i>Trabulsiella guamensis</i>	This patent
	392	<i>Yersinia bercovieri</i>	This patent
	393	<i>Yersinia enterocolitica</i>	This patent
35	394	<i>Yersinia frederiksenii</i>	This patent
	395	<i>Yersinia intermedia</i>	This patent
	396	<i>Yersinia pseudotuberculosis</i>	This patent
	397	<i>Yersinia rohdei</i>	This patent
	398	<i>Yokenella regensburgei</i>	This patent
40	399	<i>Yarrowia lipolytica</i>	This patent
	400	<i>Absidia corymbifera</i>	This patent
	401	<i>Alternaria alternata</i>	This patent
	402	<i>Aspergillus flavus</i>	This patent
	403	<i>Aspergillus fumigatus</i>	This patent
45	404	<i>Aspergillus fumigatus</i>	This patent
	405	<i>Aspergillus niger</i>	This patent
	406	<i>Blastoschizomyces capitatus</i>	This patent
	407	<i>Candida albicans</i>	This patent
	408	<i>Candida albicans</i>	This patent
50	409	<i>Candida albicans</i>	This patent
	410	<i>Candida albicans</i>	This patent
	411	<i>Candida albicans</i>	This patent
	412	<i>Candida dubliniensis</i>	This patent
	413	<i>Candida catenulata</i>	This patent
55	414	<i>Candida dubliniensis</i>	This patent
	415	<i>Candida dubliniensis</i>	This patent
	416	<i>Candida famata</i>	This patent
	417	<i>Candida glabrata</i>	WO98/20157
	418	<i>Candida guilliermondii</i>	This patent
60	419	<i>Candida haemulonii</i>	This patent
	420	<i>Candida inconspicua</i>	This patent
	421	<i>Candida kefyr</i>	This patent
	422	<i>Candida krusei</i>	WO98/20157
	423	<i>Candida lambica</i>	This patent
65	424	<i>Candida lusitaniae</i>	This patent
	425	<i>Candida norvegensis</i>	This patent

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	426	<i>Candida parapsilosis</i>	WO98/20157	<i>tuf</i> (EF-1)
	427	<i>Candida rugosa</i>	This patent	<i>tuf</i> (EF-1)
	428	<i>Candida sphaerica</i>	This patent	<i>tuf</i> (EF-1)
	429	<i>Candida tropicalis</i>	WO98/20157	<i>tuf</i> (EF-1)
	430	<i>Candida utilis</i>	This patent	<i>tuf</i> (EF-1)
10	431	<i>Candida viswanathii</i>	This patent	<i>tuf</i> (EF-1)
	432	<i>Candida zeylanoides</i>	This patent	<i>tuf</i> (EF-1)
	433	<i>Coccidioides immitis</i>	This patent	<i>tuf</i> (EF-1)
	434	<i>Cryptococcus albidus</i>	This patent	<i>tuf</i> (EF-1)
	435	<i>Exophiala jeanselmei</i>	This patent	<i>tuf</i> (EF-1)
15	436	<i>Fusarium oxysporum</i>	This patent	<i>tuf</i> (EF-1)
	437	<i>Geotrichum</i> sp.	This patent	<i>tuf</i> (EF-1)
	438	<i>Histoplasma capsulatum</i>	This patent	<i>tuf</i> (EF-1)
	439	<i>Issatchenkia orientalis</i> Kudrjanzev	This patent	<i>tuf</i> (EF-1)
	440	<i>Malassezia furfur</i>	This patent	<i>tuf</i> (EF-1)
20	441	<i>Malassezia pachydermatis</i>	This patent	<i>tuf</i> (EF-1)
	442	<i>Malbranchea filamentosa</i>	This patent	<i>tuf</i> (EF-1)
	443	<i>Metschnikowia pulcherrima</i>	This patent	<i>tuf</i> (EF-1)
	444	<i>Paecilomyces lilacinus</i>	This patent	<i>tuf</i> (EF-1)
	445	<i>Paracoccidioides brasiliensis</i>	This patent	<i>tuf</i> (EF-1)
25	446	<i>Penicillium marneffei</i>	This patent	<i>tuf</i> (EF-1)
	447	<i>Pichia anomala</i>	This patent	<i>tuf</i> (EF-1)
	448	<i>Pichia anomala</i>	This patent	<i>tuf</i> (EF-1)
	449	<i>Pseudallescheria boydii</i>	This patent	<i>tuf</i> (EF-1)
	450	<i>Rhizopus oryzae</i>	This patent	<i>tuf</i> (EF-1)
30	451	<i>Rhodotorula minuta</i>	This patent	<i>tuf</i> (EF-1)
	452	<i>Sporobolomyces salmonicolor</i>	This patent	<i>tuf</i> (EF-1)
	453	<i>Sporothrix schenckii</i>	This patent	<i>tuf</i> (EF-1)
	454	<i>Stephanoascus ciferrii</i>	This patent	<i>tuf</i> (EF-1)
	455	<i>Trichophyton mentagrophytes</i>	This patent	<i>tuf</i> (EF-1)
35	456	<i>Trichosporon cutaneum</i>	This patent	<i>tuf</i> (EF-1)
	457	<i>Wangiella dermatitidis</i>	This patent	<i>tuf</i> (EF-1)
	458	<i>Aspergillus fumigatus</i>	This patent	<i>atpD</i>
	459	<i>Blastoschizomyces capitatus</i>	This patent	<i>atpD</i>
	460	<i>Candida albicans</i>	This patent	<i>atpD</i>
40	461	<i>Candida dubliniensis</i>	This patent	<i>atpD</i>
	462	<i>Candida famata</i>	This patent	<i>atpD</i>
	463	<i>Candida glabrata</i>	This patent	<i>atpD</i>
	464	<i>Candida guilliermondii</i>	This patent	<i>atpD</i>
	465	<i>Candida haemulonii</i>	This patent	<i>atpD</i>
45	466	<i>Candida inconspicua</i>	This patent	<i>atpD</i>
	467	<i>Candida kefyr</i>	This patent	<i>atpD</i>
	468	<i>Candida krusei</i>	This patent	<i>atpD</i>
	469	<i>Candida lambica</i>	This patent	<i>atpD</i>
	470	<i>Candida lusitanae</i>	This patent	<i>atpD</i>
50	471	<i>Candida norvegensis</i>	This patent	<i>atpD</i>
	472	<i>Candida parapsilosis</i>	This patent	<i>atpD</i>
	473	<i>Candida rugosa</i>	This patent	<i>atpD</i>
	474	<i>Candida sphaerica</i>	This patent	<i>atpD</i>
	475	<i>Candida tropicalis</i>	This patent	<i>atpD</i>
55	476	<i>Candida utilis</i>	This patent	<i>atpD</i>
	477	<i>Candida viswanathii</i>	This patent	<i>atpD</i>
	478	<i>Candida zeylanoides</i>	This patent	<i>atpD</i>
	479	<i>Coccidioides immitis</i>	This patent	<i>atpD</i>
	480	<i>Cryptococcus albidus</i>	This patent	<i>atpD</i>
60	481	<i>Fusarium oxysporum</i>	This patent	<i>atpD</i>
	482	<i>Geotrichum</i> sp.	This patent	<i>atpD</i>
	483	<i>Histoplasma capsulatum</i>	This patent	<i>atpD</i>
	484	<i>Malassezia furfur</i>	This patent	<i>atpD</i>
	485	<i>Malassezia pachydermatis</i>	This patent	<i>atpD</i>
65	486	<i>Metschnikowia pulcherrima</i>	This patent	<i>atpD</i>
	487	<i>Penicillium marneffei</i>	This patent	<i>atpD</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	488	<i>Pichia anomala</i>	This patent	<i>atpD</i>
	489	<i>Pichia anomala</i>	This patent	<i>atpD</i>
	490	<i>Rhodotorula minuta</i>	This patent	<i>atpD</i>
	491	<i>Rhodotorula mucilaginosa</i>	This patent	<i>atpD</i>
	492	<i>Sporobolomyces salmonicolor</i>	This patent	<i>atpD</i>
10	493	<i>Sporothrix schenckii</i>	This patent	<i>atpD</i>
	494	<i>Stephanoascus ciferrii</i>	This patent	<i>atpD</i>
	495	<i>Trichophyton mentagrophytes</i>	This patent	<i>atpD</i>
	496	<i>Wangiella dermatitidis</i>	This patent	<i>atpD</i>
	497	<i>Yarrowia lipolytica</i>	This patent	<i>atpD</i>
15	498	<i>Aspergillus fumigatus</i>	This patent	<i>tuf</i> (M)
	499	<i>Blastoschizomyces capitatus</i>	This patent	<i>tuf</i> (M)
	500	<i>Candida rugosa</i>	This patent	<i>tuf</i> (M)
	501	<i>Coccidioides immitis</i>	This patent	<i>tuf</i> (M)
	502	<i>Fusarium oxysporum</i>	This patent	<i>tuf</i> (M)
20	503	<i>Histoplasma capsulatum</i>	This patent	<i>tuf</i> (M)
	504	<i>Paracoccidioides brasiliensis</i>	This patent	<i>tuf</i> (M)
	505	<i>Penicillium marneffeii</i>	This patent	<i>tuf</i> (M)
	506	<i>Pichia anomala</i>	This patent	<i>tuf</i> (M)
	507	<i>Trichophyton mentagrophytes</i>	This patent	<i>tuf</i> (M)
25	508	<i>Yarrowia lipolytica</i>	This patent	<i>tuf</i> (M)
	509	<i>Babesia bigemina</i>	This patent	<i>tuf</i> (EF-1)
	510	<i>Babesia bovis</i>	This patent	<i>tuf</i> (EF-1)
	511	<i>Crithidia fasciculata</i>	This patent	<i>tuf</i> (EF-1)
	512	<i>Entamoeba histolytica</i>	This patent	<i>tuf</i> (EF-1)
30	513	<i>Giardia lamblia</i>	This patent	<i>tuf</i> (EF-1)
	514	<i>Leishmania tropica</i>	This patent	<i>tuf</i> (EF-1)
	515	<i>Leishmania aethiopica</i>	This patent	<i>tuf</i> (EF-1)
	516	<i>Leishmania tropica</i>	This patent	<i>tuf</i> (EF-1)
	517	<i>Leishmania donovani</i>	This patent	<i>tuf</i> (EF-1)
35	518	<i>Leishmania infantum</i>	This patent	<i>tuf</i> (EF-1)
	519	<i>Leishmania enriettii</i>	This patent	<i>tuf</i> (EF-1)
	520	<i>Leishmania gerbilli</i>	This patent	<i>tuf</i> (EF-1)
	521	<i>Leishmania hertigi</i>	This patent	<i>tuf</i> (EF-1)
	522	<i>Leishmania major</i>	This patent	<i>tuf</i> (EF-1)
40	523	<i>Leishmania amazonensis</i>	This patent	<i>tuf</i> (EF-1)
	524	<i>Leishmania mexicana</i>	This patent	<i>tuf</i> (EF-1)
	525	<i>Leishmania tarentolae</i>	This patent	<i>tuf</i> (EF-1)
	526	<i>Leishmania tropica</i>	This patent	<i>tuf</i> (EF-1)
	527	<i>Neospora caninum</i>	This patent	<i>tuf</i> (EF-1)
45	528	<i>Trichomonas vaginalis</i>	This patent	<i>tuf</i> (EF-1)
	529	<i>Trypanosoma brucei</i> subsp. <i>brucei</i>	This patent	<i>tuf</i> (EF-1)
	530	<i>Crithidia fasciculata</i>	This patent	<i>atpD</i>
	531	<i>Leishmania tropica</i>	This patent	<i>atpD</i>
	532	<i>Leishmania aethiopica</i>	This patent	<i>atpD</i>
50	533	<i>Leishmania donovani</i>	This patent	<i>atpD</i>
	534	<i>Leishmania infantum</i>	This patent	<i>atpD</i>
	535	<i>Leishmania gerbilli</i>	This patent	<i>atpD</i>
	536	<i>Leishmania hertigi</i>	This patent	<i>atpD</i>
	537	<i>Leishmania major</i>	This patent	<i>atpD</i>
55	538	<i>Leishmania amazonensis</i>	This patent	<i>atpD</i>
	607	<i>Enterococcus faecalis</i>	WO98/20157	<i>tuf</i>
	608	<i>Enterococcus faecium</i>	WO98/20157	<i>tuf</i>
	609	<i>Enterococcus gallinarum</i>	WO98/20157	<i>tuf</i>
	610	<i>Haemophilus influenzae</i>	WO98/20157	<i>tuf</i>
60	611	<i>Staphylococcus epidermidis</i>	WO98/20157	<i>tuf</i>
	612	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	This patent	<i>tuf</i>
		serotype Paratyphi A		
	613	<i>Serratia ficaria</i>	This patent	<i>tuf</i>
	614	<i>Enterococcus malodoratus</i>	This patent	<i>tuf</i> (C)
65	615	<i>Enterococcus durans</i>	This patent	<i>tuf</i> (C)
	616	<i>Enterococcus pseudoavium</i>	This patent	<i>tuf</i> (C)

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	617	<i>Enterococcus dispar</i>	This patent	<i>tuf</i> (C)
	618	<i>Enterococcus avium</i>	This patent	<i>tuf</i> (C)
	619	<i>Saccharomyces cerevisiae</i>	Database	<i>tuf</i> (M)
	621	<i>Enterococcus faecium</i>	This patent	<i>tuf</i> (C)
	622	<i>Saccharomyces cerevisiae</i>	This patent	<i>tuf</i> (EF-1)
10	623	<i>Cryptococcus neoformans</i>	This patent	<i>tuf</i> (EF-1)
	624	<i>Candida albicans</i>	WO98/20157	<i>tuf</i> (EF-1)
	662	<i>Corynebacterium diphtheriae</i>	WO98/20157	<i>tuf</i>
	663	<i>Candida catenulata</i>	This patent	<i>atpD</i>
	665	<i>Saccharomyces cerevisiae</i>	Database	<i>tuf</i> (EF-1)
15	666	<i>Saccharomyces cerevisiae</i>	Database	<i>atpD</i>
	667	<i>Trypanosoma cruzi</i>	This patent	<i>atpD</i>
	668	<i>Corynebacterium glutamicum</i>	Database	<i>tuf</i>
	669	<i>Escherichia coli</i>	Database	<i>atpD</i>
	670	<i>Helicobacter pylori</i>	Database	<i>atpD</i>
20	671	<i>Clostridium acetobutylicum</i>	Database	<i>atpD</i>
	672	<i>Cytophaga lytica</i>	Database	<i>atpD</i>
	673	<i>Ehrlichia risticii</i>	This patent	<i>atpD</i>
	674	<i>Vibrio cholerae</i>	This patent	<i>atpD</i>
	675	<i>Vibrio cholerae</i>	This patent	<i>tuf</i>
25	676	<i>Leishmania enriettii</i>	This patent	<i>atpD</i>
	677	<i>Babesia microti</i>	This patent	<i>tuf</i> (EF-1)
	678	<i>Cryptococcus neoformans</i>	This patent	<i>atpD</i>
	679	<i>Cryptococcus neoformans</i>	This patent	<i>atpD</i>
	680	<i>Cunninghamella bertholletiae</i>	This patent	<i>atpD</i>
30	684	<i>Candida tropicalis</i>	Database	<i>atpD</i> (V)
	685	<i>Enterococcus hirae</i>	Database	<i>atpD</i> (V)
	686	<i>Chlamydia pneumoniae</i>	Database	<i>atpD</i> (V)
	687	<i>Halobacterium salinarum</i>	Database	<i>atpD</i> (V)
	688	<i>Homo sapiens</i>	Database	<i>atpD</i> (V)
35	689	<i>Plasmodium falciparum</i>	Database	<i>atpD</i> (V)
	690	<i>Saccharomyces cerevisiae</i>	Database	<i>atpD</i> (V)
	691	<i>Schizosaccharomyces pombe</i>	Database	<i>atpD</i> (V)
	692	<i>Trypanosoma congolense</i>	Database	<i>atpD</i> (V)
	693	<i>Thermus thermophilus</i>	Database	<i>atpD</i> (V)
40	698	<i>Escherichia coli</i>	WO98/20157	<i>tuf</i>
	709	<i>Borrelia burgdorferi</i>	Database	<i>atpD</i> (V)
	710	<i>Treponema pallidum</i>	Database	<i>atpD</i> (V)
	711	<i>Chlamydia trachomatis</i>	Genome project	<i>atpD</i> (V)
	712	<i>Enterococcus faecalis</i>	Genome project	<i>atpD</i> (V)
45	713	<i>Methanosarcina barkeri</i>	Database	<i>atpD</i> (V)
	714	<i>Methanococcus jannaschii</i>	Database	<i>atpD</i> (V)
	715	<i>Porphyromonas gingivalis</i>	Genome project	<i>atpD</i> (V)
	716	<i>Streptococcus pneumoniae</i>	Genome project	<i>atpD</i> (V)
	717	<i>Burkholderia mallei</i>	This patent	<i>tuf</i>
50	718	<i>Burkholderia pseudomallei</i>	This patent	<i>tuf</i>
	719	<i>Clostridium beijerinckii</i>	This patent	<i>tuf</i>
	720	<i>Clostridium innocuum</i>	This patent	<i>tuf</i>
	721	<i>Clostridium novyi</i>	This patent	<i>tuf</i>
	722	<i>Clostridium septicum</i>	This patent	<i>tuf</i>
55	723	<i>Clostridium tertium</i>	This patent	<i>tuf</i>
	724	<i>Clostridium tetani</i>	This patent	<i>tuf</i>
	725	<i>Enterococcus malodoratus</i>	This patent	<i>tuf</i>
	726	<i>Enterococcus sulfureus</i>	This patent	<i>tuf</i>
	727	<i>Lactococcus garvieae</i>	This patent	<i>tuf</i>
60	728	<i>Mycoplasma pirum</i>	This patent	<i>tuf</i>
	729	<i>Mycoplasma salivarium</i>	This patent	<i>tuf</i>
	730	<i>Neisseria polysaccharea</i>	This patent	<i>tuf</i>
	731	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	This patent	<i>tuf</i>
		serotype Enteritidis		
65				

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	732	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Gallinarum	This patent	<i>tuf</i>
	733	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Paratyphi B	This patent	<i>tuf</i>
10	734	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Virchow	This patent	<i>tuf</i>
	735	<i>Serratia grimesii</i>	This patent	<i>tuf</i>
	736	<i>Clostridium difficile</i>	This patent	<i>tuf</i>
	737	<i>Burkholderia pseudomallei</i>	This patent	<i>atpD</i>
	738	<i>Clostridium bifermentans</i>	This patent	<i>atpD</i>
15	739	<i>Clostridium beijerinckii</i>	This patent	<i>atpD</i>
	740	<i>Clostridium difficile</i>	This patent	<i>atpD</i>
	741	<i>Clostridium ramosum</i>	This patent	<i>atpD</i>
	742	<i>Clostridium septicum</i>	This patent	<i>atpD</i>
	743	<i>Clostridium tertium</i>	This patent	<i>atpD</i>
20	744	<i>Comamonas acidovorans</i>	This patent	<i>atpD</i>
	745	<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	This patent	<i>atpD</i>
	746	<i>Neisseria canis</i>	This patent	<i>atpD</i>
	747	<i>Neisseria cinerea</i>	This patent	<i>atpD</i>
	748	<i>Neisseria cuniculi</i>	This patent	<i>atpD</i>
25	749	<i>Neisseria elongata</i> subsp. <i>elongata</i>	This patent	<i>atpD</i>
	750	<i>Neisseria flavescens</i>	This patent	<i>atpD</i>
	751	<i>Neisseria gonorrhoeae</i>	This patent	<i>atpD</i>
	752	<i>Neisseria gonorrhoeae</i>	This patent	<i>atpD</i>
	753	<i>Neisseria lactamica</i>	This patent	<i>atpD</i>
30	754	<i>Neisseria meningitidis</i>	This patent	<i>atpD</i>
	755	<i>Neisseria mucosa</i>	This patent	<i>atpD</i>
	756	<i>Neisseria subflava</i>	This patent	<i>atpD</i>
	757	<i>Neisseria weaveri</i>	This patent	<i>atpD</i>
	758	<i>Neisseria animalis</i>	This patent	<i>atpD</i>
35	759	<i>Proteus penneri</i>	This patent	<i>atpD</i>
	760	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Enteritidis	This patent	<i>atpD</i>
	761	<i>Yersinia pestis</i>	This patent	<i>atpD</i>
	762	<i>Burkholderia mallei</i>	This patent	<i>atpD</i>
40	763	<i>Clostridium sordellii</i>	This patent	<i>atpD</i>
	764	<i>Clostridium novyi</i>	This patent	<i>atpD</i>
	765	<i>Clostridium botulinum</i>	This patent	<i>atpD</i>
	766	<i>Clostridium histolyticum</i>	This patent	<i>atpD</i>
	767	<i>Peptostreptococcus prevotii</i>	This patent	<i>atpD</i>
45	768	<i>Absidia corymbifera</i>	This patent	<i>atpD</i>
	769	<i>Alternaria alternata</i>	This patent	<i>atpD</i>
	770	<i>Aspergillus flavus</i>	This patent	<i>atpD</i>
	771	<i>Mucor circinelloides</i>	This patent	<i>atpD</i>
	772	<i>Piedraia hortai</i>	This patent	<i>atpD</i>
50	773	<i>Pseudallescheria boydii</i>	This patent	<i>atpD</i>
	774	<i>Rhizopus oryzae</i>	This patent	<i>atpD</i>
	775	<i>Scopulariopsis koningii</i>	This patent	<i>atpD</i>
	776	<i>Trichophyton mentagrophytes</i>	This patent	<i>atpD</i>
	777	<i>Trichophyton tonsurans</i>	This patent	<i>atpD</i>
55	778	<i>Trichosporon cutaneum</i>	This patent	<i>atpD</i>
	779	<i>Cladophialophora carrionii</i>	This patent	<i>tuf</i> (EF-1)
	780	<i>Cunninghamella bertholletiae</i>	This patent	<i>tuf</i> (EF-1)
	781	<i>Curvularia lunata</i>	This patent	<i>tuf</i> (EF-1)
	782	<i>Fonsecaea pedrosoi</i>	This patent	<i>tuf</i> (EF-1)
60	783	<i>Microsporum audouinii</i>	This patent	<i>tuf</i> (EF-1)
	784	<i>Mucor circinelloides</i>	This patent	<i>tuf</i> (EF-1)
	785	<i>Phialophora verrucosa</i>	This patent	<i>tuf</i> (EF-1)
	786	<i>Saksenaea vasiformis</i>	This patent	<i>tuf</i> (EF-1)
	787	<i>Syncephalastrum racemosum</i>	This patent	<i>tuf</i> (EF-1)
65	788	<i>Trichophyton tonsurans</i>	This patent	<i>tuf</i> (EF-1)
	789	<i>Trichophyton mentagrophytes</i>	This patent	<i>tuf</i> (EF-1)

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	790	<i>Bipolaris hawaiiensis</i>	This patent	<i>tuf</i> (EF-1)
	791	<i>Aspergillus fumigatus</i>	This patent	<i>tuf</i> (M)
	792	<i>Trichophyton mentagrophytes</i>	This patent	<i>tuf</i> (M)
	827	<i>Clostridium novyi</i>	This patent	<i>atpD</i> (V)
	828	<i>Clostridium difficile</i>	This patent	<i>atpD</i> (V)
10	829	<i>Clostridium septicum</i>	This patent	<i>atpD</i> (V)
	830	<i>Clostridium botulinum</i>	This patent	<i>atpD</i> (V)
	831	<i>Clostridium perfringens</i>	This patent	<i>atpD</i> (V)
	832	<i>Clostridium tetani</i>	This patent	<i>atpD</i> (V)
	833	<i>Streptococcus pyogenes</i>	Database	<i>atpD</i> (V)
15	834	<i>Babesia bovis</i>	This patent	<i>atpD</i> (V)
	835	<i>Cryptosporidium parvum</i>	This patent	<i>atpD</i> (V)
	836	<i>Leishmania infantum</i>	This patent	<i>atpD</i> (V)
	837	<i>Leishmania major</i>	This patent	<i>atpD</i> (V)
	838	<i>Leishmania tarentolae</i>	This patent	<i>atpD</i> (V)
20	839	<i>Trypanosoma brucei</i>	This patent	<i>atpD</i> (V)
	840	<i>Trypanosoma cruzi</i>	This patent	<i>tuf</i> (EF-1)
	841	<i>Trypanosoma cruzi</i>	This patent	<i>tuf</i> (EF-1)
	842	<i>Trypanosoma cruzi</i>	This patent	<i>tuf</i> (EF-1)
	843	<i>Babesia bovis</i>	This patent	<i>tuf</i> (M)
25	844	<i>Leishmania aethiopica</i>	This patent	<i>tuf</i> (M)
	845	<i>Leishmania amazonensis</i>	This patent	<i>tuf</i> (M)
	846	<i>Leishmania donovani</i>	This patent	<i>tuf</i> (M)
	847	<i>Leishmania infantum</i>	This patent	<i>tuf</i> (M)
	848	<i>Leishmania enriettii</i>	This patent	<i>tuf</i> (M)
30	849	<i>Leishmania gerbilli</i>	This patent	<i>tuf</i> (M)
	850	<i>Leishmania major</i>	This patent	<i>tuf</i> (M)
	851	<i>Leishmania mexicana</i>	This patent	<i>tuf</i> (M)
	852	<i>Leishmania tarentolae</i>	This patent	<i>tuf</i> (M)
	853	<i>Trypanosoma cruzi</i>	This patent	<i>tuf</i> (M)
35	854	<i>Trypanosoma cruzi</i>	This patent	<i>tuf</i> (M)
	855	<i>Trypanosoma cruzi</i>	This patent	<i>tuf</i> (M)
	856	<i>Babesia bigemina</i>	This patent	<i>atpD</i>
	857	<i>Babesia bovis</i>	This patent	<i>atpD</i>
	858	<i>Babesia microti</i>	This patent	<i>atpD</i>
40	859	<i>Leishmania guyanensis</i>	This patent	<i>atpD</i>
	860	<i>Leishmania mexicana</i>	This patent	<i>atpD</i>
	861	<i>Leishmania tropica</i>	This patent	<i>atpD</i>
	862	<i>Leishmania tropica</i>	This patent	<i>atpD</i>
	863	<i>Bordetella pertussis</i>	Database	<i>tuf</i>
45	864	<i>Trypanosoma brucei brucei</i>	Database	<i>tuf</i> (EF-1)
	865	<i>Cryptosporidium parvum</i>	This patent	<i>tuf</i> (EF-1)
	866	<i>Staphylococcus saprophyticus</i>	This patent	<i>atpD</i>
	867	<i>Zoogloea ramigera</i>	This patent	<i>atpD</i>
	868	<i>Staphylococcus saprophyticus</i>	This patent	<i>tuf</i>
50	869	<i>Enterococcus casseliflavus</i>	This patent	<i>tuf</i>
	870	<i>Enterococcus casseliflavus</i>	This patent	<i>tuf</i>
	871	<i>Enterococcus flavescens</i>	This patent	<i>tuf</i>
	872	<i>Enterococcus gallinarum</i>	This patent	<i>tuf</i>
	873	<i>Enterococcus gallinarum</i>	This patent	<i>tuf</i>
55	874	<i>Staphylococcus haemolyticus</i>	This patent	<i>tuf</i>
	875	<i>Staphylococcus epidermidis</i>	This patent	<i>tuf</i>
	876	<i>Staphylococcus epidermidis</i>	This patent	<i>tuf</i>
	877	<i>Staphylococcus epidermidis</i>	This patent	<i>tuf</i>
	878	<i>Staphylococcus epidermidis</i>	This patent	<i>tuf</i>
60	879	<i>Enterococcus gallinarum</i>	This patent	<i>tuf</i>
	880	<i>Pseudomonas aeruginosa</i>	This patent	<i>tuf</i>
	881	<i>Enterococcus casseliflavus</i>	This patent	<i>tuf</i>
	882	<i>Enterococcus casseliflavus</i>	This patent	<i>tuf</i>
	883	<i>Enterococcus faecalis</i>	This patent	<i>tuf</i>
65	884	<i>Enterococcus faecalis</i>	This patent	<i>tuf</i>
	885	<i>Enterococcus faecium</i>	This patent	<i>tuf</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	886 <i>Enterococcus faecium</i>	This patent	<i>tuf</i>
	887 <i>Zoogloea ramigera</i>	This patent	<i>tuf</i>
	888 <i>Enterococcus faecalis</i>	This patent	<i>tuf</i>
	889 <i>Aspergillus fumigatus</i>	This patent	<i>atpD</i>
	890 <i>Penicillium marneffei</i>	This patent	<i>atpD</i>
10	891 <i>Paecilomyces lilacinus</i>	This patent	<i>atpD</i>
	892 <i>Penicillium marneffei</i>	This patent	<i>atpD</i>
	893 <i>Sporothrix schenckii</i>	This patent	<i>atpD</i>
	894 <i>Malbranchea filamentosa</i>	This patent	<i>atpD</i>
	895 <i>Paecilomyces lilacinus</i>	This patent	<i>atpD</i>
15	896 <i>Aspergillus niger</i>	This patent	<i>atpD</i>
	897 <i>Aspergillus fumigatus</i>	This patent	<i>tuf</i> (EF-1)
	898 <i>Penicillium marneffei</i>	This patent	<i>tuf</i> (EF-1)
	899 <i>Piedraia hortai</i>	This patent	<i>tuf</i> (EF-1)
	900 <i>Paecilomyces lilacinus</i>	This patent	<i>tuf</i> (EF-1)
20	901 <i>Paracoccidioides brasiliensis</i>	This patent	<i>tuf</i> (EF-1)
	902 <i>Sporothrix schenckii</i>	This patent	<i>tuf</i> (EF-1)
	903 <i>Penicillium marneffei</i>	This patent	<i>tuf</i> (EF-1)
	904 <i>Curvularia lunata</i>	This patent	<i>tuf</i> (M)
	905 <i>Aspergillus niger</i>	This patent	<i>tuf</i> (M)
25	906 <i>Bipolaris hawaiiensis</i>	This patent	<i>tuf</i> (M)
	907 <i>Aspergillus flavus</i>	This patent	<i>tuf</i> (M)
	908 <i>Alternaria alternata</i>	This patent	<i>tuf</i> (M)
	909 <i>Penicillium marneffei</i>	This patent	<i>tuf</i> (M)
	910 <i>Penicillium marneffei</i>	This patent	<i>tuf</i> (M)
30	918 <i>Escherichia coli</i>	Database	<i>recA</i>
	929 <i>Bacteroides fragilis</i>	This patent	<i>atpD</i> (V)
	930 <i>Bacteroides distasonis</i>	This patent	<i>atpD</i> (V)
	931 <i>Porphyromonas asaccharolytica</i>	This patent	<i>atpD</i> (V)
	932 <i>Listeria monocytogenes</i>	This patent	<i>tuf</i>
35	939 <i>Saccharomyces cerevisiae</i>	Database	<i>recA</i> (Rad51)
	940 <i>Saccharomyces cerevisiae</i>	Database	<i>recA</i> (Dmc1)
	941 <i>Cryptococcus humicola</i>	This patent	<i>atpD</i>
	942 <i>Escherichia coli</i>	This patent	<i>atpD</i>
	943 <i>Escherichia coli</i>	This patent	<i>atpD</i>
40	944 <i>Escherichia coli</i>	This patent	<i>atpD</i>
	945 <i>Escherichia coli</i>	This patent	<i>atpD</i>
	946 <i>Neisseria polysaccharea</i>	This patent	<i>atpD</i>
	947 <i>Neisseria sicca</i>	This patent	<i>atpD</i>
	948 <i>Streptococcus mitis</i>	This patent	<i>atpD</i>
45	949 <i>Streptococcus mitis</i>	This patent	<i>atpD</i>
	950 <i>Streptococcus mitis</i>	This patent	<i>atpD</i>
	951 <i>Streptococcus oralis</i>	This patent	<i>atpD</i>
	952 <i>Streptococcus pneumoniae</i>	This patent	<i>atpD</i>
	953 <i>Streptococcus pneumoniae</i>	This patent	<i>atpD</i>
50	954 <i>Streptococcus pneumoniae</i>	This patent	<i>atpD</i>
	955 <i>Streptococcus pneumoniae</i>	This patent	<i>atpD</i>
	956 <i>Babesia microti</i>	This patent	<i>atpD</i> (V)
	957 <i>Entamoeba histolytica</i>	This patent	<i>atpD</i> (V)
	958 <i>Fusobacterium nucleatum</i> subsp. <i>polymorphum</i>	This patent	<i>atpD</i> (V)
55	959 <i>Leishmania aethiopica</i>	This patent	<i>atpD</i> (V)
	960 <i>Leishmania tropica</i>	This patent	<i>atpD</i> (V)
	961 <i>Leishmania guyanensis</i>	This patent	<i>atpD</i> (V)
	962 <i>Leishmania donovani</i>	This patent	<i>atpD</i> (V)
	963 <i>Leishmania hertigi</i>	This patent	<i>atpD</i> (V)
60	964 <i>Leishmania mexicana</i>	This patent	<i>atpD</i> (V)
	965 <i>Leishmania tropica</i>	This patent	<i>atpD</i> (V)
	966 <i>Peptostreptococcus anaerobius</i>	This patent	<i>atpD</i> (V)
	967 <i>Bordetella pertussis</i>	This patent	<i>tuf</i>
	968 <i>Bordetella pertussis</i>	This patent	<i>tuf</i>
65	969 <i>Enterococcus columbae</i>	This patent	<i>tuf</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitcal species	Source	Gene*
5	970	<i>Enterococcus flavescens</i>	This patent	<i>tuf</i>
	971	<i>Streptococcus pneumoniae</i>	This patent	<i>tuf</i>
	972	<i>Escherichia coli</i>	This patent	<i>tuf</i>
	973	<i>Escherichia coli</i>	This patent	<i>tuf</i>
	974	<i>Escherichia coli</i>	This patent	<i>tuf</i>
10	975	<i>Escherichia coli</i>	This patent	<i>tuf</i>
	976	<i>Mycobacterium avium</i>	This patent	<i>tuf</i>
	977	<i>Streptococcus pneumoniae</i>	This patent	<i>tuf</i>
	978	<i>Mycobacterium gordonae</i>	This patent	<i>tuf</i>
	979	<i>Streptococcus pneumoniae</i>	This patent	<i>tuf</i>
15	980	<i>Mycobacterium tuberculosis</i>	This patent	<i>tuf</i>
	981	<i>Staphylococcus warneri</i>	This patent	<i>tuf</i>
	982	<i>Streptococcus mitis</i>	This patent	<i>tuf</i>
	983	<i>Streptococcus mitis</i>	This patent	<i>tuf</i>
	984	<i>Streptococcus mitis</i>	This patent	<i>tuf</i>
20	985	<i>Streptococcus oralis</i>	This patent	<i>tuf</i>
	986	<i>Streptococcus pneumoniae</i>	This patent	<i>tuf</i>
	987	<i>Enterococcus hirae</i>	This patent	<i>tuf</i> (C)
	988	<i>Enterococcus mundtii</i>	This patent	<i>tuf</i> (C)
	989	<i>Enterococcus raffinosus</i>	This patent	<i>tuf</i> (C)
25	990	<i>Bacillus anthracis</i>	This patent	<i>recA</i>
	991	<i>Prevotella melaninogenica</i>	This patent	<i>recA</i>
	992	<i>Enterococcus casseliflavus</i>	This patent	<i>tuf</i>
	993	<i>Streptococcus pyogenes</i>	Database	<i>speA</i>
	1002	<i>Streptococcus pyogenes</i>	WO98/20157	<i>tuf</i>
30	1003	<i>Bacillus cereus</i>	This patent	<i>recA</i>
	1004	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1005	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1006	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1007	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
35	1008	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1009	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1010	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1011	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1012	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
40	1013	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1014	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1015	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1016	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1017	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
45	1018	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1019	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1020	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1021	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1022	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
50	1023	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1024	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1025	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1026	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1027	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
55	1028	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1029	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1030	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1031	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1032	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
60	1033	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1034	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1035	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1036	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1037	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
65				

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	1038	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1039	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1040	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1041	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1042	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
10	1043	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1044	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1045	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1046	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1047	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
15	1048	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1049	<i>Enterococcus faecium</i>	This patent	<i>vanA</i>
	1050	<i>Enterococcus gallinarum</i>	This patent	<i>vanA</i>
	1051	<i>Enterococcus faecium</i>	This patent	<i>vanA</i>
	1052	<i>Enterococcus faecium</i>	This patent	<i>vanA</i>
20	1053	<i>Enterococcus faecium</i>	This patent	<i>vanA</i>
	1054	<i>Enterococcus faecalis</i>	This patent	<i>vanA</i>
	1055	<i>Enterococcus gallinarum</i>	This patent	<i>vanA</i>
	1056	<i>Enterococcus faecium</i>	This patent	<i>vanA</i>
	1057	<i>Enterococcus flavescens</i>	This patent	<i>vanA</i>
25	1058	<i>Enterococcus gallinarum</i>	This patent	<i>vanC1</i>
	1059	<i>Enterococcus gallinarum</i>	This patent	<i>vanC1</i>
	1060	<i>Enterococcus casseliflavus</i>	This patent	<i>vanC2</i>
	1061	<i>Enterococcus casseliflavus</i>	This patent	<i>vanC2</i>
	1062	<i>Enterococcus casseliflavus</i>	This patent	<i>vanC2</i>
30	1063	<i>Enterococcus casseliflavus</i>	This patent	<i>vanC2</i>
	1064	<i>Enterococcus flavescens</i>	This patent	<i>vanC3</i>
	1065	<i>Enterococcus flavescens</i>	This patent	<i>vanC3</i>
	1066	<i>Enterococcus flavescens</i>	This patent	<i>vanC3</i>
	1067	<i>Enterococcus faecium</i>	This patent	<i>vanXY</i>
35	1068	<i>Enterococcus faecium</i>	This patent	<i>vanXY</i>
	1069	<i>Enterococcus faecium</i>	This patent	<i>vanXY</i>
	1070	<i>Enterococcus faecalis</i>	This patent	<i>vanXY</i>
	1071	<i>Enterococcus gallinarum</i>	This patent	<i>vanXY</i>
	1072	<i>Enterococcus faecium</i>	This patent	<i>vanXY</i>
40	1073	<i>Enterococcus flavescens</i>	This patent	<i>vanXY</i>
	1074	<i>Enterococcus faecium</i>	This patent	<i>vanXY</i>
	1075	<i>Enterococcus gallinarum</i>	This patent	<i>vanXY</i>
	1076	<i>Escherichia coli</i>	Database	<i>stx₁</i>
	1077	<i>Escherichia coli</i>	Database	<i>stx₂</i>
45	1093	<i>Staphylococcus saprophyticus</i>	This patent	unknown
	1117	<i>Enterococcus faecium</i>	Database	<i>vanB</i>
	1138	<i>Enterococcus gallinarum</i>	Database	<i>vanC1</i>
	1139	<i>Enterococcus faecium</i>	Database	<i>vanA</i>
	1140	<i>Enterococcus casseliflavus</i>	Database	<i>vanC2</i>
50	1141	<i>Enterococcus faecium</i>	Database	<i>vanHAXY</i>
	1169	<i>Streptococcus pneumoniae</i>	Database	<i>pbp1a</i>
	1172	<i>Streptococcus pneumoniae</i>	Database	<i>pbp2b</i>
	1173	<i>Streptococcus pneumoniae</i>	Database	<i>pbp2x</i>
	1178	<i>Staphylococcus aureus</i>	Database	<i>mecA</i>
55	1183	<i>Streptococcus pneumoniae</i>	Database	<i>hexA</i>
	1184	<i>Streptococcus pneumoniae</i>	This patent	<i>hexA</i>
	1185	<i>Streptococcus pneumoniae</i>	This patent	<i>hexA</i>
	1186	<i>Streptococcus pneumoniae</i>	This patent	<i>hexA</i>
	1187	<i>Streptococcus pneumoniae</i>	This patent	<i>hexA</i>
60				

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	1188	<i>Streptococcus oralis</i>	This patent	<i>hexA</i>
	1189	<i>Streptococcus mitis</i>	This patent	<i>hexA</i>
	1190	<i>Streptococcus mitis</i>	This patent	<i>hexA</i>
	1191	<i>Streptococcus mitis</i>	This patent	<i>hexA</i>
	1198	<i>Staphylococcus saprophyticus</i>	This patent	unknown
10	1215	<i>Streptococcus pyogenes</i>	Database	<i>pcp</i>
	1230	<i>Escherichia coli</i>	Database	<i>tuf</i> (EF-G)
	1242	<i>Enterococcus faecium</i>	Database	<i>ddl</i>
	1243	<i>Enterococcus faecalis</i>	Database	<i>mtlF</i> , <i>mtlD</i>
	1244	<i>Staphylococcus aureus</i> subsp. <i>aureus</i>	This patent	unknown
15	1245	<i>Bacillus anthracis</i>	This patent	<i>atpD</i>
	1246	<i>Bacillus mycoides</i>	This patent	<i>atpD</i>
	1247	<i>Bacillus thuringiensis</i>	This patent	<i>atpD</i>
	1248	<i>Bacillus thuringiensis</i>	This patent	<i>atpD</i>
	1249	<i>Bacillus thuringiensis</i>	This patent	<i>atpD</i>
20	1250	<i>Bacillus weihenstephanensis</i>	This patent	<i>atpD</i>
	1251	<i>Bacillus thuringiensis</i>	This patent	<i>atpD</i>
	1252	<i>Bacillus thuringiensis</i>	This patent	<i>atpD</i>
	1253	<i>Bacillus cereus</i>	This patent	<i>atpD</i>
	1254	<i>Bacillus cereus</i>	This patent	<i>atpD</i>
25	1255	<i>Staphylococcus aureus</i>	This patent	<i>gyrA</i>
	1256	<i>Bacillus weihenstephanensis</i>	This patent	<i>atpD</i>
	1257	<i>Bacillus anthracis</i>	This patent	<i>atpD</i>
	1258	<i>Bacillus thuringiensis</i>	This patent	<i>atpD</i>
	1259	<i>Bacillus cereus</i>	This patent	<i>atpD</i>
30	1260	<i>Bacillus cereus</i>	This patent	<i>atpD</i>
	1261	<i>Bacillus thuringiensis</i>	This patent	<i>atpD</i>
	1262	<i>Bacillus thuringiensis</i>	This patent	<i>atpD</i>
	1263	<i>Bacillus thuringiensis</i>	This patent	<i>atpD</i>
	1264	<i>Bacillus thuringiensis</i>	This patent	<i>atpD</i>
35	1265	<i>Bacillus anthracis</i>	This patent	<i>atpD</i>
	1266	<i>Paracoccidioides brasiliensis</i>	This patent	<i>tuf</i> (EF-1)
	1267	<i>Blastomyces dermatitidis</i>	This patent	<i>tuf</i> (EF-1)
	1268	<i>Histoplasma capsulatum</i>	This patent	<i>tuf</i> (EF-1)
	1269	<i>Trichophyton rubrum</i>	This patent	<i>tuf</i> (EF-1)
40	1270	<i>Microsporum canis</i>	This patent	<i>tuf</i> (EF-1)
	1271	<i>Aspergillus versicolor</i>	This patent	<i>tuf</i> (EF-1)
	1272	<i>Exophiala moniliae</i>	This patent	<i>tuf</i> (EF-1)
	1273	<i>Hortaea wameckii</i>	This patent	<i>tuf</i> (EF-1)
	1274	<i>Fusarium solani</i>	This patent	<i>tuf</i> (EF-1)
45	1275	<i>Aureobasidium pullulans</i>	This patent	<i>tuf</i> (EF-1)
	1276	<i>Blastomyces dermatitidis</i>	This patent	<i>tuf</i> (EF-1)
	1277	<i>Exophiala dermatitidis</i>	This patent	<i>tuf</i> (EF-1)
	1278	<i>Fusarium moniliforme</i>	This patent	<i>tuf</i> (EF-1)
	1279	<i>Aspergillus terreus</i>	This patent	<i>tuf</i> (EF-1)
50	1280	<i>Aspergillus fumigatus</i>	This patent	<i>tuf</i> (EF-1)
	1281	<i>Cryptococcus laurentii</i>	This patent	<i>tuf</i> (EF-1)
	1282	<i>Emmonsia parva</i>	This patent	<i>tuf</i> (EF-1)
	1283	<i>Fusarium solani</i>	This patent	<i>tuf</i> (EF-1)
	1284	<i>Sporothrix schenckii</i>	This patent	<i>tuf</i> (EF-1)
55	1285	<i>Aspergillus nidulans</i>	This patent	<i>tuf</i> (EF-1)
	1286	<i>Cladophialophora carrionii</i>	This patent	<i>tuf</i> (EF-1)
	1287	<i>Exserohilum rostratum</i>	This patent	<i>tuf</i> (EF-1)
	1288	<i>Bacillus thuringiensis</i>	This patent	<i>recA</i>
	1289	<i>Bacillus thuringiensis</i>	This patent	<i>recA</i>
60	1299	<i>Staphylococcus aureus</i>	Database	<i>gyrA</i>
	1300	<i>Escherichia coli</i>	Database	<i>gyrA</i>
	1307	<i>Staphylococcus aureus</i>	Database	<i>gyrB</i>
	1320	<i>Escherichia coli</i>	Database	<i>parC</i> (<i>grlA</i>)
	1321	<i>Staphylococcus aureus</i>	Database	<i>parC</i> (<i>grlA</i>)
65	1328	<i>Staphylococcus aureus</i>	Database	<i>parE</i> (<i>grlB</i>)

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	1348 unidentified bacterium	Database	<i>aac2la</i>
	1351 <i>Pseudomonas aeruginosa</i>	Database	<i>aac3lb</i>
	1356 <i>Serratia marcescens</i>	Database	<i>aac3llb</i>
	1361 <i>Escherichia coli</i>	Database	<i>aac3IVa</i>
	1366 <i>Enterobacter cloacae</i>	Database	<i>aac3VIa</i>
10	1371 <i>Citrobacter koseri</i>	Database	<i>aac6la</i>
	1376 <i>Serratia marcescens</i>	Database	<i>aac6lc</i>
	1381 <i>Escherichia coli</i>	Database	<i>ant3la</i>
	1386 <i>Staphylococcus aureus</i>	Database	<i>ant4la</i>
	1391 <i>Escherichia coli</i>	Database	<i>aph3la</i>
15	1396 <i>Escherichia coli</i>	Database	<i>aph3lla</i>
	1401 <i>Enterococcus faecalis</i>	Database	<i>aph3llla</i>
	1406 <i>Acinetobacter baumannii</i>	Database	<i>aph3VIa</i>
	1411 <i>Pseudomonas aeruginosa</i>	Database	<i>blaCARB</i>
	1416 <i>Klebsiella pneumoniae</i>	Database	<i>blaCMY-2</i>
20	1423 <i>Escherichia coli</i>	Database	<i>blaCTX-M-1</i>
	1428 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Typhimurium	Database	<i>blaCTX-M-2</i>
	1433 <i>Pseudomonas aeruginosa</i>	Database	<i>blaIMP</i>
	1438 <i>Escherichia coli</i>	Database	<i>blaOXA2</i>
	1439 <i>Pseudomonas aeruginosa</i>	Database	<i>blaOXA10</i>
25	1442 <i>Pseudomonas aeruginosa</i>	Database	<i>blaPER1</i>
	1445 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Typhimurium	Database	<i>blaPER2</i>
	1452 <i>Staphylococcus epidermidis</i>	Database	<i>dfrA</i>
	1461 <i>Escherichia coli</i>	Database	<i>dhfrIa</i>
	1470 <i>Escherichia coli</i>	Database	<i>dhfrIb</i>
30	1475 <i>Escherichia coli</i>	Database	<i>dhfrV</i>
	1480 <i>Proteus mirabilis</i>	Database	<i>dhfrVI</i>
	1489 <i>Escherichia coli</i>	Database	<i>dhfrVII</i>
	1494 <i>Escherichia coli</i>	Database	<i>dhfrVIII</i>
	1499 <i>Escherichia coli</i>	Database	<i>dhfrIX</i>
35	1504 <i>Escherichia coli</i>	Database	<i>dhfrXII</i>
	1507 <i>Escherichia coli</i>	Database	<i>dhfrXIII</i>
	1512 <i>Escherichia coli</i>	Database	<i>dhfrXV</i>
	1517 <i>Escherichia coli</i>	Database	<i>dhfrXVII</i>
	1518 <i>Acinetobacter lwoffii</i>	This patent	<i>fusA</i>
40	1519 <i>Acinetobacter lwoffii</i>	This patent	<i>fusA-tuf</i> spacer
	1520 <i>Acinetobacter lwoffii</i>	This patent	<i>tuf</i>
	1521 <i>Haemophilus influenzae</i>	This patent	<i>fusA</i>
	1522 <i>Haemophilus influenzae</i>	This patent	<i>fusA-tuf</i> spacer
	1523 <i>Haemophilus influenzae</i>	This patent	<i>tuf</i>
45	1524 <i>Proteus mirabilis</i>	This patent	<i>fusA</i>
	1525 <i>Proteus mirabilis</i>	This patent	<i>fusA-tuf</i> spacer
	1526 <i>Proteus mirabilis</i>	This patent	<i>tuf</i>
	1527 <i>Campylobacter curvus</i>	This patent	<i>atpD</i>
	1530 <i>Escherichia coli</i>	Database	<i>ereA</i>
50	1535 <i>Escherichia coli</i>	Database	<i>ereB</i>
	1540 <i>Staphylococcus haemolyticus</i>	Database	<i>linA</i>
	1545 <i>Enterococcus faecium</i>	Database	<i>linB</i>
	1548 <i>Streptococcus pyogenes</i>	Database	<i>mefA</i>
	1551 <i>Streptococcus pneumoniae</i>	Database	<i>mefE</i>
55	1560 <i>Escherichia coli</i>	Database	<i>mphA</i>
	1561 <i>Candida albicans</i>	This patent	<i>tuf</i> (EF-1)
	1562 <i>Candida dubliniensis</i>	This patent	<i>tuf</i> (EF-1)
	1563 <i>Candida famata</i>	This patent	<i>tuf</i> (EF-1)
	1564 <i>Candida glabrata</i>	This patent	<i>tuf</i> (EF-1)
60	1565 <i>Candida guilliermondii</i>	This patent	<i>tuf</i> (EF-1)
	1566 <i>Candida haemulonii</i>	This patent	<i>tuf</i> (EF-1)
	1567 <i>Candida kefyr</i>	This patent	<i>tuf</i> (EF-1)
	1568 <i>Candida lusitanae</i>	This patent	<i>tuf</i> (EF-1)

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	1569 <i>Candida sphaerica</i>	This patent	<i>tuf</i> (EF-1)
	1570 <i>Candida tropicalis</i>	This patent	<i>tuf</i> (EF-1)
	1571 <i>Candida viswanathii</i>	This patent	<i>tuf</i> (EF-1)
	1572 <i>Alcaligenes faecalis</i> subsp. <i>faecalis</i>	This patent	<i>tuf</i>
	1573 <i>Prevotella buccalis</i>	This patent	<i>tuf</i>
10	1574 <i>Succinivibrio dextrinosolvens</i>	This patent	<i>tuf</i>
	1575 <i>Tetragenococcus halophilus</i>	This patent	<i>tuf</i>
	1576 <i>Campylobacter jejuni</i> subsp. <i>jejuni</i>	This patent	<i>atpD</i>
	1577 <i>Campylobacter rectus</i>	This patent	<i>atpD</i>
	1578 <i>Enterococcus casseliflavus</i>	This patent	<i>fusA</i>
15	1579 <i>Enterococcus gallinarum</i>	This patent	<i>fusA</i>
	1580 <i>Streptococcus mitis</i>	This patent	<i>fusA</i>
	1585 <i>Enterococcus faecium</i>	Database	<i>satG</i>
	1590 Cloning vector pFW16	Database	<i>tetM</i>
	1594 <i>Enterococcus faecium</i>	Database	<i>vanD</i>
20	1599 <i>Enterococcus faecalis</i>	Database	<i>vanE</i>
	1600 <i>Campylobacter jejuni</i> subsp. <i>doylei</i>	This patent	<i>atpD</i>
	1601 <i>Enterococcus sulfureus</i>	This patent	<i>atpD</i>
	1602 <i>Enterococcus solitarius</i>	This patent	<i>atpD</i>
	1603 <i>Campylobacter sputorum</i> subsp. <i>sputorum</i>	This patent	<i>atpD</i>
25	1604 <i>Enterococcus pseudoavium</i>	This patent	<i>atpD</i>
	1607 <i>Klebsiella ornithinolytica</i>	This patent	<i>gyrA</i>
	1608 <i>Klebsiella oxytoca</i>	This patent	<i>gyrA</i>
	1613 <i>Staphylococcus aureus</i>	Database	<i>vatB</i>
	1618 <i>Staphylococcus cohnii</i>	Database	<i>vatC</i>
30	1623 <i>Staphylococcus aureus</i>	Database	<i>vga</i>
	1628 <i>Staphylococcus aureus</i>	Database	<i>vgaB</i>
	1633 <i>Staphylococcus aureus</i>	Database	<i>vgb</i>
	1638 <i>Aspergillus fumigatus</i>	This patent	<i>atpD</i>
	1639 <i>Aspergillus fumigatus</i>	This patent	<i>atpD</i>
35	1640 <i>Bacillus mycoides</i>	This patent	<i>atpD</i>
	1641 <i>Bacillus mycoides</i>	This patent	<i>atpD</i>
	1642 <i>Bacillus mycoides</i>	This patent	<i>atpD</i>
	1643 <i>Bacillus pseudomycoides</i>	This patent	<i>atpD</i>
	1644 <i>Bacillus pseudomycoides</i>	This patent	<i>atpD</i>
40	1645 <i>Budvicia aquatica</i>	This patent	<i>atpD</i>
	1646 <i>Buttiauxella agrestis</i>	This patent	<i>atpD</i>
	1647 <i>Candida norvegica</i>	This patent	<i>atpD</i>
	1648 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1649 <i>Campylobacter lari</i>	This patent	<i>atpD</i>
45	1650 <i>Coccidioides immitis</i>	This patent	<i>atpD</i>
	1651 <i>Emmonsia parva</i>	This patent	<i>atpD</i>
	1652 <i>Erwinia amylovora</i>	This patent	<i>atpD</i>
	1653 <i>Fonsecaea pedrosoi</i>	This patent	<i>atpD</i>
	1654 <i>Fusarium moniliforme</i>	This patent	<i>atpD</i>
50	1655 <i>Klebsiella oxytoca</i>	This patent	<i>atpD</i>
	1656 <i>Microsporum audouinii</i>	This patent	<i>atpD</i>
	1657 <i>Obesumbacterium proteus</i>	This patent	<i>atpD</i>
	1658 <i>Paracoccidioides brasiliensis</i>	This patent	<i>atpD</i>
	1659 <i>Plesiomonas shigelloides</i>	This patent	<i>atpD</i>
55	1660 <i>Shewanella putrefaciens</i>	This patent	<i>atpD</i>
	1662 <i>Campylobacter curvus</i>	This patent	<i>tuf</i>
	1663 <i>Campylobacter rectus</i>	This patent	<i>tuf</i>
	1664 <i>Fonsecaea pedrosoi</i>	This patent	<i>tuf</i>
	1666 <i>Microsporum audouinii</i>	This patent	<i>tuf</i>
60	1667 <i>Piedraia hortai</i>	This patent	<i>tuf</i>
	1668 <i>Escherichia coli</i>	Database	<i>tuf</i>
	1669 <i>Saksenaea vasiformis</i>	This patent	<i>tuf</i>
	1670 <i>Trichophyton tonsurans</i>	This patent	<i>tuf</i>
	1671 <i>Enterobacter aerogenes</i>	This patent	<i>atpD</i>
65	1672 <i>Bordetella pertussis</i>	Database	<i>atpD</i>
	1673 <i>Arcanobacterium haemolyticum</i>	This patent	<i>tuf</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	1674 <i>Butyrivibrio fibrisolvens</i>	This patent	tuf
	1675 <i>Campylobacter jejuni</i> subsp. <i>doylei</i>	This patent	tuf
	1676 <i>Campylobacter lari</i>	This patent	tuf
	1677 <i>Campylobacter sputorum</i> subsp. <i>sputorum</i>	This patent	tuf
	1678 <i>Campylobacter upsaliensis</i>	This patent	tuf
10	1679 <i>Globicatella sanguis</i>	This patent	tuf
	1680 <i>Lactobacillus acidophilus</i>	This patent	tuf
	1681 <i>Leuconostoc mesenteroides</i> subsp. <i>dextranicum</i>	This patent	tuf
	1682 <i>Prevotella buccalis</i>	This patent	tuf
	1683 <i>Ruminococcus bromii</i>	This patent	tuf
15	1684 <i>Paracoccidioides brasiliensis</i>	This patent	atpD
	1685 <i>Candida norvegica</i>	This patent	tuf (EF-1)
	1686 <i>Aspergillus nidulans</i>	This patent	tuf
	1687 <i>Aspergillus terreus</i>	This patent	tuf
	1688 <i>Candida norvegica</i>	This patent	tuf
20	1689 <i>Candida parapsilosis</i>	This patent	tuf
	1702 <i>Streptococcus gordonii</i>	WO98/20157	recA
	1703 <i>Streptococcus mutans</i>	WO98/20157	recA
	1704 <i>Streptococcus pneumoniae</i>	WO98/20157	recA
	1705 <i>Streptococcus pyogenes</i>	WO98/20157	recA
25	1706 <i>Streptococcus salivarius</i> subsp. <i>thermophilus</i>	WO98/20157	recA
	1707 <i>Escherichia coli</i>	WO98/20157	oxa
	1708 <i>Enterococcus faecalis</i>	WO98/20157	blaZ
	1709 <i>Pseudomonas aeruginosa</i>	WO98/20157	aac6'-IIa
	1710 <i>Staphylococcus aureus</i>	WO98/20157	ermA
30	1711 <i>Escherichia coli</i>	WO98/20157	ermB
	1712 <i>Staphylococcus aureus</i>	WO98/20157	ermC
	1713 <i>Enterococcus faecalis</i>	WO98/20157	vanB
	1714 <i>Campylobacter jejuni</i> subsp. <i>jejuni</i>	This patent	recA
	1715 <i>Abiotrophia adiacens</i>	WO98/20157	tuf
35	1716 <i>Abiotrophia defectiva</i>	WO98/20157	tuf
	1717 <i>Corynebacterium accolens</i>	WO98/20157	tuf
	1718 <i>Corynebacterium genitalium</i>	WO98/20157	tuf
	1719 <i>Corynebacterium jeikeium</i>	WO98/20157	tuf
	1720 <i>Corynebacterium pseudodiphtheriticum</i>	WO98/20157	tuf
40	1721 <i>Corynebacterium striatum</i>	WO98/20157	tuf
	1722 <i>Enterococcus avium</i>	WO98/20157	tuf
	1723 <i>Gardnerella vaginalis</i>	WO98/20157	tuf
	1724 <i>Listeria innocua</i>	WO98/20157	tuf
	1725 <i>Listeria ivanovii</i>	WO98/20157	tuf
45	1726 <i>Listeria monocytogenes</i>	WO98/20157	tuf
	1727 <i>Listeria seeligeri</i>	WO98/20157	tuf
	1728 <i>Staphylococcus aureus</i>	WO98/20157	tuf
	1729 <i>Staphylococcus saprophyticus</i>	WO98/20157	tuf
	1730 <i>Staphylococcus simulans</i>	WO98/20157	tuf
50	1731 <i>Streptococcus agalactiae</i>	WO98/20157	tuf
	1732 <i>Streptococcus pneumoniae</i>	WO98/20157	tuf
	1733 <i>Streptococcus salivarius</i>	WO98/20157	tuf
	1734 <i>Agrobacterium radiobacter</i>	WO98/20157	tuf
	1735 <i>Bacillus subtilis</i>	WO98/20157	tuf
55	1736 <i>Bacteroides fragilis</i>	WO98/20157	tuf
	1737 <i>Borrelia burgdorferi</i>	WO98/20157	tuf
	1738 <i>Brevibacterium linens</i>	WO98/20157	tuf
	1739 <i>Chlamydia trachomatis</i>	WO98/20157	tuf
	1740 <i>Fibrobacter succinogenes</i>	WO98/20157	tuf
60	1741 <i>Flavobacterium ferrugineum</i>	WO98/20157	tuf
	1742 <i>Helicobacter pylori</i>	WO98/20157	tuf
	1743 <i>Micrococcus luteus</i>	WO98/20157	tuf
	1744 <i>Mycobacterium tuberculosis</i>	WO98/20157	tuf
	1745 <i>Mycoplasma genitalium</i>	WO98/20157	tuf
65	1746 <i>Neisseria gonorrhoeae</i>	WO98/20157	tuf

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	1747 <i>Rickettsia prowazekii</i>	WO98/20157	tuf
	1748 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	WO98/20157	tuf
	serotype Typhimurium		
	1749 <i>Shewanella putrefaciens</i>	WO98/20157	tuf
	1750 <i>Stigmatella aurantiaca</i>	WO98/20157	tuf
10	1751 <i>Thiomonas cuprina</i>	WO98/20157	tuf
	1752 <i>Treponema pallidum</i>	WO98/20157	tuf
	1753 <i>Ureaplasma urealyticum</i>	WO98/20157	tuf
	1754 <i>Wolinella succinogenes</i>	WO98/20157	tuf
	1755 <i>Burkholderia cepacia</i>	WO98/20157	tuf
15	1756 <i>Bacillus anthracis</i>	This patent	recA
	1757 <i>Bacillus anthracis</i>	This patent	recA
	1758 <i>Bacillus cereus</i>	This patent	recA
	1759 <i>Bacillus cereus</i>	This patent	recA
	1760 <i>Bacillus mycoides</i>	This patent	recA
20	1761 <i>Bacillus pseudomycoides</i>	This patent	recA
	1762 <i>Bacillus thuringiensis</i>	This patent	recA
	1763 <i>Bacillus thuringiensis</i>	This patent	recA
	1764 <i>Klebsiella oxytoca</i>	This patent	gyrA
	1765 <i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	This patent	gyrA
25	1766 <i>Klebsiella planticola</i>	This patent	gyrA
	1767 <i>Klebsiella pneumoniae</i>	This patent	gyrA
	1768 <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	This patent	gyrA
	1769 <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	This patent	gyrA
	1770 <i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	This patent	gyrA
30	1771 <i>Klebsiella terrigena</i>	This patent	gyrA
	1772 <i>Legionella pneumophila</i> subsp. <i>pneumophila</i>	This patent	gyrA
	1773 <i>Proteus mirabilis</i>	This patent	gyrA
	1774 <i>Providencia rettgeri</i>	This patent	gyrA
	1775 <i>Proteus vulgaris</i>	This patent	gyrA
35	1776 <i>Yersinia enterocolitica</i>	This patent	gyrA
	1777 <i>Klebsiella oxytoca</i>	This patent	parC (grlA)
	1778 <i>Klebsiella oxytoca</i>	This patent	parC (grlA)
	1779 <i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	This patent	parC (grlA)
	1780 <i>Klebsiella planticola</i>	This patent	parC (grlA)
40	1781 <i>Klebsiella pneumoniae</i>	This patent	parC (grlA)
	1782 <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	This patent	parC (grlA)
	1783 <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	This patent	parC (grlA)
	1784 <i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	This patent	parC (grlA)
	1785 <i>Klebsiella terrigena</i>	This patent	parC (grlA)
45	1786 <i>Bacillus cereus</i>	This patent	fusA
	1787 <i>Bacillus cereus</i>	This patent	fusA
	1788 <i>Bacillus anthracis</i>	This patent	fusA
	1789 <i>Bacillus cereus</i>	This patent	fusA
	1790 <i>Bacillus anthracis</i>	This patent	fusA
50	1791 <i>Bacillus pseudomycoides</i>	This patent	fusA
	1792 <i>Bacillus cereus</i>	This patent	fusA
	1793 <i>Bacillus anthracis</i>	This patent	fusA
	1794 <i>Bacillus cereus</i>	This patent	fusA
	1795 <i>Bacillus weihenstephanensis</i>	This patent	fusA
55	1796 <i>Bacillus mycoides</i>	This patent	fusA
	1797 <i>Bacillus thuringiensis</i>	This patent	fusA
	1798 <i>Bacillus weihenstephanensis</i>	This patent	fusA-tuf spacer
	1799 <i>Bacillus thuringiensis</i>	This patent	fusA-tuf spacer
	1800 <i>Bacillus anthracis</i>	This patent	fusA-tuf spacer
60	1801 <i>Bacillus pseudomycoides</i>	This patent	fusA-tuf spacer
	1802 <i>Bacillus anthracis</i>	This patent	fusA-tuf spacer
	1803 <i>Bacillus cereus</i>	This patent	fusA-tuf spacer
	1804 <i>Bacillus cereus</i>	This patent	fusA-tuf spacer
	1805 <i>Bacillus mycoides</i>	This patent	fusA-tuf spacer
65	1806 <i>Bacillus cereus</i>	This patent	fusA-tuf spacer

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	1807 <i>Bacillus cereus</i>	This patent	<i>fusA-tuf</i> spacer
	1808 <i>Bacillus cereus</i>	This patent	<i>fusA-tuf</i> spacer
	1809 <i>Bacillus anthracis</i>	This patent	<i>fusA-tuf</i> spacer
	1810 <i>Bacillus mycoides</i>	This patent	<i>tuf</i>
	1811 <i>Bacillus thuringiensis</i>	This patent	<i>tuf</i>
10	1812 <i>Bacillus cereus</i>	This patent	<i>tuf</i>
	1813 <i>Bacillus weihenstephanensis</i>	This patent	<i>tuf</i>
	1814 <i>Bacillus anthracis</i>	This patent	<i>tuf</i>
	1815 <i>Bacillus cereus</i>	This patent	<i>tuf</i>
15	1816 <i>Bacillus cereus</i>	This patent	<i>tuf</i>
	1817 <i>Bacillus anthracis</i>	This patent	<i>tuf</i>
	1818 <i>Bacillus cereus</i>	This patent	<i>tuf</i>
	1819 <i>Bacillus anthracis</i>	This patent	<i>tuf</i>
	1820 <i>Bacillus pseudomyoides</i>	This patent	<i>tuf</i>
20	1821 <i>Bacillus cereus</i>	This patent	<i>tuf</i>
	1822 <i>Streptococcus oralis</i>	This patent	<i>fusA</i>
	1823 <i>Budvicia aquatica</i>	This patent	<i>fusA</i>
	1824 <i>Buttiauxella agrestis</i>	This patent	<i>fusA</i>
	1825 <i>Klebsiella oxytoca</i>	This patent	<i>fusA</i>
25	1826 <i>Plesiomonas shigelloides</i>	This patent	<i>fusA</i>
	1827 <i>Shewanella putrefaciens</i>	This patent	<i>fusA</i>
	1828 <i>Obesumbacterium proteus</i>	This patent	<i>fusA</i>
	1829 <i>Klebsiella oxytoca</i>	This patent	<i>fusA-tuf</i> spacer
	1830 <i>Budvicia aquatica</i>	This patent	<i>fusA-tuf</i> spacer
30	1831 <i>Plesiomonas shigelloides</i>	This patent	<i>fusA-tuf</i> spacer
	1832 <i>Obesumbacterium proteus</i>	This patent	<i>fusA-tuf</i> spacer
	1833 <i>Shewanella putrefaciens</i>	This patent	<i>fusA-tuf</i> spacer
	1834 <i>Buttiauxella agrestis</i>	This patent	<i>fusA-tuf</i> spacer
	1835 <i>Campylobacter coli</i>	This patent	<i>tuf</i>
35	1836 <i>Campylobacter fetus</i> subsp. <i>fetus</i>	This patent	<i>tuf</i>
	1837 <i>Campylobacter fetus</i> subsp. <i>venerealis</i>	This patent	<i>tuf</i>
	1838 <i>Buttiauxella agrestis</i>	This patent	<i>tuf</i>
	1839 <i>Klebsiella oxytoca</i>	This patent	<i>tuf</i>
	1840 <i>Plesiomonas shigelloides</i>	This patent	<i>tuf</i>
40	1841 <i>Shewanella putrefaciens</i>	This patent	<i>tuf</i>
	1842 <i>Obesumbacterium proteus</i>	This patent	<i>tuf</i>
	1843 <i>Budvicia aquatica</i>	This patent	<i>tuf</i>
	1844 <i>Abiotrophia adiacens</i>	This patent	<i>atpD</i>
	1845 <i>Arcanobacterium haemolyticum</i>	This patent	<i>atpD</i>
45	1846 <i>Basidiobolus ranarum</i>	This patent	<i>atpD</i>
	1847 <i>Blastomyces dermatitidis</i>	This patent	<i>atpD</i>
	1848 <i>Blastomyces dermatitidis</i>	This patent	<i>atpD</i>
	1849 <i>Campylobacter coli</i>	This patent	<i>atpD</i>
	1850 <i>Campylobacter fetus</i> subsp. <i>fetus</i>	This patent	<i>atpD</i>
50	1851 <i>Campylobacter fetus</i> subsp. <i>venerealis</i>	This patent	<i>atpD</i>
	1852 <i>Campylobacter gracilis</i>	This patent	<i>atpD</i>
	1853 <i>Campylobacter jejuni</i> subsp. <i>jejuni</i>	This patent	<i>atpD</i>
	1854 <i>Enterococcus cecorum</i>	This patent	<i>atpD</i>
	1855 <i>Enterococcus columbae</i>	This patent	<i>atpD</i>
55	1856 <i>Enterococcus dispar</i>	This patent	<i>atpD</i>
	1857 <i>Enterococcus malodoratus</i>	This patent	<i>atpD</i>
	1858 <i>Enterococcus mundtii</i>	This patent	<i>atpD</i>
	1859 <i>Enterococcus raffinosus</i>	This patent	<i>atpD</i>
	1860 <i>Globicatella sanguis</i>	This patent	<i>atpD</i>
60	1861 <i>Lactococcus garvieae</i>	This patent	<i>atpD</i>
	1862 <i>Lactococcus lactis</i>	This patent	<i>atpD</i>
	1863 <i>Listeria ivanovii</i>	This patent	<i>atpD</i>
	1864 <i>Succinivibrio dextrinosolvens</i>	This patent	<i>atpD</i>
	1865 <i>Tetragenococcus halophilus</i>	This patent	<i>atpD</i>
65	1866 <i>Campylobacter fetus</i> subsp. <i>fetus</i>	This patent	<i>recA</i>
	1867 <i>Campylobacter fetus</i> subsp. <i>venerealis</i>	This patent	<i>recA</i>
	1868 <i>Campylobacter jejuni</i> subsp. <i>jejuni</i>	This patent	<i>recA</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	1869 <i>Enterococcus avium</i>	This patent	<i>recA</i>
	1870 <i>Enterococcus faecium</i>	This patent	<i>recA</i>
	1871 <i>Listeria monocytogenes</i>	This patent	<i>recA</i>
	1872 <i>Streptococcus mitis</i>	This patent	<i>recA</i>
	1873 <i>Streptococcus oralis</i>	This patent	<i>recA</i>
10	1874 <i>Aspergillus fumigatus</i>	This patent	<i>tuf</i> (M)
	1875 <i>Aspergillus versicolor</i>	This patent	<i>tuf</i> (M)
	1876 <i>Basidiobolus ranarum</i>	This patent	<i>tuf</i> (M)
	1877 <i>Campylobacter gracilis</i>	This patent	<i>tuf</i>
	1878 <i>Campylobacter jejuni</i> subsp. <i>jejuni</i>	This patent	<i>tuf</i>
15	1879 <i>Coccidioides immitis</i>	This patent	<i>tuf</i> (M)
	1880 <i>Erwinia amylovora</i>	This patent	<i>tuf</i>
	1881 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Typhimurium	This patent	<i>tuf</i>
	1899 <i>Klebsiella pneumoniae</i>	Database	<i>blaSHV</i>
	1900 <i>Klebsiella pneumoniae</i>	Database	<i>blaSHV</i>
20	1901 <i>Escherichia coli</i>	Database	<i>blaSHV</i>
	1902 <i>Klebsiella pneumoniae</i>	Database	<i>blaSHV</i>
	1903 <i>Klebsiella pneumoniae</i>	Database	<i>blaSHV</i>
	1904 <i>Escherichia coli</i>	Database	<i>blaSHV</i>
	1905 <i>Pseudomonas aeruginosa</i>	Database	<i>blaSHV</i>
25	1927 <i>Neisseria meningitidis</i>	Database	<i>blaTEM</i>
	1928 <i>Escherichia coli</i>	Database	<i>blaTEM</i>
	1929 <i>Klebsiella oxytoca</i>	Database	<i>blaTEM</i>
	1930 <i>Escherichia coli</i>	Database	<i>blaTEM</i>
	1931 <i>Escherichia coli</i>	Database	<i>blaTEM</i>
30	1932 <i>Escherichia coli</i>	Database	<i>blaTEM</i>
	1933 <i>Escherichia coli</i>	Database	<i>blaTEM</i>
	1954 <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	Database	<i>gyrA</i>
	1956 <i>Candida inconspicua</i>	This patent	<i>tuf</i> (M)
	1957 <i>Candida utilis</i>	This patent	<i>tuf</i> (M)
35	1958 <i>Candida zeylanoides</i>	This patent	<i>tuf</i> (M)
	1959 <i>Candida catenulata</i>	This patent	<i>tuf</i> (M)
	1960 <i>Candida krusei</i>	This patent	<i>tuf</i> (M)
	1965 Plasmid pGS05	Database	<i>sull</i>
	1970 Transposon Tn10	Database	<i>tetB</i>
40	1985 <i>Cryptococcus neoformans</i>	Database	<i>tuf</i> (EF-1)
	1986 <i>Cryptococcus neoformans</i>	Database	<i>tuf</i> (EF-1)
	1987 <i>Saccharomyces cerevisiae</i>	Database	<i>tuf</i> (EF-1)
	1988 <i>Saccharomyces cerevisiae</i>	Database	<i>tuf</i> (EF-1)
	1989 <i>Eremothecium gossypii</i>	Database	<i>tuf</i> (EF-1)
45	1990 <i>Eremothecium gossypii</i>	Database	<i>tuf</i> (EF-1)
	1991 <i>Aspergillus oryzae</i>	Database	<i>tuf</i> (EF-1)
	1992 <i>Aureobasidium pullulans</i>	Database	<i>tuf</i> (EF-1)
	1993 <i>Histoplasma capsulatum</i>	Database	<i>tuf</i> (EF-1)
	1994 <i>Neurospora crassa</i>	Database	<i>tuf</i> (EF-1)
50	1995 <i>Podospora anserina</i>	Database	<i>tuf</i> (EF-1)
	1996 <i>Podospora curvicola</i>	Database	<i>tuf</i> (EF-1)
	1997 <i>Sordaria macrospora</i>	Database	<i>tuf</i> (EF-1)
	1998 <i>Trichoderma reesei</i>	Database	<i>tuf</i> (EF-1)
	2004 <i>Candida albicans</i>	Database	<i>tuf</i> (M)
55	2005 <i>Schizosaccharomyces pombe</i>	Database	<i>tuf</i> (M)
	2010 <i>Klebsiella pneumoniae</i>	Database	<i>blaTEM</i>
	2011 <i>Klebsiella pneumoniae</i>	Database	<i>blaTEM</i>
	2013 <i>Kluyvera ascorbata</i>	This patent	<i>gyrA</i>
	2014 <i>Kluyvera georgiana</i>	This patent	<i>gyrA</i>
60	2047 <i>Streptococcus pneumoniae</i>	Database	<i>pbp1A</i>
	2048 <i>Streptococcus pneumoniae</i>	Database	<i>pbp1A</i>
	2049 <i>Streptococcus pneumoniae</i>	Database	<i>pbp1A</i>

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Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	2050 <i>Streptococcus pneumoniae</i>	Database	<i>pbp1A</i>
	2051 <i>Streptococcus pneumoniae</i>	Database	<i>pbp1A</i>
	2052 <i>Streptococcus pneumoniae</i>	Database	<i>pbp1A</i>
	2053 <i>Streptococcus pneumoniae</i>	Database	<i>pbp1A</i>
	2054 <i>Streptococcus pneumoniae</i>	Database	<i>gyrA</i>
10	2055 <i>Streptococcus pneumoniae</i>	Database	<i>parC</i>
	2056 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp1A</i>
	2057 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp1A</i>
	2058 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp1A</i>
	2059 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp1A</i>
15	2060 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp1A</i>
	2061 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp1A</i>
	2062 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp1A</i>
	2063 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp1A</i>
	2064 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp1A</i>
20	2072 <i>Mycobacterium tuberculosis</i>	Database	<i>rpoB</i>
	2097 <i>Mycoplasma pneumoniae</i>	Database	<i>tuf</i>
	2101 <i>Mycobacterium tuberculosis</i>	Database	<i>inhA</i>
	2105 <i>Mycobacterium tuberculosis</i>	Database	<i>embB</i>
	2129 <i>Clostridium difficile</i>	Database	<i>cdtA</i>
25	2130 <i>Clostridium difficile</i>	Database	<i>cdtB</i>
	2137 <i>Pseudomonas putida</i>	Genome project	<i>tuf</i>
	2138 <i>Pseudomonas aeruginosa</i>	Genome project	<i>tuf</i>
	2139 <i>Campylobacter jejuni</i>	Database	<i>atpD</i>
	2140 <i>Streptococcus pneumoniae</i>	Database	<i>pbp1a</i>
30	2144 <i>Staphylococcus aureus</i>	Database	<i>mupA</i>
	2147 <i>Escherichia coli</i>	Database	<i>catI</i>
	2150 <i>Escherichia coli</i>	Database	<i>catIII</i>
	2153 <i>Shigella flexneri</i>	Database	<i>catIII</i>
	2156 <i>Clostridium perfringens</i>	Database	<i>catP</i>
35	2159 <i>Staphylococcus aureus</i>	Database	<i>cat</i>
	2162 <i>Staphylococcus aureus</i>	Database	<i>cat</i>
	2165 <i>Salmonella typhimurium</i>	Database	<i>ppfl</i> -like
	2183 <i>Alcaligenes faecalis</i> subsp. <i>faecalis</i>	This patent	<i>tuf</i>
	2184 <i>Campylobacter coli</i>	This patent	<i>fusA</i>
40	2185 <i>Succinivibrio dextrinosolvens</i>	This patent	<i>tuf</i>
	2186 <i>Tetragenococcus halophilus</i>	This patent	<i>tuf</i>
	2187 <i>Campylobacter jejuni</i> subsp. <i>jejuni</i>	This patent	<i>fusA</i>
	2188 <i>Campylobacter jejuni</i> subsp. <i>jejuni</i>	This patent	<i>fusA</i>
	2189 <i>Leishmania guyanensis</i>	This patent	<i>atpD</i>
45	2190 <i>Trypanosoma brucei brucei</i>	This patent	<i>atpD</i>
	2191 <i>Aspergillus nidulans</i>	This patent	<i>atpD</i>
	2192 <i>Leishmania panamensis</i>	This patent	<i>atpD</i>
	2193 <i>Aspergillus nidulans</i>	This patent	<i>tuf</i> (M)
	2194 <i>Aureobasidium pullulans</i>	This patent	<i>tuf</i> (M)
50	2195 <i>Emmonsia parva</i>	This patent	<i>tuf</i> (M)
	2196 <i>Exserohilum rostratum</i>	This patent	<i>tuf</i> (M)
	2197 <i>Fusarium moniliforme</i>	This patent	<i>tuf</i> (M)
	2198 <i>Fusarium solani</i>	This patent	<i>tuf</i> (M)
	2199 <i>Histoplasma capsulatum</i>	This patent	<i>tuf</i> (M)
55	2200 <i>Kocuria kristinae</i>	This patent	<i>tuf</i>
	2201 <i>Vibrio mimicus</i>	This patent	<i>tuf</i>
	2202 <i>Citrobacter freundii</i>	This patent	<i>recA</i>
	2203 <i>Clostridium botulinum</i>	This patent	<i>recA</i>
	2204 <i>Francisella tularensis</i>	This patent	<i>recA</i>
60	2205 <i>Peptostreptococcus anaerobius</i>	This patent	<i>recA</i>
	2206 <i>Peptostreptococcus asaccharolyticus</i>	This patent	<i>recA</i>
	2207 <i>Providencia stuartii</i>	This patent	<i>recA</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	2208 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Paratyphi A	This patent	<i>recA</i>
	2209 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Typhimurium	This patent	<i>recA</i>
	2210 <i>Staphylococcus saprophyticus</i>	This patent	<i>recA</i>
10	2211 <i>Yersinia pseudotuberculosis</i>	This patent	<i>recA</i>
	2212 <i>Zoogloea ramigera</i>	This patent	<i>recA</i>
	2214 <i>Abiotrophia adiacens</i>	This patent	<i>fusA</i>
	2215 <i>Acinetobacter baumannii</i>	This patent	<i>fusA</i>
	2216 <i>Actinomyces meyeri</i>	This patent	<i>fusA</i>
15	2217 <i>Clostridium difficile</i>	This patent	<i>fusA</i>
	2218 <i>Corynebacterium diphtheriae</i>	This patent	<i>fusA</i>
	2219 <i>Enterobacter cloacae</i>	This patent	<i>fusA</i>
	2220 <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	This patent	<i>fusA</i>
	2221 <i>Listeria monocytogenes</i>	This patent	<i>fusA</i>
20	2222 <i>Mycobacterium avium</i>	This patent	<i>fusA</i>
	2223 <i>Mycobacterium gordonae</i>	This patent	<i>fusA</i>
	2224 <i>Mycobacterium kansasii</i>	This patent	<i>fusA</i>
	2225 <i>Mycobacterium terrae</i>	This patent	<i>fusA</i>
	2226 <i>Neisseria polysaccharea</i>	This patent	<i>fusA</i>
25	2227 <i>Staphylococcus epidermidis</i>	This patent	<i>fusA</i>
	2228 <i>Staphylococcus haemolyticus</i>	This patent	<i>fusA</i>
	2229 <i>Succinivibrio dextrinosolvens</i>	This patent	<i>fusA</i>
	2230 <i>Tetragenococcus halophilus</i>	This patent	<i>fusA</i>
	2231 <i>Veillonella parvula</i>	This patent	<i>fusA</i>
30	2232 <i>Yersinia pseudotuberculosis</i>	This patent	<i>fusA</i>
	2233 <i>Zoogloea ramigera</i>	This patent	<i>fusA</i>
	2234 <i>Aeromonas hydrophila</i>	This patent	<i>fusA</i>
	2235 <i>Abiotrophia adiacens</i>	This patent	<i>fusA-tuf</i> spacer
	2236 <i>Acinetobacter baumannii</i>	This patent	<i>fusA-tuf</i> spacer
35	2237 <i>Actinomyces meyeri</i>	This patent	<i>fusA-tuf</i> spacer
	2238 <i>Clostridium difficile</i>	This patent	<i>fusA-tuf</i> spacer
	2239 <i>Corynebacterium diphtheriae</i>	This patent	<i>fusA-tuf</i> spacer
	2240 <i>Enterobacter cloacae</i>	This patent	<i>fusA-tuf</i> spacer
	2241 <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	This patent	<i>fusA-tuf</i> spacer
40	2242 <i>Listeria monocytogenes</i>	This patent	<i>fusA-tuf</i> spacer
	2243 <i>Mycobacterium avium</i>	This patent	<i>fusA-tuf</i> spacer
	2244 <i>Mycobacterium gordonae</i>	This patent	<i>fusA-tuf</i> spacer
	2245 <i>Mycobacterium kansasii</i>	This patent	<i>fusA-tuf</i> spacer
	2246 <i>Mycobacterium terrae</i>	This patent	<i>fusA-tuf</i> spacer
45	2247 <i>Neisseria polysaccharea</i>	This patent	<i>fusA-tuf</i> spacer
	2248 <i>Staphylococcus epidermidis</i>	This patent	<i>fusA-tuf</i> spacer
	2249 <i>Staphylococcus haemolyticus</i>	This patent	<i>fusA-tuf</i> spacer
	2255 <i>Abiotrophia adiacens</i>	This patent	<i>tuf</i>
	2256 <i>Acinetobacter baumannii</i>	This patent	<i>tuf</i>
50	2257 <i>Actinomyces meyeri</i>	This patent	<i>tuf</i>
	2258 <i>Clostridium difficile</i>	This patent	<i>tuf</i>
	2259 <i>Corynebacterium diphtheriae</i>	This patent	<i>tuf</i>
	2260 <i>Enterobacter cloacae</i>	This patent	<i>tuf</i>
	2261 <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	This patent	<i>tuf</i>
55	2262 <i>Listeria monocytogenes</i>	This patent	<i>tuf</i>
	2263 <i>Mycobacterium avium</i>	This patent	<i>tuf</i>
	2264 <i>Mycobacterium gordonae</i>	This patent	<i>tuf</i>
	2265 <i>Mycobacterium kansasii</i>	This patent	<i>tuf</i>
	2266 <i>Mycobacterium terrae</i>	This patent	<i>tuf</i>
60	2267 <i>Neisseria polysaccharea</i>	This patent	<i>tuf</i>
	2268 <i>Staphylococcus epidermidis</i>	This patent	<i>tuf</i>
	2269 <i>Staphylococcus haemolyticus</i>	This patent	<i>tuf</i>
	2270 <i>Aeromonas hydrophila</i>	This patent	<i>tuf</i>
	2271 <i>Bilophila wadsworthia</i>	This patent	<i>tuf</i>
65	2272 <i>Brevundimonas diminuta</i>	This patent	<i>tuf</i>
	2273 <i>Streptococcus mitis</i>	This patent	<i>pbp1a</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	2274 <i>Streptococcus mitis</i>	This patent	<i>pbp1a</i>
	2275 <i>Streptococcus mitis</i>	This patent	<i>pbp1a</i>
	2276 <i>Streptococcus oralis</i>	This patent	<i>pbp1a</i>
	2277 <i>Escherichia coli</i>	This patent	<i>gyrA</i>
	2278 <i>Escherichia coli</i>	This patent	<i>gyrA</i>
10	2279 <i>Escherichia coli</i>	This patent	<i>gyrA</i>
	2280 <i>Escherichia coli</i>	This patent	<i>gyrA</i>
	2288 <i>Enterococcus faecium</i>	Database	<i>ddl</i>
	2293 <i>Enterococcus faecium</i>	Database	<i>vanA</i>
15	2296 <i>Enterococcus faecalis</i>	Database	<i>vanB</i>

* *tuf* indicates *tuf* sequences, *tuf* (C) indicates *tuf* sequences divergent from main (usually A and B) copies of the elongation factor-Tu, *tuf* (EF-1) indicates *tuf* sequences of the eukaryotic type (elongation factor 1 α), *tuf* (M) indicates *tuf* sequences from organellar (mostly mitochondrial) origin.

fusA indicates *fusA* sequences; *fusA-tuf* spacer indicates the intergenic region between *fusA* and *tuf*.

atpD indicates *atpD* sequences of the F-type, *atpD* (V) indicates *atpD* sequences of the V-type.

recA indicates *recA* sequences, *recA*(Rad51) indicates *rad51* sequences or homologs and *recA*(Dmc1) indicates *dmc1* sequences or homologs.

Table 8. Bacterial species used to test the specificity of the *Streptococcus agalactiae*-specific amplification primers derived from *tuf* sequences.

5	Strain	Reference number	Strain	Reference number
	<i>Streptococcus acidominimus</i>	ATCC 51726	<i>Bacteroides caccae</i>	ATCC 43185
	<i>Streptococcus agalactiae</i>	ATCC 12403	<i>Bacteroides vulgatus</i>	ATCC 8482
	<i>Streptococcus agalactiae</i>	ATCC 12973	<i>Bacteroides fragilis</i>	ATCC 25285
10	<i>Streptococcus agalactiae</i>	ATCC 13813	<i>Candida albicans</i>	ATCC 11006
	<i>Streptococcus agalactiae</i>	ATCC 27591	<i>Clostridium innocuum</i>	ATCC 14501
	<i>Streptococcus agalactiae</i>	CDCs 1073	<i>Clostridium ramosum</i>	ATCC 25582
	<i>Streptococcus anginosus</i>	ATCC 27335	<i>Lactobacillus casei</i> subsp. <i>casei</i>	ATCC 393
	<i>Streptococcus anginosus</i>	ATCC 33397	<i>Clostridium septicum</i>	ATCC 12464
15	<i>Streptococcus bovis</i>	ATCC 33317	<i>Corynebacterium cervicis</i>	NCTC 10604
	<i>Streptococcus anginosus</i>	ATCC 27823	<i>Corynebacterium genitalium</i>	ATCC 33031
	<i>Streptococcus cricetus</i>	ATCC 19642	<i>Corynebacterium urealyticum</i>	ATCC 43042
	<i>Streptococcus cristatus</i>	ATCC 51100	<i>Enterococcus faecalis</i>	ATCC 29212
	<i>Streptococcus downei</i>	ATCC 33748	<i>Enterococcus faecium</i>	ATCC 19434
20	<i>Streptococcus dysgalactiae</i>	ATCC 43078	<i>Eubacterium lentum</i>	ATCC 43055
	<i>Streptococcus equi</i> subsp. <i>equi</i>	ATCC 9528	<i>Eubacterium nodutum</i>	ATCC 33099
	<i>Streptococcus ferus</i>	ATCC 33477	<i>Gardnerella vaginalis</i>	ATCC 14018
	<i>Streptococcus gordonii</i>	ATCC 10558	<i>Lactobacillus acidophilus</i>	ATCC 4356
	<i>Streptococcus macacae</i>	ATCC 35911	<i>Lactobacillus crispatus</i>	ATCC 33820
25	<i>Streptococcus mitis</i>	ATCC 49456	<i>Lactobacillus gasseri</i>	ATCC 33323
	<i>Streptococcus mutans</i>	ATCC 25175	<i>Lactobacillus johnsonii</i>	ATCC 33200
	<i>Streptococcus oralis</i>	ATCC 35037	<i>Lactococcus lactis</i> subsp. <i>lactis</i>	ATCC 19435
	<i>Streptococcus parasanguinis</i>	ATCC 15912	<i>Lactococcus lactis</i> subsp. <i>lactis</i>	ATCC 11454
	<i>Streptococcus parauberis</i>	DSM 6631	<i>Listeria innocua</i>	ATCC 33090
30	<i>Streptococcus pneumoniae</i>	ATCC 27336	<i>Micrococcus luteus</i>	ATCC 9341
	<i>Streptococcus pyogenes</i>	ATCC 19615	<i>Escherichia coli</i>	ATCC 25922
	<i>Streptococcus rattii</i>	ATCC 19645	<i>Micrococcus lylae</i>	ATCC 27566
	<i>Streptococcus salivarius</i>	ATCC 7073	<i>Porphyromonas asaccharolytica</i>	ATCC 25260
	<i>Streptococcus sanguinis</i>	ATCC 10556	<i>Prevotella corporis</i>	ATCC 33547
35	<i>Streptococcus sobrinus</i>	ATCC 27352	<i>Prevotella melanogenica</i>	ATCC 25845
	<i>Streptococcus suis</i>	ATCC 43765	<i>Staphylococcus aureus</i>	ATCC 13301
	<i>Streptococcus uberis</i>	ATCC 19436	<i>Staphylococcus epidermidis</i>	ATCC 14990
	<i>Streptococcus vestibularis</i>	ATCC 49124	<i>Staphylococcus saprophyticus</i>	ATCC 15305

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Table 9. Bacterial species used to test the specificity of the *Streptococcus agalactiae*-specific amplification primers derived from *atpD* sequences.

5	Strain		Reference number	
	Strain		Reference number	
10	<i>Streptococcus acidominimus</i>	ATCC 51726	<i>Streptococcus gordonii</i>	ATCC 10558
	<i>Streptococcus agalactiae</i>	ATCC 12400	<i>Streptococcus macacae</i>	ATCC 35911
	<i>Streptococcus agalactiae</i>	ATCC 12403	<i>Streptococcus mitis</i>	ATCC 49456
	<i>Streptococcus agalactiae</i>	ATCC 12973	<i>Streptococcus mutans</i>	ATCC 25175
	<i>Streptococcus agalactiae</i>	ATCC 13813	<i>Streptococcus oralis</i>	ATCC 35037
15	<i>Streptococcus agalactiae</i>	ATCC 27591	<i>Streptococcus parasanguinis</i>	ATCC 15912
	<i>Streptococcus agalactiae</i>	CDCs-1073	<i>Streptococcus parauberis</i>	DSM 6631
	<i>Streptococcus anginosus</i>	ATCC 27335	<i>Streptococcus pneumoniae</i>	ATCC 27336
	<i>Streptococcus anginosus</i>	ATCC 27823	<i>Streptococcus pyogenes</i>	ATCC 19615
	<i>Streptococcus bovis</i>	ATCC 33317	<i>Streptococcus rattii</i>	ATCC 19645
20	<i>Streptococcus cricetus</i>	ATCC 19642	<i>Streptococcus salivarius</i>	ATCC 7073
	<i>Streptococcus cristatus</i>	ATCC 51100	<i>Streptococcus sanguinis</i>	ATCC 10556
	<i>Streptococcus downei</i>	ATCC 33748	<i>Streptococcus sobrinus</i>	ATCC 27352
	<i>Streptococcus dysgalactiae</i>	ATCC 43078	<i>Streptococcus suis</i>	ATCC 43765
	<i>Streptococcus equi</i> subsp. <i>equi</i>	ATCC 9528	<i>Streptococcus uberis</i>	ATCC 19436
	<i>Streptococcus ferus</i>	ATCC 33477	<i>Streptococcus vestibularis</i>	ATCC 49124

Table 10. Bacterial species used to test the specificity of the *Enterococcus*-specific amplification primers derived from *tuf* sequences.

	Strain	Reference number	Strain	Reference number
5	Gram-positive species (n=74)			
	<i>Abiotrophia adiacens</i>	ATCC 49176	<i>Listeria innocua</i>	ATCC 33090
	<i>Abiotrophia defectiva</i>	ATCC 49175	<i>Listeria ivanovii</i>	ATCC 19119
	<i>Bacillus cereus</i>	ATCC 14579	<i>Listeria monocytogenes</i>	ATCC 15313
	<i>Bacillus subtilis</i>	ATCC 27370	<i>Listeria seeligeri</i>	ATCC 35967
10	<i>Bifidobacterium adolescentis</i>	ATCC 27534	<i>Micrococcus luteus</i>	ATCC 9341
	<i>Bifidobacterium breve</i>	ATCC 15700	<i>Pediococcus acidilacti</i>	ATCC 33314
	<i>Bifidobacterium dentium</i>	ATCC 27534	<i>Pediococcus pentosaceus</i>	ATCC 33316
	<i>Bifidobacterium longum</i>	ATCC 15707	<i>Peptococcus niger</i>	ATCC 27731
	<i>Clostridium perfringens</i>	ATCC 3124	<i>Peptostreptococcus anaerobius</i>	ATCC 27337
15	<i>Clostridium septicum</i>	ATCC 12464	<i>Peptostreptococcus indolicus</i>	ATCC 29247
	<i>Corynebacterium aquaticus</i>	ATCC 14665	<i>Peptostreptococcus micros</i>	ATCC 33270
	<i>Corynebacterium pseudodiphtheriticum</i>	ATCC 10700	<i>Propionibacterium acnes</i>	ATCC 6919
	<i>Enterococcus avium</i>	ATCC 14025	<i>Staphylococcus aureus</i>	ATCC 43300
20	<i>Enterococcus casseliflavus</i>	ATCC 25788	<i>Staphylococcus capitis</i>	ATCC 27840
	<i>Enterococcus cecorum</i>	ATCC 43199	<i>Staphylococcus epidermidis</i>	ATCC 14990
	<i>Enterococcus columbae</i>	ATCC 51263	<i>Staphylococcus haemolyticus</i>	ATCC 29970
	<i>Enterococcus dispar</i>	ATCC 51266	<i>Staphylococcus hominis</i>	ATCC 27844
	<i>Enterococcus durans</i>	ATCC 19432	<i>Staphylococcus lugdunensis</i>	ATCC 43809
25	<i>Enterococcus faecalis</i>	ATCC 29212	<i>Staphylococcus saprophyticus</i>	ATCC 15305
	<i>Enterococcus faecium</i>	ATCC 19434	<i>Staphylococcus simulans</i>	ATCC 27848
	<i>Enterococcus flavescens</i>	ATCC 49996	<i>Staphylococcus warneri</i>	ATCC 27836
	<i>Enterococcus gallinarum</i>	ATCC 49573	<i>Streptococcus agalactiae</i>	ATCC 13813
	<i>Enterococcus hirae</i>	ATCC 8044	<i>Streptococcus anginosus</i>	ATCC 33397
30	<i>Enterococcus malodoratus</i>	ATCC 43197	<i>Streptococcus bovis</i>	ATCC 33317
	<i>Enterococcus mundtii</i>	ATCC 43186	<i>Streptococcus constellatus</i>	ATCC 27823
	<i>Enterococcus pseudoavium</i>	ATCC 49372	<i>Streptococcus cristatus</i>	ATCC 51100
	<i>Enterococcus raffinosus</i>	ATCC 49427	<i>Streptococcus intermedius</i>	ATCC 27335
	<i>Enterococcus saccharolyticus</i>	ATCC 43076	<i>Streptococcus mitis</i>	ATCC 49456
35	<i>Enterococcus solitarius</i>	ATCC 49428	<i>Streptococcus mitis</i>	ATCC 3639
	<i>Enterococcus sulfureus</i>	ATCC 49903	<i>Streptococcus mutans</i>	ATCC 27175
	<i>Eubacterium lentum</i>	ATCC 49903	<i>Streptococcus parasanguinis</i>	ATCC 15912
	<i>Gemella haemolysans</i>	ATCC 10379	<i>Streptococcus pneumoniae</i>	ATCC 27736
	<i>Gemella morbillorum</i>	ATCC 27842	<i>Streptococcus pneumoniae</i>	ATCC 6303
40	<i>Lactobacillus acidophilus</i>	ATCC 4356	<i>Streptococcus pyogenes</i>	ATCC 19615
	<i>Leuconostoc mesenteroides</i>	ATCC 19225	<i>Streptococcus salivarius</i>	ATCC 7073
	<i>Listeria grayi</i>	ATCC 19120	<i>Streptococcus sanguinis</i>	ATCC 10556
	<i>Listeria grayi</i>	ATCC 19123	<i>Streptococcus suis</i>	ATCC 43765

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Table 10. Bacterial species used to test the specificity of the *Enterococcus*-specific amplification primers derived from *tuf* sequences (continued).

	Strain	Reference number	Strain	Reference number
5	Gram-negative species (n=39)			
	<i>Acidominococcus fermentans</i>	ATCC 2508	<i>Hafnia alvei</i>	ATCC 13337
	<i>Acinetobacter baumannii</i>	ATCC 19606	<i>Klebsiella oxytoca</i>	ATCC 13182
	<i>Alcaligenes faecalis</i>	ATCC 8750	<i>Meganomonas hypermegas</i>	ATCC 25560
	<i>Anaerobiospirillum</i>	ATCC 29305	<i>Mitsukoella multiacidus</i>	ATCC 27723
10	<i>succiniproducens</i>		<i>Moraxella catarrhalis</i>	ATCC 43628
	<i>Anaerorhabdus furcosus</i>	ATCC 25662	<i>Morganella morganii</i>	ATCC 25830
	<i>Bacteroides distasonis</i>	ATCC 8503	<i>Neisseria meningitidis</i>	ATCC 13077
	<i>Bacteroides thetaiotaomicron</i>	ATCC 29741	<i>Pasteurella aerogenes</i>	ATCC 27883
	<i>Bacteroides vulgatus</i>	ATCC 8482	<i>Proteus vulgaris</i>	ATCC 13315
15	<i>Bordetella pertussis</i>	LSPQ 3702	<i>Providencia alcalifaciens</i>	ATCC 9886
	<i>Bulkholderia cepacia</i>	LSPQ 2217	<i>Providencia rettgeri</i>	ATCC 9250
	<i>Butyrvibrio fibrinosolvens</i>	ATCC 19171	<i>Pseudomonas aeruginosa</i>	ATCC 27853
	<i>Cardiobacterium hominis</i>	ATCC 15826	<i>Salmonella typhimurium</i>	ATCC 14028
	<i>Citrobacter freundii</i>	ATCC 8090	<i>Serratia marcescens</i>	ATCC 13880
20	<i>Desulfovibrio vulgaris</i>	ATCC 29579	<i>Shigella flexneri</i>	ATCC 12022
	<i>Edwardsiellae tarda</i>	ATCC 15947	<i>Shigella sonnei</i>	ATCC 29930
	<i>Enterobacter cloacae</i>	ATCC 13047	<i>Succinivibrio dextrinosolvens</i>	ATCC 19716
	<i>Escherichia coli</i>	ATCC 25922	<i>Tissierella praeacuta</i>	ATCC 25539
	<i>Fusobacterium russii</i>	ATCC 25533	<i>Veillonella parvula</i>	ATCC 10790
25	<i>Haemophilus influenzae</i>	ATCC 9007	<i>Yersinia enterocolitica</i>	ATCC 9610

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases.

	Species	Strain	Accession number	Coding gene*
	<u>tuf sequences</u>			
	Bacteria			
5	<i>Actinobacillus actinomycetemcomitans</i>	HK1651	Genome project ²	<i>tuf</i>
	<i>Actinobacillus actinomycetemcomitans</i>	HK1651	Genome project ²	<i>tuf</i> (EF-G)
	<i>Agrobacterium tumefaciens</i>		X99673	<i>tuf</i>
	<i>Agrobacterium tumefaciens</i>		X99673	<i>tuf</i> (EF-G)
	<i>Agrobacterium tumefaciens</i>		X99674	<i>tuf</i>
10	<i>Anacystis nidulans</i>	PCC 6301	X17442	<i>tuf</i>
	<i>Aquifex aeolicus</i>	VF5	AE000669	<i>tuf</i>
	<i>Aquifex aeolicus</i>	VF5	AE000669	<i>tuf</i> (EF-G)
	<i>Aquifex pyrophilus</i>		Genome project ²	<i>tuf</i> (EF-G)
	<i>Aquifex pyrophilus</i>		Y15787	<i>tuf</i>
15	<i>Bacillus anthracis</i>	Ames	Genome project ²	<i>tuf</i>
	<i>Bacillus anthracis</i>	Ames	Genome project ²	<i>tuf</i> (EF-G)
	<i>Bacillus halodurans</i>	C-125	AB017508	<i>tuf</i>
	<i>Bacillus halodurans</i>	C-125	AB017508	<i>tuf</i> (EF-G)
	<i>Bacillus stearothermophilus</i>	CCM 2184	AJ000260	<i>tuf</i>
20	<i>Bacillus subtilis</i>	168	D64127	<i>tuf</i>
	<i>Bacillus subtilis</i>	168	D64127	<i>tuf</i> (EF-G)
	<i>Bacillus subtilis</i>	DSM 10	Z99104	<i>tuf</i>
	<i>Bacillus subtilis</i>	DSM 10	Z99104	<i>tuf</i> (EF-G)
	<i>Bacteroides forsythus</i>	ATCC 43037	AB035466	<i>tuf</i>
25	<i>Bacteroides fragilis</i>	DSM 1151	- ¹	<i>tuf</i>
	<i>Bordetella bronchiseptica</i>	RB50	Genome project ²	<i>tuf</i>
	<i>Bordetella pertussis</i>	Tohama 1	Genome project ²	<i>tuf</i>
	<i>Bordetella pertussis</i>	Tohama 1	Genome project ²	<i>tuf</i> (EF-G)
	<i>Borrelia burgdorferi</i>	B31	U78193	<i>tuf</i>
30	<i>Borrelia burgdorferi</i>		AE001155	<i>tuf</i> (EF-G)
	<i>Brevibacterium linens</i>	DSM 20425	X76863	<i>tuf</i>
	<i>Buchnera aphidicola</i>	Ap	Y12307	<i>tuf</i>
	<i>Burkholderia pseudomallei</i>	K96243	Genome project ²	<i>tuf</i> (EF-G)
	<i>Campylobacter jejuni</i>	NCTC 11168	Y17167	<i>tuf</i>
35	<i>Campylobacter jejuni</i>	NCTC 11168	CJ11168X2	<i>tuf</i> (EF-G)
	<i>Chlamydia pneumoniae</i>	CWL029	AE001592	<i>tuf</i>
	<i>Chlamydia pneumoniae</i>	CWL029	AE001639	<i>tuf</i> (EF-G)
	<i>Chlamydia trachomatis</i>		M74221	<i>tuf</i>
	<i>Chlamydia trachomatis</i>	D/UW-3/CX	AE001317	<i>tuf</i> (EF-G)
40	<i>Chlamydia trachomatis</i>	D/UW-3/CX	AE001305	<i>tuf</i>
	<i>Chlamydia trachomatis</i>	F/IC-Cal-13	L22216	<i>tuf</i>
	<i>Chlorobium vibrioforme</i>	DSM 263	X77033	<i>tuf</i>
	<i>Chloroflexus aurantiacus</i>	DSM 636	X76865	<i>tuf</i>
	<i>Clostridium acetobutylicum</i>	ATCC 824	Genome project ²	<i>tuf</i>
45	<i>Clostridium difficile</i>	630	Genome project ²	<i>tuf</i>
	<i>Clostridium difficile</i>	630	Genome project ²	<i>tuf</i> (EF-G)
	<i>Corynebacterium diphtheriae</i>	NCTC 13129	Genome project ²	<i>tuf</i>
	<i>Corynebacterium diphtheriae</i>	NCTC 13129	Genome project ²	<i>tuf</i> (EF-G)
	<i>Corynebacterium glutamicum</i>	ASO 19	X77034	<i>tuf</i>
50	<i>Corynebacterium glutamicum</i>	MJ-233	E09634	<i>tuf</i>
	<i>Coxiella burnetii</i>	Nine Mile phase I	AF136604	<i>tuf</i>
	<i>Cytophaga lytica</i>	DSM 2039	X77035	<i>tuf</i>
	<i>Deinococcus radiodurans</i>	R1	AE001891	<i>tuf</i> (EF-G)
	<i>Deinococcus radiodurans</i>	R1	AE180092	<i>tuf</i>
55				

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Deinococcus radiodurans</i>	R1	AE002041	<i>tuf</i>
	<i>Deinonema</i> sp.		- ¹	<i>tuf</i>
	<i>Eikenella corrodens</i>	ATCC 23834	Z12610	<i>tuf</i>
	<i>Eikenella corrodens</i>	ATCC 23834	Z12610	<i>tuf</i> (EF-G)
5	<i>Enterococcus faecalis</i>		Genome project ²	<i>tuf</i> (EF-G)
	<i>Escherichia coli</i>		J01690	<i>tuf</i>
	<i>Escherichia coli</i>		J01717	<i>tuf</i>
	<i>Escherichia coli</i>		X00415	<i>tuf</i> (EF-G)
	<i>Escherichia coli</i>		X57091	<i>tuf</i>
10	<i>Escherichia coli</i>	K-12 MG1655	U00006	<i>tuf</i>
	<i>Escherichia coli</i>	K-12 MG1655	U00096	<i>tuf</i>
	<i>Escherichia coli</i>	K-12 MG1655	AE000410	<i>tuf</i> (EF-G)
	<i>Fervidobacterium islandicum</i>	DSM 5733	Y15788	<i>tuf</i>
	<i>Fibrobacter succinogenes</i>	S85	X76866	<i>tuf</i>
15	<i>Flavobacterium ferrigeneum</i>	DSM 13524	X76867	<i>tuf</i>
	<i>Flexistipes sinusarabici</i>		X59461	<i>tuf</i>
	<i>Gloeobacter violaceus</i>	PCC 7421	U09433	<i>tuf</i>
	<i>Gloeotheca</i> sp.	PCC 6501	U09434	<i>tuf</i>
	<i>Haemophilus actinomycetemcomitans</i>	HK1651	Genome project ²	<i>tuf</i>
20	<i>Haemophilus ducreyi</i>	35000	AF087414	<i>tuf</i> (EF-G)
	<i>Haemophilus influenzae</i>	Rd	U32739	<i>tuf</i>
	<i>Haemophilus influenzae</i>	Rd	U32746	<i>tuf</i>
	<i>Haemophilus influenzae</i>	Rd	U32739	<i>tuf</i> (EF-G)
	<i>Helicobacter pylori</i>	26695	AE000511	<i>tuf</i>
25	<i>Helicobacter pylori</i>	J99	AE001539	<i>tuf</i> (EF-G)
	<i>Helicobacter pylori</i>	J99	AE001541	<i>tuf</i>
	<i>Herpetosiphon aurantiacus</i>	Hpga1	X76868	<i>tuf</i>
	<i>Klebsiella pneumoniae</i>	M6H 78578	Genome project ²	<i>tuf</i>
	<i>Klebsiella pneumoniae</i>	M6H 78578	Genome project ²	<i>tuf</i> (EF-G)
30	<i>Lactobacillus paracasei</i>		E13922	<i>tuf</i>
	<i>Legionella pneumophila</i>	Philadelphia-1	Genome project ²	<i>tuf</i>
	<i>Leptospira interrogans</i>		AF115283	<i>tuf</i>
	<i>Leptospira interrogans</i>		AF115283	<i>tuf</i> (EF-G)
	<i>Micrococcus luteus</i>	IFO 3333	M17788	<i>tuf</i> (EF-G)
35	<i>Micrococcus luteus</i>	IFO 3333	M17788	<i>tuf</i>
	<i>Moraxella</i> sp.	TAC II 25	AJ249258	<i>tuf</i>
	<i>Mycobacterium avium</i>	104	Genome project ²	<i>tuf</i>
	<i>Mycobacterium avium</i>	104	Genome project ²	<i>tuf</i> (EF-G)
	<i>Mycobacterium bovis</i>	AF2122/97	Genome project ²	<i>tuf</i>
40	<i>Mycobacterium bovis</i>	AF2122/97	Genome project ²	<i>tuf</i> (EF-G)
	<i>Mycobacterium leprae</i>		L13276	<i>tuf</i>
	<i>Mycobacterium leprae</i>		Z14314	<i>tuf</i>
	<i>Mycobacterium leprae</i>		Z14314	<i>tuf</i> (EF-G)
	<i>Mycobacterium leprae</i>	Thai 53	D13869	<i>tuf</i>
45	<i>Mycobacterium tuberculosis</i>	Erdmann	S40925	<i>tuf</i>
	<i>Mycobacterium tuberculosis</i>	H37Rv	AL021943	<i>tuf</i> (EF-G)
	<i>Mycobacterium tuberculosis</i>	H37Rv	Z84395	<i>tuf</i>
	<i>Mycobacterium tuberculosis</i>	y42	AD000005	<i>tuf</i>
	<i>Mycobacterium tuberculosis</i>	CSU#93	Genome project ²	<i>tuf</i>
50	<i>Mycobacterium tuberculosis</i>	CSU#93	Genome project ²	<i>tuf</i> (EF-G)
	<i>Mycoplasma capricolum</i>	PG-31	X16462	<i>tuf</i>
	<i>Mycoplasma genitalium</i>	G37	U39732	<i>tuf</i>
	<i>Mycoplasma genitalium</i>	G37	U39689	<i>tuf</i> (EF-G)
	<i>Mycoplasma hominis</i>		X57136	<i>tuf</i>
55	<i>Mycoplasma hominis</i>	PG21	M57675	<i>tuf</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Mycoplasma pneumoniae</i>	M129	AE000019	<i>tuf</i>
	<i>Mycoplasma pneumoniae</i>	M129	AE000058	<i>tuf</i> (EF-G)
	<i>Neisseria gonorrhoeae</i>	MS11	L36380	<i>tuf</i>
	<i>Neisseria gonorrhoeae</i>	MS11	L36380	<i>tuf</i> (EF-G)
5	<i>Neisseria meningitidis</i>	Z2491	Genome project ²	<i>tuf</i> (EF-G)
	<i>Neisseria meningitidis</i>	Z2491	Genome project ²	<i>tuf</i>
	<i>Pasteurella multocida</i>	Pm70	Genome project ²	<i>tuf</i>
	<i>Peptococcus niger</i>	DSM 20745	X76869	<i>tuf</i>
	<i>Phormidium ectocarp</i>	PCC 7375	U09443	<i>tuf</i>
10	<i>Planobispora rosea</i>	ATCC 53773	U67308	<i>tuf</i>
	<i>Planobispora rosea</i>	ATCC 53733	X98830	<i>tuf</i>
	<i>Planobispora rosea</i>	ATCC 53733	X98830	<i>tuf</i> (EF-G)
	<i>Plectonema boryanum</i>	PCC 73110	U09444	<i>tuf</i>
	<i>Porphyromonas gingivalis</i>	W83	Genome project ²	<i>tuf</i>
15	<i>Porphyromonas gingivalis</i>	W83	Genome project ²	<i>tuf</i> (EF-G)
	<i>Porphyromonas gingivalis</i>	FDC 381	AB035461	<i>tuf</i>
	<i>Porphyromonas gingivalis</i>	W83	AB035462	<i>tuf</i>
	<i>Porphyromonas gingivalis</i>	SUNY 1021	AB035463	<i>tuf</i>
	<i>Porphyromonas gingivalis</i>	A7A1-28	AB035464	<i>tuf</i>
20	<i>Porphyromonas gingivalis</i>	ATCC 33277	AB035465	<i>tuf</i>
	<i>Porphyromonas gingivalis</i>	ATCC 33277	AB035471	<i>tuf</i> (EF-G)
	<i>Prochlorothrix hollandica</i>		U09445	<i>tuf</i>
	<i>Pseudomonas aeruginosa</i>	PAO-1	Genome project ²	<i>tuf</i>
	<i>Pseudomonas putida</i>		Genome project ²	<i>tuf</i>
25	<i>Rickettsia prowazekii</i>	Madrid E	AJ235272	<i>tuf</i>
	<i>Rickettsia prowazekii</i>	Madrid E	AJ235270	<i>tuf</i> (EF-G)
	<i>Rickettsia prowazekii</i>	Madrid E	Z54171	<i>tuf</i> (EF-G)
	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype <i>Typhimurium</i>		X64591	<i>tuf</i> (EF-G)
30	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype <i>Typhimurium</i>	LT2 trpE91	X55116	<i>tuf</i>
	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype <i>Typhimurium</i>	LT2 trpE91	X55117	<i>tuf</i>
	<i>Serpulina hyodysenteriae</i>	B204	U51635	<i>tuf</i>
35	<i>Serratia marcescens</i>		AF058451	<i>tuf</i>
	<i>Shewanella putrefaciens</i>	DSM 50426	- ¹	<i>tuf</i>
	<i>Shewanella putrefaciens</i>	MR-1	Genome project ²	<i>tuf</i>
	<i>Spirochaeta aurantia</i>	DSM 1902	X76874	<i>tuf</i>
	<i>Staphylococcus aureus</i>		AJ237696	<i>tuf</i> (EF-G)
40	<i>Staphylococcus aureus</i>	EMRSA-16	Genome project ²	<i>tuf</i>
	<i>Staphylococcus aureus</i>	NCTC 8325	Genome project ²	<i>tuf</i>
	<i>Staphylococcus aureus</i>	COL	Genome project ²	<i>tuf</i>
	<i>Staphylococcus aureus</i>	EMRSA-16	Genome project ²	<i>tuf</i> (EF-G)
	<i>Stigmatella aurantiaca</i>	DW4	X82820	<i>tuf</i>
45	<i>Stigmatella aurantiaca</i>	Sg a1	X76870	<i>tuf</i>
	<i>Streptococcus mutans</i>	GS-5 Kuramitsu	U75481	<i>tuf</i>
	<i>Streptococcus mutans</i>	UAB159	Genome project ²	<i>tuf</i>
	<i>Streptococcus oralis</i>	NTCC 11427	P331701	<i>tuf</i>
	<i>Streptococcus pyogenes</i>		Genome project ²	<i>tuf</i> (EF-G)
50	<i>Streptococcus pyogenes</i>	M1-GAS	Genome project ²	<i>tuf</i>
	<i>Streptomyces aureofaciens</i>	ATCC 10762	AF007125	<i>tuf</i>
	<i>Streptomyces cinnamomeus</i>	Tue89	X98831	<i>tuf</i>
	<i>Streptomyces coelicolor</i>	A3(2)	AL031013	<i>tuf</i> (EF-G)
	<i>Streptomyces coelicolor</i>	A3(2)	X77039	<i>tuf</i> (EF-G)
55	<i>Streptomyces coelicolor</i>	M145	X77039	<i>tuf</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Streptomyces collinus</i>	BSM 40733	S79408	<i>tuf</i>
	<i>Streptomyces netropsis</i>	Tu1063	AF153618	<i>tuf</i>
	<i>Streptomyces ramocissimus</i>		X67057	<i>tuf</i>
	<i>Streptomyces ramocissimus</i>		X67058	<i>tuf</i>
5	<i>Streptomyces ramocissimus</i>		X67057	<i>tuf</i> (EF-G)
	<i>Synechococcus</i> sp.	PCC 6301	X17442	<i>tuf</i> (EF-G)
	<i>Synechococcus</i> sp.	PCC 6301	X17442	<i>tuf</i>
	<i>Synechocystis</i> sp.	PCC 6803	D90913	<i>tuf</i> (EF-G)
	<i>Synechocystis</i> sp.	PCC 6803	D90913	<i>tuf</i>
10	<i>Synechocystis</i> sp.	PCC 6803	X65159	<i>tuf</i> (EF-G)
	<i>Taxeobacter occealus</i>	Myx 2105	X77036	<i>tuf</i>
	<i>Thermotoga maritima</i>		Genome project ²	<i>tuf</i> (EF-G)
	<i>Thermotoga maritima</i>		M27479	<i>tuf</i>
	<i>Thermus aquaticus</i>	EP 00276	X66322	<i>tuf</i>
15	<i>Thermus thermophilus</i>	HB8	X16278	<i>tuf</i> (EF-G)
	<i>Thermus thermophilus</i>	HB8	X05977	<i>tuf</i>
	<i>Thermus thermophilus</i>	HB8	X06657	<i>tuf</i>
	<i>Thiomonas cuprina</i>	DSM 5495	U78300	<i>tuf</i>
	<i>Thiomonas cuprina</i>	DSM 5495	U78300	<i>tuf</i> (EF-G)
20	<i>Thiomonas cuprina</i>	Hoe5	X76871	<i>tuf</i>
	<i>Treponema denticola</i>		Genome project ²	<i>tuf</i>
	<i>Treponema denticola</i>		Genome project ²	<i>tuf</i> (EF-G)
	<i>Treponema pallidum</i>		AE001202	<i>tuf</i>
	<i>Treponema pallidum</i>		AE001222	<i>tuf</i> (EF-G)
25	<i>Treponema pallidum</i>		AE001248	<i>tuf</i> (EF-G)
	<i>Ureaplasma urealyticum</i>	ATCC 33697	Z34275	<i>tuf</i>
	<i>Ureaplasma urealyticum</i>	serovar 3 biovar 1	AE002151	<i>tuf</i>
	<i>Ureaplasma urealyticum</i>	serovar 3 biovar 1	AE002151	<i>tuf</i> (EF-G)
	<i>Vibrio cholerae</i>	N16961	Genome project ²	<i>tuf</i>
30	<i>Wolinella succinogenes</i>	DSM 1740	X76872	<i>tuf</i>
	<i>Yersinia pestis</i>	CO-92	Genome project ²	<i>tuf</i>
	<i>Yersinia pestis</i>	CO-92	Genome project ²	<i>tuf</i> (EF-G)
35	Archaeobacteria			
	<i>Archaeoglobus fulgidus</i>		Genome project ²	<i>tuf</i> (EF-G)
	<i>Halobacterium marismortui</i>		X16677	<i>tuf</i>
	<i>Methanobacterium thermoautrophicum</i>	delta H	AE000877	<i>tuf</i>
40	<i>Methanococcus jannaschii</i>	ATCC 43067	U67486	<i>tuf</i>
	<i>Methanococcus vanniellii</i>		X05698	<i>tuf</i>
	<i>Pyrococcus abyssi</i>	Orsay	AJ248285	<i>tuf</i>
	<i>Thermoplasma acidophilum</i>	DSM 1728	X53866	<i>tuf</i>
45	Fungi			
	<i>Absidia glauca</i>	CBS 101.48	X54730	<i>tuf</i> (EF-1)
	<i>Arxula adenivorans</i>	Ls3	Z47379	<i>tuf</i> (EF-1)
50	<i>Aspergillus oryzae</i>	KBN616	AB007770	<i>tuf</i> (EF-1)
	<i>Aureobasidium pullulans</i>	R106	U19723	<i>tuf</i> (EF-1)
	<i>Candida albicans</i>	SC5314	Genome project ²	<i>tuf</i> (M)
	<i>Candida albicans</i>	SC5314	M29934	<i>tuf</i> (EF-1)
	<i>Candida albicans</i>	SC5314	M29935	<i>tuf</i> (EF-1)
55	<i>Cryptococcus neoformans</i>	B3501	U81803	<i>tuf</i> (EF-1)

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Cryptococcus neoformans</i>	M1-106	U81804	<i>tuf</i> (EF-1)
	<i>Eremothecium gossypii</i>	ATCC 10895	X73978	<i>tuf</i> (EF-1)
	<i>Eremothecium gossypii</i>		A29820	<i>tuf</i> (EF-1)
	<i>Fusarium oxysporum</i>	NRRL 26037	AF008498	<i>tuf</i> (EF-1)
5	<i>Histoplasma capsulatum</i>	186AS	U14100	<i>tuf</i> (EF-1)
	<i>Podospora anserina</i>		X74799	<i>tuf</i> (EF-1)
	<i>Podospora curvicolle</i>	VLV	X96614	<i>tuf</i> (EF-1)
	<i>Prototheca wickerhamii</i>	263-11	AJ245645	<i>tuf</i> (EF-1)
	<i>Puccinia graminis</i>	race 32	X73529	<i>tuf</i> (EF-1)
10	<i>Reclinomonas americana</i>	ATCC 50394	AF007261	<i>tuf</i> (M)
	<i>Rhizomucor racemosus</i>	ATCC 1216B	X17475	<i>tuf</i> (EF-1)
	<i>Rhizomucor racemosus</i>	ATCC 1216B	J02605	<i>tuf</i> (EF-1)
	<i>Rhizomucor racemosus</i>	ATCC 1216B	X17476	<i>tuf</i> (EF-1)
	<i>Rhodotorula mucilaginosa</i>		AF016239	<i>tuf</i> (EF-1)
15	<i>Saccharomyces cerevisiae</i>		K00428	<i>tuf</i> (M)
	<i>Saccharomyces cerevisiae</i>		M59369	<i>tuf</i> (EF-G)
	<i>Saccharomyces cerevisiae</i>		X00779	<i>tuf</i> (EF-1)
	<i>Saccharomyces cerevisiae</i>		X01638	<i>tuf</i> (EF-1)
	<i>Saccharomyces cerevisiae</i>		M10992	<i>tuf</i> (EF-1)
20	<i>Saccharomyces cerevisiae</i>	Alpha S288	X78993	<i>tuf</i> (EF-1)
	<i>Saccharomyces cerevisiae</i>		M15666	<i>tuf</i> (EF-1)
	<i>Saccharomyces cerevisiae</i>		Z35987	<i>tuf</i> (EF-1)
	<i>Saccharomyces cerevisiae</i>	S288C (AB972)	U51033	<i>tuf</i> (EF-1)
	<i>Schizophyllum commune</i>	1-40	X94913	<i>tuf</i> (EF-1)
25	<i>Schizosaccharomyces pombe</i>	972h-	AL021816	<i>tuf</i> (EF-1)
	<i>Schizosaccharomyces pombe</i>	972h-	AL021813	<i>tuf</i> (EF-1)
	<i>Schizosaccharomyces pombe</i>	972h-	D82571	<i>tuf</i> (EF-1)
	<i>Schizosaccharomyces pombe</i>		U42189	<i>tuf</i> (EF-1)
	<i>Schizosaccharomyces pombe</i>	PR745	D89112	<i>tuf</i> (EF-1)
30	<i>Sordaria macrospora</i>	OOO	X96615	<i>tuf</i> (EF-1)
	<i>Trichoderma reesei</i>	QM9414	Z23012	<i>tuf</i> (EF-1)
	<i>Yarrowia lipolytica</i>		AF054510	<i>tuf</i> (EF-1)
35	Parasites			
	<i>Blastocystis hominis</i>	HE87-1	D64080	<i>tuf</i> (EF-1)
	<i>Cryptosporidium parvum</i>		U69697	<i>tuf</i> (EF-1)
	<i>Eimeria tenella</i>	LS18	AI755521	<i>tuf</i> (EF-1)
40	<i>Entamoeba histolytica</i>	HM1:IMSS	X83565	<i>tuf</i> (EF-1)
	<i>Entamoeba histolytica</i>	NIH 200	M92073	<i>tuf</i> (EF-1)
	<i>Giardia lamblia</i>		D14342	<i>tuf</i> (EF-1)
	<i>Kentrophoros</i> sp.		AF056101	<i>tuf</i> (EF-1)
	<i>Leishmania amazonensis</i>	IFLA/BR/67/PH8	M92653	<i>tuf</i> (EF-1)
45	<i>Leishmania braziliensis</i>		U72244	<i>tuf</i> (EF-1)
	<i>Onchocerca volvulus</i>		M64333	<i>tuf</i> (EF-1)
	<i>Porphyra purpurea</i>	Avonport	U08844	<i>tuf</i> (EF-1)
	<i>Plasmodium berghei</i>	ANKA	AJ224150	<i>tuf</i> (EF-1)
	<i>Plasmodium falciparum</i>	K1	X60488	<i>tuf</i> (EF-1)
50	<i>Plasmodium knowlesi</i>	line H	AJ224153	<i>tuf</i> (EF-1)
	<i>Toxoplasma gondii</i>	RH	Y11431	<i>tuf</i> (EF-1)
	<i>Trichomonas tenax</i>	ATCC 30207	D78479	<i>tuf</i> (EF-1)
	<i>Trypanosoma brucei</i>	LVH/75/	U10562	<i>tuf</i> (EF-1)
		USAMRU-K/18		
55	<i>Trypanosoma cruzi</i>	Y	L76077	<i>tuf</i> (EF-1)

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
Human and plants				
	<i>Arabidopsis thaliana</i>	Columbia	X89227	<i>tuf</i> (EF-1)
5	<i>Glycine max</i>	Ceresia	X89058	<i>tuf</i> (EF-1)
	<i>Glycine max</i>	Ceresia	Y15107	<i>tuf</i> (EF-1)
	<i>Glycine max</i>	Ceresia	Y15108	<i>tuf</i> (EF-1)
	<i>Glycine max</i>	Maple Arrow	X66062	<i>tuf</i> (EF-1)
	<i>Homo sapiens</i>		X03558	<i>tuf</i> (EF-1)
10	<i>Pyramimonas disomata</i>		AB008010	<i>tuf</i>
<u>atpD sequences</u>				
15	Bacteria			
	<i>Acetobacterium woodi</i>	DSM 1030	U10505	<i>atpD</i>
	<i>Actinobacillus actinomycetemcomitans</i>	HK1651	Genome project ²	<i>atpD</i>
	<i>Bacillus anthracis</i>	Ames	Genome project ²	<i>atpD</i>
20	<i>Bacillus firmus</i>	OF4	M60117	<i>atpD</i>
	<i>Bacillus megaterium</i>	QM B1551	M20255	<i>atpD</i>
	<i>Bacillus stearothermophilus</i>		D38058	<i>atpD</i>
	<i>Bacillus stearothermophilus</i>	IFO1035	D38060	<i>atpD</i>
	<i>Bacillus subtilis</i>	168	Z28592	<i>atpD</i>
25	<i>Bacteroides fragilis</i>	DSM 2151	M22247	<i>atpD</i>
	<i>Bordetella bronchiseptica</i>	RB50	Genome project ²	<i>atpD</i>
	<i>Bordetella pertussis</i>	Tohama 1	Genome project ²	<i>atpD</i>
	<i>Borrelia burgdorferi</i>	B31	AE001122	<i>atpD</i> (V)
	<i>Burkholderia cepacia</i>	DSM50181	X76877	<i>atpD</i>
30	<i>Burkholderia pseudomallei</i>	K96243	Genome project ²	<i>atpD</i>
	<i>Campylobacter jejuni</i>	NCTC 11168	CJ11168X1	<i>atpD</i>
	<i>Chlamydia pneumoniae</i>		Genome project ²	<i>atpD</i> (V)
	<i>Chlamydia trachomatis</i>	MoPn	Genome project ²	<i>atpD</i> (V)
	<i>Chlorobium vibrioforme</i>	DSM 263	X76873	<i>atpD</i>
35	<i>Citrobacter freundii</i>	JEO503	AF037156	<i>atpD</i>
	<i>Clostridium acetobutylicum</i>	ATCC 824	Genome project ²	<i>atpD</i>
	<i>Clostridium acetobutylicum</i>	DSM 792	AF101055	<i>atpD</i>
	<i>Clostridium difficile</i>	630	Genome project ²	<i>atpD</i>
	<i>Corynebacterium diphtheriae</i>	NCTC13129	Genome project ²	<i>atpD</i>
40	<i>Corynebacterium glutamicum</i>	ASO 19	X76875	<i>atpD</i>
	<i>Corynebacterium glutamicum</i>	MJ-233	E09634	<i>atpD</i>
	<i>Cytophaga lytica</i>	DSM 2039	M22535	<i>atpD</i>
	<i>Enterobacter aerogenes</i>	DSM 30053	- ³	<i>atpD</i>
	<i>Enterococcus faecalis</i>	V583	Genome project ²	<i>atpD</i> (V)
45	<i>Enterococcus hirae</i>		M90060	<i>atpD</i>
	<i>Enterococcus hirae</i>	ATCC 9790	D17462	<i>atpD</i> (V)
	<i>Escherichia coli</i>		J01594	<i>atpD</i>
	<i>Escherichia coli</i>		M25464	<i>atpD</i>
	<i>Escherichia coli</i>		V00267	<i>atpD</i>
50	<i>Escherichia coli</i>		V00311	<i>atpD</i>
	<i>Escherichia coli</i>	K12 MG1655	L10328	<i>atpD</i>
	<i>Flavobacterium ferrugineum</i>	DSM 13524	- ³	<i>atpD</i>
	<i>Haemophilus actinomycetemcomitans</i>		Genome project ²	<i>atpD</i>
	<i>Haemophilus influenzae</i>	Rd	U32730	<i>atpD</i>
55	<i>Helicobacter pylori</i>	NCTC 11638	AF004014	<i>atpD</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Helicobacter pylori</i>	26695	Genome project ²	<i>atpD</i>
	<i>Helicobacter pylori</i>	J99	Genome project ²	<i>atpD</i>
	<i>Klebsiella pneumoniae</i>	M6H 78578	Genome project ²	<i>atpD</i>
	<i>Lactobacillus casei</i>	DSM 20021	X64542	<i>atpD</i>
5	<i>Legionella pneumophila</i>	Philadelphia-1	Genome project ²	<i>atpD</i>
	<i>Moorella thermoacetica</i>	ATCC 39073	U64318	<i>atpD</i>
	<i>Mycobacterium avium</i>	104	Genome project ²	<i>atpD</i>
	<i>Mycobacterium bovis</i>	AF2122/97	Genome project ²	<i>atpD</i>
	<i>Mycobacterium leprae</i>		U15186	<i>atpD</i>
10	<i>Mycobacterium leprae</i>		Genome project ²	<i>atpD</i>
	<i>Mycobacterium tuberculosis</i>	H37Rv	Z73419	<i>atpD</i>
	<i>Mycobacterium tuberculosis</i>	CSU#93	Genome project ²	<i>atpD</i>
	<i>Mycoplasma gallisepticum</i>		X64256	<i>atpD</i>
	<i>Mycoplasma genitalium</i>	G37	U39725	<i>atpD</i>
15	<i>Mycoplasma pneumoniae</i>	M129	U43738	<i>atpD</i>
	<i>Neisseria gonorrhoeae</i>	FA 1090	Genome project ²	<i>atpD</i>
	<i>Neisseria meningitidis</i>	Z2491	Genome project ²	<i>atpD</i>
	<i>Pasteurella multocida</i>	Pm70	Genome project ²	<i>atpD</i>
	<i>Pectinatus frisingensis</i>	DSM 20465	X64543	<i>atpD</i>
20	<i>Peptococcus niger</i>	DSM 20475	X76878	<i>atpD</i>
	<i>Pirellula marina</i>	IFAM 1313	X57204	<i>atpD</i>
	<i>Porphyromonas gingivalis</i>	W83	Genome project ²	<i>atpD</i> (V)
	<i>Propionigenium modestum</i>	DSM 2376	X58461	<i>atpD</i>
	<i>Pseudomonas aeruginosa</i>	PAO1	Genome project ²	<i>atpD</i>
25	<i>Pseudomonas putida</i>		Genome project ²	<i>atpD</i>
	<i>Rhodobacter capsulatus</i>	B100	X99599	<i>atpD</i>
	<i>Rhodospirillum rubrum</i>		X02499	<i>atpD</i>
	<i>Rickettsia prowazekii</i>	F-12	AF036246	<i>atpD</i>
	<i>Rickettsia prowazekii</i>	Madrid	Genome project ²	<i>atpD</i>
30	<i>Ruminococcus albus</i>	7ATCC	AB006151	<i>atpD</i>
	<i>Salmonella bongori</i>	JEO4162	AF037155	<i>atpD</i>
	<i>Salmonella bongori</i>	BR1859	AF037154	<i>atpD</i>
	<i>Salmonella choleraesuis</i>	S83769	AF037146	<i>atpD</i>
	subsp. <i>arizonae</i>			
35	<i>Salmonella choleraesuis</i>	u24	AF037147	<i>atpD</i>
	subsp. <i>arizonae</i>			
	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Dublin	K228	AF037140	<i>atpD</i>
	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Dublin	K771	AF037139	<i>atpD</i>
40	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Dublin			
	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Infantis	Div36-86	AF037142	<i>atpD</i>
	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Tennessee	Div95-86	AF037143	<i>atpD</i>
45	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Typhimurium	LT2	AF037141	<i>atpD</i>
	<i>Salmonella choleraesuis</i>	DS210/89	AF037149	<i>atpD</i>
	subsp. <i>diarizonae</i>			
	<i>Salmonella choleraesuis</i>	JEO307	AF037148	<i>atpD</i>
50	subsp. <i>diarizonae</i>			
	<i>Salmonella choleraesuis</i>	S109671	AF037150	<i>atpD</i>
	subsp. <i>diarizonae</i>			
	<i>Salmonella choleraesuis</i>	S84366	AF037151	<i>atpD</i>
	subsp. <i>houtenae</i>			
55	<i>Salmonella choleraesuis</i>	S84098	AF037152	<i>atpD</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	subsp. <i>houtenae</i>			
	<i>Salmonella choleraesuis</i>	BR2047	AF037153	<i>atpD</i>
	subsp. <i>indica</i>			
	<i>Salmonella choleraesuis</i>	NSC72	AF037144	<i>atpD</i>
5	subsp. <i>salamae</i>			
	<i>Salmonella choleraesuis</i>	S114655	AF037145	<i>atpD</i>
	subsp. <i>salamae</i>			
	<i>Shewanella putrefaciens</i>	MR-1	Genome project ²	<i>atpD</i>
	<i>Staphylococcus aureus</i>	COL	Genome project ²	<i>atpD</i>
10	<i>Stigmatella aurantiaca</i>	Sga1	X76879	<i>atpD</i>
	<i>Streptococcus bovis</i>	JB-1	AB009314	<i>atpD</i>
	<i>Streptococcus mutans</i>	GS-5	U31170	<i>atpD</i>
	<i>Streptococcus mutans</i>	UAB159	Genome project ²	<i>atpD</i>
	<i>Streptococcus pneumoniae</i>	Type 4	Genome project ²	<i>atpD</i> (V)
15	<i>Streptococcus pneumoniae</i>	Type 4	Genome project ²	<i>atpD</i>
	<i>Streptococcus pyogenes</i>	M1-GAS	Genome project ²	<i>atpD</i> (V)
	<i>Streptococcus pyogenes</i>	M1-GAS	Genome project ²	<i>atpD</i>
	<i>Streptococcus sanguinis</i>	10904	AF001955	<i>atpD</i>
	<i>Streptomyces lividans</i>	1326	Z22606	<i>atpD</i>
20	<i>Thermus thermophilus</i>	HB8	D63799	<i>atpD</i> (V)
	<i>Thiobacillus ferrooxidans</i>	ATCC 33020	M81087	<i>atpD</i>
	<i>Treponema pallidum</i>	Nichols	AE001228	<i>atpD</i> (V)
	<i>Vibrio alginolyticus</i>		X16050	<i>atpD</i>
	<i>Vibrio cholerae</i>	N16961	Genome project ²	<i>atpD</i>
25	<i>Wolinella succinogenes</i>	DSM 1470	X76880	<i>atpD</i>
	<i>Yersinia enterocolitica</i>	NCTC 10460	AF037157	<i>atpD</i>
	<i>Yersinia pestis</i>	CO-92	Genome project ²	<i>atpD</i>
30	Archaeobacteria			
	<i>Archaeoglobus fulgidus</i>	DSM 4304	AE001023	<i>atpD</i> (V)
	<i>Halobacterium salinarum</i>		S56356	<i>atpD</i> (V)
	<i>Haloferax volcanii</i>	WR 340	X79516	<i>atpD</i>
35	<i>Methanococcus jannaschii</i>	DSM 2661	U67477	<i>atpD</i> (V)
	<i>Methanosarcina barkeri</i>	DSM 800	J04836	<i>atpD</i> (V)
	Fungi			
40	<i>Candida albicans</i>	SC5314	Genome project ²	<i>atpD</i>
	<i>Candida tropicalis</i>		M64984	<i>atpD</i> (V)
	<i>Kluyveromyces lactis</i>	2359/152	U37764	<i>atpD</i>
	<i>Neurospora crassa</i>		X53720	<i>atpD</i>
45	<i>Saccharomyces cerevisiae</i>		M12082	<i>atpD</i>
	<i>Saccharomyces cerevisiae</i>	X2180-1A	J05409	<i>atpD</i> (V)
	<i>Schizosaccharomyces pombe</i>	972 h-	S47814	<i>atpD</i> (V)
	<i>Schizosaccharomyces pombe</i>	972 h-	M57956	<i>atpD</i>
50	Parasites			
	<i>Giardia lamblia</i>	WB	U18938	<i>atpD</i>
	<i>Plasmodium falciparum</i>	3D7	L08200	<i>atpD</i> (V)
55	<i>Trypanosoma congolense</i>	IL3000	Z25814	<i>atpD</i> (V)

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
Human and plants				
5	<i>Homo sapiens</i> <i>Homo sapiens</i>		L09234 M27132	<i>atpD</i> (V) <i>atpD</i>
	<u>recA sequences</u>			
10	Bacteria			
	<i>Acetobacter aceti</i>	no. 1023	S60630	<i>recA</i>
	<i>Acetobacter altoacetigenes</i>	MH-24	E05290	<i>recA</i>
15	<i>Acetobacter polyoxogenes</i>	NBI 1028	D13183	<i>recA</i>
	<i>Acholeplasma laidlawii</i>	8195	M81465	<i>recA</i>
	<i>Acidiphilium facilis</i>	ATCC 35904	D16538	<i>recA</i>
	<i>Acidothermus cellulolyticus</i>	ATCC 43068	AJ006705	<i>recA</i>
	<i>Acinetobacter calcoaceticus</i>	BD413/ADP1	L26100	<i>recA</i>
20	<i>Actinobacillus actinomycetemcomitans</i>	HK1651	Genome project ²	<i>recA</i>
	<i>Aeromonas salmonicida</i>	A449	U83688	<i>recA</i>
	<i>Agrobacterium tumefaciens</i>	C58	L07902	<i>recA</i>
	<i>Allochromatium vinosum</i>		AJ000677	<i>recA</i>
	<i>Aquifex aeolicus</i>	VF5	AE000775	<i>recA</i>
25	<i>Aquifex pyrophilus</i>	Kol5a	L23135	<i>recA</i>
	<i>Azotobacter vinelandii</i>		S96898	<i>recA</i>
	<i>Bacillus stearothermophilus</i>	10	Genome project ²	<i>recA</i>
	<i>Bacillus subtilis</i>	PB1831	U87792	<i>recA</i>
	<i>Bacillus subtilis</i>	168	Z99112	<i>recA</i>
30	<i>Bacteroides fragilis</i>		M63029	<i>recA</i>
	<i>Bifidobacterium breve</i>	NCFB 2258	AF094756	<i>recA</i>
	<i>Blastochloris viridis</i>	DSM 133	AF022175	<i>recA</i>
	<i>Bordetella pertussis</i>	165	X53457	<i>recA</i>
	<i>Bordetella pertussis</i>	Tohama I	Genome project ²	<i>recA</i>
35	<i>Borrelia burgdorferi</i>	Sh-2-82	U23457	<i>recA</i>
	<i>Borrelia burgdorferi</i>	B31	AE001124	<i>recA</i>
	<i>Brevibacterium flavum</i>	MJ-233	E10390	<i>recA</i>
	<i>Brucella abortus</i>	2308	L00679	<i>recA</i>
	<i>Burkholderia cepacia</i>	ATCC 17616	U70431	<i>recA</i>
40	<i>Burkholderia cepacia</i>		D90120	<i>recA</i>
	<i>Burkholderia pseudomallei</i>	K96243	Genome project ²	<i>recA</i>
	<i>Campylobacter fetus</i> subsp. <i>fetus</i>	23D	AF020677	<i>recA</i>
	<i>Campylobacter jejuni</i>	81-176	U03121	<i>recA</i>
	<i>Campylobacter jejuni</i>	NCTC 11168	AL139079	<i>recA</i>
45	<i>Chlamydia trachomatis</i>	L2	U16739	<i>recA</i>
	<i>Chlamydia trachomatis</i>	D/UW-3/CX	AE001335	<i>recA</i>
	<i>Chlamydophila pneumoniae</i>	CWL029	AE001658	<i>recA</i>
	<i>Chloroflexus aurantiacus</i>	J-10-fl	AF037259	<i>recA</i>
	<i>Clostridium acetobutylicum</i>		M94057	<i>recA</i>
50	<i>Clostridium perfringens</i>	13	U61497	<i>recA</i>
	<i>Corynebacterium diphtheriae</i>	NCTC13129	Genome project ²	<i>recA</i>
	<i>Corynebacterium glutamicum</i>	AS019	U14965	<i>recA</i>
	<i>Corynebacterium pseudotuberculosis</i>	C231	U30387	<i>recA</i>
	<i>Deinococcus radiodurans</i>	KD8301	AB005471	<i>recA</i>
55	<i>Deinococcus radiodurans</i>	R1	U01876	<i>recA</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Enterobacter agglomerans</i>	339	L03291	<i>recA</i>
	<i>Enterococcus faecalis</i>	OGIX	M81466	<i>recA</i>
	<i>Erwinia carotovora</i>		X55554	<i>recA</i>
	<i>Escherichia coli</i>		J01672	<i>recA</i>
5	<i>Escherichia coli</i>		X55552	<i>recA</i>
	<i>Escherichia coli</i>	K-12	AE000354	<i>recA</i>
	<i>Frankia alni</i>	Arl3	AJ006707	<i>recA</i>
	<i>Gluconobacter oxydans</i>		U21001	<i>recA</i>
	<i>Haemophilus influenzae</i>	Rd	U32687	<i>recA</i>
10	<i>Haemophilus influenzae</i>	Rd	U32741	<i>recA</i>
	<i>Haemophilus influenzae</i>	Rd	L07529	<i>recA</i>
	<i>Helicobacter pylori</i>	69A	Z35478	<i>recA</i>
	<i>Helicobacter pylori</i>	26695	AE000536	<i>recA</i>
	<i>Helicobacter pylori</i>	J99	AE001453	<i>recA</i>
15	<i>Klebsiella pneumoniae</i>	M6H 78578	Genome project ²	<i>recA</i>
	<i>Lactococcus lactis</i>	ML3	M88106	<i>recA</i>
	<i>Legionella pneumophila</i>		X55453	<i>recA</i>
	<i>Leptospira biflexa</i>	serovar patoc	U32625	<i>recA</i>
	<i>Leptospira interrogans</i>	serovar pomona	U29169	<i>recA</i>
20	<i>Magnetospirillum magnetotacticum</i>	MS-1	X17371	<i>recA</i>
	<i>Methylobacillus flagellatus</i>	MFK1	M35325	<i>recA</i>
	<i>Methylomonas clara</i>	ATCC 31226	X59514	<i>recA</i>
	<i>Mycobacterium avium</i>	104	Genome project ²	<i>recA</i>
	<i>Mycobacterium bovis</i>	AF122/97	Genome project ²	<i>recA</i>
25	<i>Mycobacterium leprae</i>		X73822	<i>recA</i>
	<i>Mycobacterium tuberculosis</i>	H37Rv	X58485	<i>recA</i>
	<i>Mycobacterium tuberculosis</i>	CSU#93	Genome project ²	<i>recA</i>
	<i>Mycoplasma genitalium</i>	G37	U39717	<i>recA</i>
	<i>Mycoplasma mycoides</i>	GM9	L22073	<i>recA</i>
30	<i>Mycoplasma pneumoniae</i>	ATCC 29342	MPAE000033	<i>recA</i>
	<i>Mycoplasma pulmonis</i>	KD735	L22074	<i>recA</i>
	<i>Myxococcus xanthus</i>		L40368	<i>recA</i>
	<i>Myxococcus xanthus</i>		L40367	<i>recA</i>
	<i>Neisseria animalis</i>	NCTC 10212	U57910	<i>recA</i>
35	<i>Neisseria cinerea</i>	LCDC 81-176	AJ223869	<i>recA</i>
	<i>Neisseria cinerea</i>	LNP 1646	U57906	<i>recA</i>
	<i>Neisseria cinerea</i>	NCTC 10294	AJ223871	<i>recA</i>
	<i>Neisseria cinerea</i>	Vedros M601	AJ223870	<i>recA</i>
	<i>Neisseria elongata</i>	CCUG 2131	AJ223882	<i>recA</i>
40	<i>Neisseria elongata</i>	CCUG 4165A	AJ223880	<i>recA</i>
	<i>Neisseria elongata</i>	NCTC 10660	AJ223881	<i>recA</i>
	<i>Neisseria elongata</i>	NCTC 11050	AJ223878	<i>recA</i>
	<i>Neisseria elongata</i>	NHITCC 2376	AJ223877	<i>recA</i>
	<i>Neisseria elongata</i>	CCUG 4557	AJ223879	<i>recA</i>
45	subsp. <i>intermedia</i>			
	<i>Neisseria flava</i>	Bangor 9	AJ223873	<i>recA</i>
	<i>Neisseria flavescens</i>	LNP 444	U57907	<i>recA</i>
	<i>Neisseria gonorrhoeae</i>	CH95	U57902	<i>recA</i>
	<i>Neisseria gonorrhoeae</i>	FA19	X64842	<i>recA</i>
50	<i>Neisseria gonorrhoeae</i>	MS11	X17374	<i>recA</i>
	<i>Neisseria gonorrhoeae</i>		Genome project ²	<i>recA</i>
	<i>Neisseria lactamica</i>	CCUC 7757	AJ223866	<i>recA</i>
	<i>Neisseria lactamica</i>	CCUG 7852	Y11819	<i>recA</i>
	<i>Neisseria lactamica</i>	LCDC 77-143	Y11818	<i>recA</i>
55	<i>Neisseria lactamica</i>	LCDC 80-111	AJ223864	<i>recA</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Neisseria lactamica</i>	LCDC 845	AJ223865	<i>recA</i>
	<i>Neisseria lactamica</i>	NCTC 10617	U57905	<i>recA</i>
	<i>Neisseria lactamica</i>	NCTC 10618	AJ223863	<i>recA</i>
	<i>Neisseria meningitidis</i>	44/46	X64849	<i>recA</i>
5	<i>Neisseria meningitidis</i>	Bangor 13	AJ223868	<i>recA</i>
	<i>Neisseria meningitidis</i>	HF116	X64848	<i>recA</i>
	<i>Neisseria meningitidis</i>	HF130	X64844	<i>recA</i>
	<i>Neisseria meningitidis</i>	HF46	X64847	<i>recA</i>
	<i>Neisseria meningitidis</i>	M470	X64850	<i>recA</i>
10	<i>Neisseria meningitidis</i>	N94II	X64846	<i>recA</i>
	<i>Neisseria meningitidis</i>	NCTC 8249	AJ223867	<i>recA</i>
	<i>Neisseria meningitidis</i>	P63	X64845	<i>recA</i>
	<i>Neisseria meningitidis</i>	S3446	U57903	<i>recA</i>
	<i>Neisseria meningitidis</i>	FAM18	Genome project ²	<i>recA</i>
15	<i>Neisseria mucosa</i>	LNP 405	U57908	<i>recA</i>
	<i>Neisseria mucosa</i>	Vedros M1801	AJ223875	<i>recA</i>
	<i>Neisseria perflava</i>	CCUG 17915	AJ223876	<i>recA</i>
	<i>Neisseria perflava</i>	LCDC 85402	AJ223862	<i>recA</i>
	<i>Neisseria pharyngis</i> var. <i>flava</i>	NCTC 4590	U57909	<i>recA</i>
20	<i>Neisseria polysaccharea</i>	CCUG 18031	Y11815	<i>recA</i>
	<i>Neisseria polysaccharea</i>	CCUG 24845	Y11816	<i>recA</i>
	<i>Neisseria polysaccharea</i>	CCUG 24846	Y11814	<i>recA</i>
	<i>Neisseria polysaccharea</i>	INS MA 3008	Y11817	<i>recA</i>
	<i>Neisseria polysaccharea</i>	NCTC 11858	U57904	<i>recA</i>
25	<i>Neisseria sicca</i>	NRL 30016	AJ223872	<i>recA</i>
	<i>Neisseria subflava</i>	NRL 30017	AJ223874	<i>recA</i>
	<i>Paracoccus denitrificans</i>	DSM 413	U59631	<i>recA</i>
	<i>Pasteurella multocida</i>		X99324	<i>recA</i>
	<i>Porphyromonas gingivalis</i>	W83	U70054	<i>recA</i>
30	<i>Prevotella ruminicola</i>	JCM 8958	U61227	<i>recA</i>
	<i>Proteus mirabilis</i>	pG1300	X14870	<i>recA</i>
	<i>Proteus vulgaris</i>		X55555	<i>recA</i>
	<i>Pseudomonas aeruginosa</i>		X05691	<i>recA</i>
	<i>Pseudomonas aeruginosa</i>	PAM 7	X52261	<i>recA</i>
35	<i>Pseudomonas aeruginosa</i>	PAO12	D13090	<i>recA</i>
	<i>Pseudomonas fluorescens</i>	OE 28.3	M96558	<i>recA</i>
	<i>Pseudomonas putida</i>		L12684	<i>recA</i>
	<i>Pseudomonas putida</i>	PpS145	U70864	<i>recA</i>
	<i>Rhizobium leguminosarum</i>	VF39	X59956	<i>recA</i>
40	biovar <i>viciae</i>			
	<i>Rhizobium phaseoli</i>	CNPAF512	X62479	<i>recA</i>
	<i>Rhodobacter capsulatus</i>	J50	X82183	<i>recA</i>
	<i>Rhodobacter sphaeroides</i>	2.4.1	X72705	<i>recA</i>
	<i>Rhodopseudomonas palustris</i>	N 7	D84467	<i>recA</i>
45	<i>Rickettsia prowazekii</i>	Madrid E	AJ235273	<i>recA</i>
	<i>Rickettsia prowazekii</i>	Madrid E	U01959	<i>recA</i>
	<i>Serratia marcescens</i>		M22935	<i>recA</i>
	<i>Shigella flexneri</i>		X55553	<i>recA</i>
	<i>Shigella sonnei</i>	KNIH104S	AF101227	<i>recA</i>
50	<i>Sinorhizobium meliloti</i>	2011	X59957	<i>recA</i>
	<i>Staphylococcus aureus</i>		L25893	<i>recA</i>
	<i>Streptococcus gordonii</i>	Challis V288	L20574	<i>recA</i>
	<i>Streptococcus mutans</i>	UA96	M81468	<i>recA</i>
	<i>Streptococcus mutans</i>	GS-5	M61897	<i>recA</i>
55	<i>Streptococcus pneumoniae</i>		Z17307	<i>recA</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Streptococcus pneumoniae</i>	R800	Z34303	<i>recA</i>
	<i>Streptococcus pyogenes</i>	NZ131	U21934	<i>recA</i>
	<i>Streptococcus pyogenes</i>	D471	M81469	<i>recA</i>
	<i>Streptococcus salivarius</i>		M94062	<i>recA</i>
5	subsp. <i>thermophilus</i>			
	<i>Streptomyces ambofaciens</i>	DSM 40697	Z30324	<i>recA</i>
	<i>Streptomyces coelicolor</i>	A3(2)	AL020958	<i>recA</i>
	<i>Streptomyces lividans</i>	TK24	X76076	<i>recA</i>
	<i>Streptomyces rimosus</i>	R6	X94233	<i>recA</i>
10	<i>Streptomyces venezuelae</i>	ATCC10712	U04837	<i>recA</i>
	<i>Synechococcus</i> sp.	PR6	M29495	<i>recA</i>
	<i>Synechocystis</i> sp.	PCC6803	D90917	<i>recA</i>
	<i>Thermotoga maritima</i>		L23425	<i>recA</i>
	<i>Thermotoga maritima</i>		AE001823	<i>recA</i>
15	<i>Thermus aquaticus</i>		L20095	<i>recA</i>
	<i>Thermus thermophilus</i>	HB8	D17392	<i>recA</i>
	<i>Thiobacillus ferrooxidans</i>		M26933	<i>recA</i>
	<i>Treponema denticola</i>		Genome project ²	<i>recA</i>
	<i>Treponema pallidum</i>	Nichols	AE001243	<i>recA</i>
20	<i>Vibrio anguillarum</i>		M80525	<i>recA</i>
	<i>Vibrio cholerae</i>	017	X71969	<i>recA</i>
	<i>Vibrio cholerae</i>	2740-80	U10162	<i>recA</i>
	<i>Vibrio cholerae</i>	569B	L42384	<i>recA</i>
	<i>Vibrio cholerae</i>	M549	AF117881	<i>recA</i>
25	<i>Vibrio cholerae</i>	M553	AF117882	<i>recA</i>
	<i>Vibrio cholerae</i>	M645	AF117883	<i>recA</i>
	<i>Vibrio cholerae</i>	M793	AF117878	<i>recA</i>
	<i>Vibrio cholerae</i>	M794	AF117880	<i>recA</i>
	<i>Vibrio cholerae</i>	M967	AF117879	<i>recA</i>
30	<i>Xanthomonas citri</i>	XW47	AF006590	<i>recA</i>
	<i>Xanthomonas oryzae</i>		AF013600	<i>recA</i>
	<i>Xenorhabdus bovienii</i>	T228/1	U87924	<i>recA</i>
	<i>Xenorhabdus nematophilus</i>	AN6	AF127333	<i>recA</i>
	<i>Yersinia pestis</i>	231	X75336	<i>recA</i>
35	<i>Yersinia pestis</i>	CO-92	Genome project ²	<i>recA</i>
Fungi, parasites, human and plants				
40	<i>Anabaena variabilis</i>	ATCC 29413	M29680	<i>recA</i>
	<i>Arabidopsis thaliana</i>		U43652	<i>recA</i> (Rad51)
	<i>Candida albicans</i>		U39808	<i>recA</i> (Dmc1)
	<i>Coprinus cinereus</i>	Okayama-7	U21905	<i>recA</i> (Rad51)
	<i>Emmericella nidulans</i>		Z80341	<i>recA</i> (Rad51)
45	<i>Gallus gallus</i>		L09655	<i>recA</i> (Rad51)
	<i>Homo sapiens</i>		D13804	<i>recA</i> (Rad51)
	<i>Homo sapiens</i>		D63882	<i>recA</i> (Dmc1)
	<i>Leishmania major</i>	Friedlin	AF062379	<i>recA</i> (Rad51)
	<i>Leishmania major</i>	Friedlin	AF062380	<i>recA</i> (Dmc1)
50	<i>Mus musculus</i>		D58419	<i>recA</i> (Dmc1)
	<i>Neurospora crassa</i>	74-OR23-1A	D29638	<i>recA</i> (Rad51)
	<i>Saccharomyces cerevisiae</i>		D10023	<i>recA</i> (Rad51)
	<i>Schizosaccharomyces pombe</i>		Z22691	<i>recA</i> (Rad51)
	<i>Schizosaccharomyces pombe</i>	972h-	AL021817	<i>recA</i> (Dmc1)
55	<i>Tetrahymena thermophila</i>	PB9R	AF064516	<i>recA</i> (Rad51)

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

Species	Strain	Accession number	Coding gene*
<i>Trypanosoma brucei</i>	stock 427	Y13144	<i>recA</i> (Rad51)
<i>Ustilago maydis</i>		U62484	<i>recA</i> (Rad51)
<i>Xenopus laevis</i>		D38488	<i>recA</i> (Rad51)
5 <i>Xenopus laevis</i>		D38489	<i>recA</i> (Rad51)

* *tuf* indicates *tuf* sequences, including *tuf* genes, *fusA* genes and *fusA-tuf* intergenic spacers.

tuf (C) indicates *tuf* sequences divergent from main (usually A and B) copies of the elongation factor-Tu

10 *tuf* (EF-1) indicates *tuf* sequences of the eukaryotic type (elongation factor 1 α)

tuf (M) indicates *tuf* sequences from organellar (mostly mitochondrial) origin

atpD indicates *atpD* sequences of the F-type

atpD (V) indicates *atpD* sequences of the V-Type

recA indicates *recA* sequences

15 *recA* (Rad51) indicates *rad51* sequences or homologs

recA (Dmc1) indicates *dmc1* sequences or homologs

¹ Nucleotide sequences published in Arch. Microbiol. 1990 153:241-247

² These sequences are from the TIGR database (<http://www.tigr.org/tdb/tdb.html>)

³ Nucleotide sequences published in FEMS Microbiology Letters 1988 50:101-106

Table 12. Bacterial species used to test the specificity of the *Staphylococcus*-specific amplification primers derived from *tuf* sequences.

	Strain	Reference number	Strain	Reference number
5	Staphylococcal species (n=27)		Other Gram-positive bacteria (n=20)	
	<i>Staphylococcus arlettae</i>	ATCC 43957	<i>Bacillus subtilis</i>	ATCC 27370
	<i>Staphylococcus aureus</i>	ATCC 35844	<i>Enterococcus avium</i>	ATCC 14025
	subsp. <i>anaerobius</i>			
10	<i>Staphylococcus aureus</i>	ATCC 43300	<i>Enterococcus durans</i>	ATCC 19432
	subsp. <i>aureus</i>			
	<i>Staphylococcus auricularis</i>	ATCC 33753	<i>Enterococcus faecalis</i>	ATCC 19433
	<i>Staphylococcus capitis</i>	ATCC 27840	<i>Enterococcus faecium</i>	ATCC 19434
	subsp. <i>capitis</i>			
15	<i>Staphylococcus caprae</i>	ATCC 35538	<i>Enterococcus flavescens</i>	ATCC 49996
	<i>Staphylococcus carnosus</i>	ATCC 51365	<i>Enterococcus gallinarum</i>	ATCC 49573
	<i>Staphylococcus chromogenes</i>	ATCC 43764	<i>Lactobacillus acidophilus</i>	ATCC 4356
	<i>Staphylococcus cohnii</i>	DSM 20260	<i>Lactococcus lactis</i>	ATCC 11454
	subsp. <i>urealyticum</i>			
20	<i>Staphylococcus delphini</i>	ATCC 49171	<i>Listeria innocua</i>	ATCC 33090
	<i>Staphylococcus epidermidis</i>	ATCC 14990	<i>Listeria ivanovii</i>	ATCC 19119
	<i>Staphylococcus equorum</i>	ATCC 43958	<i>Listeria monocytogenes</i>	ATCC 15313
	<i>Staphylococcus felis</i>	ATCC 49168	<i>Macrococcus caseolyticus</i>	ATCC 13548
	<i>Staphylococcus gallinarum</i>	ATCC 35539	<i>Streptococcus agalactiae</i>	ATCC 13813
25	<i>Staphylococcus haemolyticus</i>	ATCC 29970	<i>Streptococcus anginosus</i>	ATCC 33397
	<i>Staphylococcus hominis</i>	ATCC 27844	<i>Streptococcus bovis</i>	ATCC 33317
	<i>Staphylococcus hyicus</i>	ATCC 11249	<i>Streptococcus mutans</i>	ATCC 25175
	<i>Staphylococcus intermedius</i>	ATCC 29663	<i>Streptococcus pneumoniae</i>	ATCC 6303
	<i>Staphylococcus kloosis</i>	ATCC 43959	<i>Streptococcus pyogenes</i>	ATCC 19615
30	<i>Staphylococcus lentus</i>	ATCC 29070	<i>Streptococcus salivarius</i>	ATCC 7073
	<i>Staphylococcus lugdunensis</i>	ATCC 43809		
	<i>Staphylococcus saprophyticus</i>	ATCC 15305		
	<i>Staphylococcus schleiferi</i>	ATCC 49545		
	subsp. <i>coagulans</i>			
35	<i>Staphylococcus sciuri</i>	ATCC 29060		
	subsp. <i>sciuri</i>			
	<i>Staphylococcus simulans</i>	ATCC 27848		
	<i>Staphylococcus warneri</i>	ATCC 27836		
	<i>Staphylococcus xylosus</i>	ATCC 29971		
40	Gram-negative bacteria (n=33)			
	<i>Acinetobacter baumannii</i>	ATCC 19606	<i>Morganella morganii</i>	ATCC 25830
	<i>Bacteroides distasonis</i>	ATCC 8503	<i>Neisseria gonorrhoeae</i>	ATCC 35201
	<i>Bacteroides fragilis</i>	ATCC 25285	<i>Neisseria meningitidis</i>	ATCC 13077
	<i>Bulkholderia cepacia</i>	ATCC 25416	<i>Proteus mirabilis</i>	ATCC 25933
45	<i>Bordetella pertussis</i>	ATCC 9797	<i>Proteus vulgaris</i>	ATCC 13315
	<i>Citrobacter freundii</i>	ATCC 8090	<i>Providencia rettgeri</i>	ATCC 9250
	<i>Enterobacter aerogenes</i>	ATCC 13048	<i>Providencia stuartii</i>	ATCC 29914
	<i>Enterobacter cloacae</i>	ATCC 13047	<i>Pseudomonas aeruginosa</i>	ATCC 27853
	<i>Escherichia coli</i>	ATCC 25922	<i>Pseudomonas fluorescens</i>	ATCC 13525
50	<i>Haemophilus influenzae</i>	ATCC 8907	<i>Salmonella choleraesuis</i>	ATCC 7001
	<i>Haemophilus parahaemolyticus</i>	ATCC 10014	<i>Salmonella typhimurium</i>	ATCC 14028
	<i>Haemophilus parainfluenzae</i>	ATCC 7901	<i>Serratia marcescens</i>	ATCC 8100
	<i>Hafnia alvei</i>	ATCC 13337	<i>Shigella flexneri</i>	ATCC 12022
	<i>Kingella indologenes</i>	ATCC 25869	<i>Shigella sonnei</i>	ATCC 29930
55	<i>Klebsiella oxytoca</i>	ATCC 13182	<i>Stenotrophomonas maltophilia</i>	ATCC 13843
	<i>Klebsiella pneumoniae</i>	ATCC 13883	<i>Yersinia enterocolitica</i>	ATCC 9610
	<i>Moraxella catarrhalis</i>	ATCC 25240		

Table 13. Bacterial species used to test the specificity of the penicillin-resistant *Streptococcus pneumoniae* assay.

	Strain	Reference number	Strain	Reference number
5	Gram-positive species (n=67)			
	<i>Abiotrophia adiacens</i>	ATCC 49175	<i>Staphylococcus hominis</i>	ATCC 27844
	<i>Abiotrophia defectiva</i>	ATCC 49176	<i>Staphylococcus lugdunensis</i>	ATCC 43809
	<i>Actinomyces pyogenes</i>	ATCC 19411	<i>Staphylococcus saprophyticus</i>	ATCC 15305
10	<i>Bacillus anthracis</i>	ATCC 4229	<i>Staphylococcus simulans</i>	ATCC 27848
	<i>Bacillus cereus</i>	ATCC 14579	<i>Staphylococcus. warneri</i>	ATCC 27836
	<i>Bifidobacterium breve</i>	ATCC 15700	<i>Streptococcus acidominimus</i>	ATCC 51726
	<i>Clostridium difficile</i>	ATCC 9689	<i>Streptococcus agalactiae</i>	ATCC 12403
	<i>Enterococcus avium</i>	ATCC 14025	<i>Streptococcus anginosus</i>	ATCC 33397
15	<i>Enterococcus casseliflavus</i>	ATCC 25788	<i>Streptococcus bovis</i>	ATCC 33317
	<i>Enterococcus dispar</i>	ATCC 51266	<i>Streptococcus constellatus</i>	ATCC 27823
	<i>Enterococcus durans</i>	ATCC 19432	<i>Streptococcus cricetus</i>	ATCC 19624
	<i>Enterococcus faecalis</i>	ATCC 29212	<i>Streptococcus cristatus</i>	ATCC 51100
	<i>Enterococcus faecium</i>	ATCC 19434	<i>Streptococcus downei</i>	ATCC 33748
20	<i>Enterococcus flavescens</i>	ATCC 49996	<i>Streptococcus dysgalactiae</i>	ATCC 43078
	<i>Enterococcus gallinarum</i>	ATCC 49573	<i>Streptococcus equi</i>	ATCC 9528
	<i>Enterococcus hirae</i>	ATCC 8043	<i>Streptococcus ferus</i>	ATCC 33477
	<i>Enterococcus mundtii</i>	ATCC 43186	<i>Streptococcus gordonii</i>	ATCC 10558
	<i>Enterococcus raffinosus</i>	ATCC 49427	<i>Streptococcus intermedius</i>	ATCC 27335
25	<i>Lactobacillus lactis</i>	ATCC 19435	<i>Streptococcus mitis</i>	ATCC 903
	<i>Lactobacillus monocytogenes</i>	ATCC 15313	<i>Streptococcus mitis</i>	LSPQ 2583
	<i>Mobiluncus curtisii</i>	ATCC 35242	<i>Streptococcus mitis</i>	ATCC 49456
	<i>Peptococcus niger</i>	ATCC 27731	<i>Streptococcus mutans</i>	ATCC 27175
	<i>Peptostreptococcus acones</i>	ATCC 6919	<i>Streptococcus oralis</i>	ATCC 10557
30	<i>Peptostreptococcus anaerobius</i>	ATCC 27337	<i>Streptococcus oralis</i>	ATCC 9811
	<i>Peptostreptococcus</i>	ATCC 2639	<i>Streptococcus oralis</i>	ATCC 35037
	<i>asaccharolyticus</i>		<i>Streptococcus parasanguinis</i>	ATCC 15912
	<i>Peptostreptococcus lactolyticus</i>	ATCC 51172	<i>Streptococcus parauberis</i>	ATCC 6631
	<i>Peptostreptococcus magnus</i>	ATCC 15794	<i>Streptococcus rattus</i>	ATCC 15912
35	<i>Peptostreptococcus prevotii</i>	ATCC 9321	<i>Streptococcus salivarius</i>	ATCC 7073
	<i>Peptostreptococcus tetradius</i>	ATCC 35098	<i>Streptococcus sanguinis</i>	ATCC10556
	<i>Staphylococcus aureus</i>	ATCC 25923	<i>Streptococcus suis</i>	ATCC 43765
	<i>Staphylococcus capitis</i>	ATCC 27840	<i>Streptococcus uberis</i>	ATCC 19436
	<i>Staphylococcus epidermidis</i>	ATCC 14990	<i>Streptococcus vestibularis</i>	ATCC 49124
40	<i>Staphylococcus haemolyticus</i>	ATCC 29970		
	Gram-negative species (n=33)			
	<i>Actinetobacter baumannii</i>	ATCC 19606	<i>Moraxella morganii</i>	ATCC 13077
	<i>Bordetella pertussis</i>	ATCC 9797	<i>Neisseria gonorrhoeae</i>	ATCC 35201
	<i>Citrobacter diversus</i>	ATCC 27028	<i>Neisseria meningitidis</i>	ATCC 13077
45	<i>Citrobacter freundii</i>	ATCC 8090	<i>Proteus mirabilis</i>	ATCC 25933
	<i>Enterobacter aerogenes</i>	ATCC 13048	<i>Proteus vulgaris</i>	ATCC 13315
	<i>Enterobacter agglomerans</i>	ATCC 27155	<i>Providencia alcalifaciens</i>	ATCC 9886
	<i>Enterobacter cloacae</i>	ATCC 13047	<i>Providencia rettgeri</i>	ATCC 9250
	<i>Escherichia coli</i>	ATCC 25922	<i>Providencia rustigianii</i>	ATCC 33673
50	<i>Haemophilus ducreyi</i>	ATCC 33940	<i>Providencia stuartii</i>	ATCC 33672
	<i>Haemophilus haemolyticus</i>	ATCC 33390	<i>Pseudomonas aeruginosa</i>	ATCC 35554
	<i>Haemophilus influenzae</i>	ATCC 9007	<i>Pseudomonas fluorescens</i>	ATCC 13525
	<i>Haemophilus parainfluenzae</i>	ATCC 7901	<i>Pseudomonas stutzeri</i>	ATCC 17588
	<i>Hafnia alvei</i>	ATCC 13337	<i>Salmonella typhimurium</i>	ATCC 14028
55	<i>Klebsiella oxytoca</i>	ATCC 13182	<i>Serratia marcescens</i>	ATCC 13880
	<i>Klebsiella pneumoniae</i>	ATCC 13883	<i>Shigella flexneri</i>	ATCC 12022
	<i>Moraxella atlantae</i>	ATCC 29525	<i>Yersinia enterocolitica</i>	ATCC 9610
	<i>Moraxella catarrhalis</i>	ATCC 43628		

Table 14. Bacterial species (n=104) detected by the platelet contaminants assay. Bold characters indicate the major bacterial contaminants found in platelet concentrates.

5	<i>Abiotrophia adiacens</i>	<i>Klebsiella oxytoca</i>	<i>Staphylococcus simulans</i>
	<i>Abiotrophia defectiva</i>	<i>Klebsiella pneumoniae</i>	<i>Staphylococcus warneri</i>
	<i>Acinetobacter baumannii</i>	<i>Legionella pneumophila</i>	<i>Stenotrophomonas maltophilia</i>
	<i>Acinetobacter lwoffii</i>	<i>Megamonas hypermegale</i>	80 <i>Streptococcus acidominimus</i>
	<i>Aerococcus viridans</i>	45 <i>Moraxella atlantae</i>	<i>Streptococcus agalactiae</i>
10	<i>Bacillus anthracis</i>	<i>Moraxella catarrhalis</i>	<i>Streptococcus anginosus</i>
	<i>Bacillus cereus</i>	<i>Morganella morganii</i>	<i>Streptococcus bovis</i>
	<i>Bacillus subtilis</i>	<i>Neisseria gonorrhoeae</i>	<i>Streptococcus constellatus</i>
	<i>Brucella abortus</i>	<i>Neisseria meningitidis</i>	85 <i>Streptococcus cricetus</i>
	<i>Burkholderia cepacia</i>	50 <i>Pasteurella aerogenes</i>	<i>Streptococcus cristatus</i>
15	<i>Citrobacter diversus</i>	<i>Pasteurella multocida</i>	<i>Streptococcus dysgalactiae</i>
	<i>Citrobacter freundii</i>	<i>Peptostreptococcus magnus</i>	<i>Streptococcus equi</i>
	<i>Enterobacter aerogenes</i>	<i>Proteus mirabilis</i>	<i>Streptococcus ferus</i>
	<i>Enterobacter agglomerans</i>	<i>Providencia alcalifaciens</i>	90 <i>Streptococcus gordonii</i>
	<i>Enterobacter cloacae</i>	55 <i>Providencia rettgeri</i>	<i>Streptococcus intermedius</i>
20	<i>Enterococcus avium</i>	<i>Providencia rustigianii</i>	<i>Streptococcus macacae</i>
	<i>Enterococcus casseliflavus</i>	<i>Providencia stuartii</i>	<i>Streptococcus mitis</i>
	<i>Enterococcus dispar</i>	<i>Pseudomonas aeruginosa</i>	<i>Streptococcus mutans</i>
	<i>Enterococcus durans</i>	<i>Pseudomonas fluorescens</i>	95 <i>Streptococcus oralis</i>
	<i>Enterococcus faecalis</i>	60 <i>Pseudomonas stutzeri</i>	<i>Streptococcus parasanguinis</i>
25	<i>Enterococcus faecium</i>	<i>Salmonella bongori</i>	<i>Streptococcus parauberis</i>
	<i>Enterococcus flavescens</i>	<i>Salmonella choleraesuis</i>	<i>Streptococcus pneumoniae</i>
	<i>Enterococcus gallinarum</i>	<i>Salmonella enteritidis</i>	<i>Streptococcus pyogenes</i>
	<i>Enterococcus mundtii</i>	<i>Salmonella gallinarum</i>	100 <i>Streptococcus rattus</i>
	<i>Enterococcus raffinosus</i>	65 <i>Salmonella typhimurium</i>	<i>Streptococcus salivarius</i>
30	<i>Enterococcus solitarius</i>	<i>Serratia liquefaciens</i>	<i>Streptococcus sanguinis</i>
	<i>Escherichia coli</i>	<i>Serratia marcescens</i>	<i>Streptococcus sobrinus</i>
	<i>Gemella morbillorum</i>	<i>Shigella flexneri</i>	<i>Streptococcus uberis</i>
	<i>Haemophilus ducreyi</i>	<i>Shigella sonnei</i>	105 <i>Streptococcus vestibularis</i>
	<i>Haemophilus haemolyticus</i>	70 <i>Staphylococcus aureus</i>	<i>Vibrio cholerae</i>
35	<i>Haemophilus influenzae</i>	<i>Staphylococcus capitis</i>	<i>Yersinia enterocolitica</i>
	<i>Haemophilus</i>	<i>Staphylococcus epidermidis</i>	<i>Yersinia pestis</i>
	<i>parahaemolyticus</i>	<i>Staphylococcus haemolyticus</i>	<i>Yersinia pseudotuberculosis</i>
	<i>Haemophilus parainfluenzae</i>	<i>Staphylococcus hominis</i>	
	<i>Hafnia alvei</i>	75 <i>Staphylococcus lugdunensis</i>	
40	<i>Kingella kingae</i>	<i>Staphylococcus saprophyticus</i>	

Table 15. Microorganism identified by commercial systems¹.

	<i>Abiotrophia adiacens</i> (<i>Streptococcus adjacens</i>)	75	<i>Alcaligenes xylosoxidans</i> subsp. <i>xylosoxidans</i>	150	<i>Brevibacterium</i> species
	<i>Abiotrophia defectiva</i> (<i>Streptococcus defectivus</i>)		<i>Allotococcus otitis</i>		<i>Brevundimonas</i> (<i>Pseudomonas</i>) <i>diminuta</i>
5	<i>Achromobacter</i> species		<i>Anaerobiospirillum succiniciproducens</i>		<i>Brevundimonas</i> (<i>Pseudomonas</i>) <i>vesicularis</i>
	<i>Acidaminococcus fermentans</i>	80	<i>Anaerovibrio lipolytica</i>		<i>Brevundimonas</i> species
	<i>Acinetobacter alcaligenes</i>		<i>Arachnia propionica</i>	155	<i>Brochothrix thermosphacta</i>
	<i>Acinetobacter anitratus</i>		<i>Arcanobacterium</i> (<i>Actinomyces</i>) <i>bernardiae</i>		<i>Brucella abortus</i>
	<i>Acinetobacter baumannii</i>		<i>Arcanobacterium</i> (<i>Actinomyces</i>) <i>pyogenes</i>		<i>Brucella canis</i>
10	<i>Acinetobacter calcoaceticus</i>		<i>Arcanobacterium haemolyticum</i>		<i>Brucella melitensis</i>
	<i>Acinetobacter calcoaceticus</i> biovar <i>anitratus</i>	85	<i>Arcobacter cryaerophilus</i> (<i>Campylobacter cryaerophila</i>)	160	<i>Brucella ovis</i>
	<i>Acinetobacter calcoaceticus</i> biovar <i>lwoffii</i>		<i>Arthrobacter globiformis</i>		<i>Brucella species</i>
15	<i>Acinetobacter genomospecies</i>		<i>Arthrobacter species</i>		<i>Brucella suis</i>
	<i>Acinetobacter haemolyticus</i>	90	<i>Arxiozyma telluris</i> (<i>Torulopsis pintolopesii</i>)		<i>Budvicia aquatica</i>
	<i>Acinetobacter johnsonii</i>		<i>Atopobium minutum</i> (<i>Lactobacillus minutus</i>)	165	<i>Burkholderia</i> (<i>Pseudomonas</i>) <i>cepacia</i>
	<i>Acinetobacter junii</i>		<i>Aureobacterium</i> species		<i>Burkholderia</i> (<i>Pseudomonas</i>) <i>gladioli</i>
	<i>Acinetobacter lwoffii</i>		<i>Bacillus amyloliquefaciens</i>		<i>Burkholderia</i> (<i>Pseudomonas</i>) <i>mallei</i>
20	<i>Acinetobacter radioresistens</i>	95	<i>Bacillus anthracis</i>		<i>Burkholderia</i> (<i>Pseudomonas</i>) <i>pseudomallei</i>
	<i>Actinobacillus actinomycetemcomitans</i>		<i>Bacillus badius</i>	170	<i>Burkholderia species</i>
	<i>Actinobacillus capsulatus</i>		<i>Bacillus cereus</i>		<i>Buttiauxella agrestis</i>
	<i>Actinobacillus equuli</i>		<i>Bacillus circulans</i>		<i>Campylobacter coli</i>
25	<i>Actinobacillus hominis</i>	100	<i>Bacillus coagulans</i>		<i>Campylobacter concisus</i>
	<i>Actinobacillus lignieresii</i>		<i>Bacillus firmus</i>		<i>Campylobacter fetus</i>
	<i>Actinobacillus pleuropneumoniae</i>		<i>Bacillus lentus</i>	175	<i>Campylobacter fetus</i> subsp. <i>fetus</i>
	<i>Actinobacillus species</i>		<i>Bacillus licheniformis</i>		<i>Campylobacter fetus</i> subsp. <i>fetus</i>
	<i>Actinobacillus suis</i>		<i>Bacillus megaterium</i>		<i>Campylobacter fetus</i> subsp. <i>fetus</i>
30	<i>Actinobacillus ureae</i>	105	<i>Bacillus mycoides</i>		<i>Campylobacter jejuni</i>
	<i>Actinomyces bovis</i>		<i>Bacillus pantothenicus</i>	180	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i>
	<i>Actinomyces israelii</i>		<i>Bacillus pumilus</i>		<i>Campylobacter lari</i>
	<i>Actinomyces meyeri</i>		<i>Bacillus species</i>		<i>Campylobacter lari</i> subsp. UPTC
	<i>Actinomyces naeslundii</i>		<i>Bacillus sphaericus</i>		<i>Campylobacter mucosalis</i>
35	<i>Actinomyces neuii</i> subsp. <i>anitratus</i>	110	<i>Bacillus stearothermophilus</i>		<i>Campylobacter species</i>
	<i>Actinomyces neuii</i> subsp. <i>neuii</i>		<i>Bacillus subtilis</i>		<i>Campylobacter sputorum</i>
	<i>Actinomyces odontolyticus</i>		<i>Bacillus thuringiensis</i>	185	<i>Campylobacter sputorum</i> subsp. <i>bubulus</i>
	<i>Actinomyces pyogenes</i>		<i>Bacteroides caccae</i>		<i>Campylobacter sputorum</i> subsp. <i>fecalis</i>
	<i>Actinomyces radingae</i>		<i>Bacteroides capillosus</i>		<i>Campylobacter sputorum</i> subsp. <i>sputorum</i>
40	<i>Actinomyces species</i>	115	<i>Bacteroides distasonis</i>		<i>Campylobacter upsaliensis</i>
	<i>Actinomyces turicensis</i>		<i>Bacteroides eggerthii</i>	190	<i>Candida</i> (<i>Clavispora</i>) <i>lusitanae</i>
	<i>Actinomyces viscosus</i>		<i>Bacteroides fragilis</i>		<i>Candida</i> (<i>Pichia</i>) <i>guilliermondii</i>
	<i>Aerococcus species</i>		<i>Bacteroides merdae</i>		<i>Candida</i> (<i>Torulopsis</i>) <i>glabrata</i>
	<i>Aerococcus viridans</i>		<i>Bacteroides ovatus</i>		<i>Candida albicans</i>
45	<i>Aeromonas caviae</i>	120	<i>Bacteroides species</i>	195	<i>Candida boidinii</i>
	<i>Aeromonas hydrophila</i>		<i>Bacteroides spianchnicus</i>		<i>Candida catenulata</i>
	<i>Aeromonas hydrophila</i> group		<i>Bacteroides stercoris</i>		<i>Candida ciferrii</i>
	<i>Aeromonas jandaei</i>		<i>Bacteroides thetaiotaomicron</i>		<i>Candida colliculosa</i>
	<i>Aeromonas salmonicida</i>		<i>Bacteroides uniformis</i>		<i>Candida conglobata</i>
50	<i>Aeromonas salmonicida</i> subsp. <i>achromogenes</i>	125	<i>Bacteroides ureolyticus</i> (<i>B. corrodens</i>)	200	<i>Candida curvata</i> (<i>Cryptococcus curvatus</i>)
	<i>Aeromonas salmonicida</i> subsp. <i>masoucida</i>		<i>Bacteroides vulgatus</i>		<i>Candida dattila</i>
	<i>Aeromonas salmonicida</i> subsp. <i>salmonicida</i>		<i>Bergeyella</i> (<i>Weeksella</i>) <i>zooheicum</i>		<i>Candida dubliniensis</i>
55	<i>Aeromonas schubertii</i>		<i>Bifidobacterium adolescentis</i>		<i>Candida famata</i>
	<i>Aeromonas sobria</i>	130	<i>Bifidobacterium bifidum</i>		<i>Candida globosa</i>
	<i>Aeromonas sobria</i>		<i>Bifidobacterium breve</i>	205	<i>Candida helenica</i>
	<i>Aeromonas species</i>		<i>Bifidobacterium dentium</i>		<i>Candida holmii</i>
	<i>Aeromonas trota</i>		<i>Bifidobacterium infantis</i>		<i>Candida humicola</i>
60	<i>Aeromonas veronii</i>		<i>Bifidobacterium species</i>		<i>Candida inconspicua</i>
	<i>Aeromonas veronii</i> biovar <i>sobria</i>		<i>Blastoschizomyces</i> (<i>Dipodascus</i>) <i>capitatus</i>	210	<i>Candida intermedia</i>
	<i>Aeromonas veronii</i> biovar <i>veronii</i>	135	<i>Bordetella avium</i>		<i>Candida kefyr</i>
	<i>Agrobacterium radiobacter</i>		<i>Bordetella bronchiseptica</i>		<i>Candida krusei</i>
	<i>Agrobacterium species</i>		<i>Bordetella parapertussis</i>		<i>Candida lambica</i>
65	<i>Agrobacterium tumefaciens</i>	140	<i>Bordetella pertussis</i>		<i>Candida magnoliae</i>
	<i>Alcaligenes denitrificans</i>		<i>Bordetella species</i>	215	<i>Candida maris</i>
	<i>Alcaligenes faecalis</i>		<i>Borrelia species</i>		<i>Candida melibiosica</i>
	<i>Alcaligenes odorans</i>		<i>Branhamella</i> (<i>Moraxella</i>) <i>catarrhalis</i>		<i>Candida membranaefaciens</i>
	<i>Alcaligenes odorans</i> (<i>Alcaligenes faecalis</i>)		<i>Branhamella species</i>		<i>Candida norvegensis</i>
70	<i>Alcaligenes species</i>	145	<i>Brevibacillus brevis</i>		<i>Candida norvegica</i>
	<i>Alcaligenes xylosoxidans</i>		<i>Brevibacillus laterosporus</i>	220	<i>Candida parapsilosis</i>
	<i>Alcaligenes xylosoxidans</i> subsp. <i>denitrificans</i>		<i>Brevibacterium casei</i>		<i>Candida paratropicalis</i>
			<i>Brevibacterium epidermidis</i>		<i>Candida pelliculosa</i>
			<i>Brevibacterium linens</i>		

Table 15. Microorganism identified by commercial systems (continued)

<i>Candida pseudotropicalis</i>		<i>Clostridium hastiforme</i>		<i>Corynebacterium urealyticum</i> (group D2)
<i>Candida pulcherrima</i>		80 <i>Clostridium histolyticum</i>		<i>Corynebacterium xerosis</i>
<i>Candida ravautii</i>		<i>Clostridium innocuum</i>		160 <i>Cryptococcus albidus</i>
5 <i>Candida rugosa</i>		<i>Clostridium limosum</i>		<i>Cryptococcus ater</i>
<i>Candida sake</i>		<i>Clostridium novyi</i>		<i>Cryptococcus cereanus</i>
<i>Candida silvicola</i>		<i>Clostridium novyi A</i>		<i>Cryptococcus gastricus</i>
<i>Candida species</i>		85 <i>Clostridium paraputrificum</i>		<i>Cryptococcus humicolus</i>
<i>Candida sphaerica</i>		<i>Clostridium perfringens</i>		165 <i>Cryptococcus lactativorus</i>
<i>Candida stellatoidea</i>		<i>Clostridium putrificum</i>		<i>Cryptococcus laurentii</i>
10 <i>Candida tenuis</i>		<i>Clostridium ramosum</i>		<i>Cryptococcus luteolus</i>
<i>Candida tropicalis</i>		<i>Clostridium septicum</i>		<i>Cryptococcus melibiosum</i>
<i>Candida utilis</i>		90 <i>Clostridium sordellii</i>		<i>Cryptococcus neoformans</i>
<i>Candida valida</i>		<i>Clostridium species</i>		170 <i>Cryptococcus species</i>
<i>Candida vini</i>		<i>Clostridium sphenoides</i>		<i>Cryptococcus terreus</i>
15 <i>Candida viswanathii</i>		<i>Clostridium sporogenes</i>		<i>Cryptococcus uniguttulatus</i>
<i>Candida zeylanoides</i>		<i>Clostridium subterminale</i>		<i>Debaryomyces hansenii</i>
<i>Capnocytophaga gingivalis</i>		95 <i>Clostridium tertium</i>		<i>Debaryomyces maramba</i>
<i>Capnocytophaga ochracea</i>		<i>Clostridium tetani</i>		175 <i>Debaryomyces polymorphus</i>
<i>Capnocytophaga species</i>		<i>Clostridium tyrobutyricum</i>		<i>Debaryomyces species</i>
20 <i>Capnocytophaga sputigena</i>		<i>Comamonas (Pseudomonas) acidovorans</i>		<i>Dermabacter hominis</i>
<i>Cardiobacterium hominis</i>		100 <i>Comamonas (Pseudomonas) testasteroni</i>		<i>Dermacoccus (Micrococcus) nishinomiyensis</i>
<i>Camobacterium divergens</i>		<i>Comamonas species</i>		180 <i>Dietzia species</i>
<i>Camobacterium piscicola</i>		<i>Corynebacterium accolens</i>		<i>Edwardsiella hoshinae</i>
CDC group ED-2		<i>Corynebacterium alermentans</i>		<i>Edwardsiella ictaluri</i>
25 CDC group EF4 (<i>Pasteurella</i> sp.)		105 <i>Corynebacterium amycolatum</i>		<i>Edwardsiella species</i>
CDC group EF-4A		<i>Corynebacterium aquaticum</i>		<i>Edwardsiella tarda</i>
CDC group EF-4B		<i>Corynebacterium argenteolactense</i>		185 <i>Eikenella corrodens</i>
CDC group EQ-Z		<i>Corynebacterium auris</i>		<i>Empedobacter brevis (Flavobacterium breve)</i>
CDC group HB-5		<i>Corynebacterium bovis</i>		<i>Enterobacter aerogenes</i>
30 CDC group II K-2		110 <i>Corynebacterium coyleae</i>		<i>Enterobacter agglomerans</i>
CDC group IV C-2 (<i>Bordetella</i> -like)		<i>Corynebacterium cystitidis</i>		190 <i>Enterobacter amnigenus</i>
CDC group M5		<i>Corynebacterium diphtheriae</i>		<i>Enterobacter amnigenus asburiae</i>
CDC group M6		<i>Corynebacterium diphtheriae</i> biotype bellanti		(CDC enteric group 17)
<i>Cedecea davisae</i>		115 <i>Corynebacterium diphtheriae</i> biotype gravis		<i>Enterobacter amnigenus biogroup 1</i>
35 <i>Cedecea lapagei</i>		<i>Corynebacterium diphtheriae</i> biotype intermedius		<i>Enterobacter amnigenus biogroup 2</i>
<i>Cedecea neteri</i>		120 <i>Corynebacterium diphtheriae</i> biotype mitis		195 <i>Enterobacter asburiae</i>
<i>Cedecea species</i>		<i>Corynebacterium flavescens</i>		<i>Enterobacter cancerogenus</i>
<i>Cellulomonas (Oerskovia) turbata</i>		<i>Corynebacterium glucuronolyticum</i>		<i>Enterobacter cloacae</i>
<i>Cellulomonas species</i>		<i>Corynebacterium glucuronolyticum-seminale</i>		<i>Enterobacter gergoviae</i>
40 <i>Chlamydia species</i>		125 <i>Corynebacterium group A</i>		<i>Enterobacter hormaechei</i>
<i>Chromobacterium violaceum</i>		<i>Corynebacterium group A-4</i>		200 <i>Enterobacter intermedius</i>
<i>Chryseobacterium (Flavobacterium) indologenes</i>		<i>Corynebacterium group A-5</i>		<i>Enterobacter sakazakii</i>
<i>Chryseobacterium (Flavobacterium) meningosepticum</i>		<i>Corynebacterium group ANF</i>		<i>Enterobacter species</i>
45 <i>Chryseobacterium gleum</i>		<i>Corynebacterium group B</i>		<i>Enterobacter taylorae</i>
<i>Chryseobacterium species</i>		130 <i>Corynebacterium group B-3</i>		<i>Enterobacter taylorae</i> (CDC enteric group 19)
<i>Chryseomonas indologenes</i>		<i>Corynebacterium group F</i>		<i>Enterococcus (Streptococcus) cecorum</i>
<i>Citromyces matritensis</i>		<i>Corynebacterium group F-1</i>		<i>Enterococcus (Streptococcus) faecalis</i> (Group D)
50 <i>Citrobacter amalonaticus</i>		<i>Corynebacterium group F-2</i>		210 <i>Enterococcus (Streptococcus) faecium</i> (Group D)
<i>Citrobacter braakii</i>		<i>Corynebacterium group G</i>		<i>Enterococcus (Streptococcus) saccharolyticus</i>
<i>Citrobacter diversus</i>		135 <i>Corynebacterium group G-1</i>		<i>Enterococcus avium</i> (Group D)
<i>Citrobacter farmeri</i>		<i>Corynebacterium group G-2</i>		215 <i>Enterococcus casseliflavus</i>
<i>Citrobacter freundii</i>		<i>Corynebacterium group I</i>		(<i>Streptococcus faecium</i> subsp. casseliflavus)
55 <i>Citrobacter freundii</i> complex		<i>Corynebacterium group I-2</i>		<i>Enterococcus durans</i> (<i>Streptococcus faecium</i> subsp. <i>durans</i>) (Group D)
<i>Citrobacter koseri</i>		<i>Corynebacterium jeikeium</i> (group JK)		220 <i>Enterococcus gallinarum</i>
<i>Citrobacter sedlakii</i>		140 <i>Corynebacterium kutscheri</i> (<i>C. murium</i>)		<i>Enterococcus hirae</i>
<i>Citrobacter species</i>		<i>Corynebacterium macginleyi</i>		<i>Enterococcus malodoratus</i>
<i>Citrobacter werkmanii</i>		<i>Corynebacterium minutissimum</i>		<i>Enterococcus mundtii</i>
60 <i>Citrobacter youngae</i>		145 <i>Corynebacterium pilosum</i>		<i>Enterococcus raffinosus</i>
<i>Clostridium acetobutylicum</i>		<i>Corynebacterium propinquum</i>		225 <i>Enterococcus species</i>
<i>Clostridium baratii</i>		<i>Corynebacterium pseudodiphtheriticum</i>		<i>Erwinia amylovora</i>
<i>Clostridium beijerinckii</i>		<i>Corynebacterium pseudotuberculosis</i>		<i>Erwinia carotovora</i>
<i>Clostridium bifementans</i>		150 <i>Corynebacterium pyogenes</i>		<i>Erwinia carotovora</i> subsp. <i>atroseptica</i>
65 <i>Clostridium botulinum</i>		<i>Corynebacterium renale</i>		<i>Erwinia carotovora</i> subsp. <i>betavascularum</i>
<i>Clostridium botulinum</i> (NP) B&F		<i>Corynebacterium renale</i> group		<i>Erwinia carotovora</i> subsp. <i>carotovora</i>
<i>Clostridium botulinum</i> (NP) E		<i>Corynebacterium seminale</i>		<i>Erwinia chrysanthemi</i>
<i>Clostridium botulinum</i> (P) A&H		<i>Corynebacterium species</i>		<i>Erwinia cypripedii</i>
<i>Clostridium botulinum</i> (P) F		<i>Corynebacterium striatum</i> (<i>C. flavidum</i>)		<i>Erwinia mallotivora</i>
70 <i>Clostridium botulinum</i> G1		155 <i>Corynebacterium ulcerans</i>		
<i>Clostridium botulinum</i> G2				
<i>Clostridium butyricum</i>				
<i>Clostridium cadaveris</i>				
<i>Clostridium chauvoei</i>				
75 <i>Clostridium clostridioforme</i>				
<i>Clostridium difficile</i>				
<i>Clostridium fallax</i>				
<i>Clostridium glycolicum</i>				

Table 15. Microorganism identified by commercial systems (continued)

<i>Erwinia nigrifluens</i>	VII	<i>Lactobacillus paracasei</i> subsp. <i>paracasei</i>
<i>Erwinia quercina</i>	80 <i>Haemophilus parainfluenzae</i> biotype VIII	<i>Lactobacillus pentosus</i>
<i>Erwinia rhapontici</i>	<i>Haemophilus paraphrohaemolyticus</i>	160 <i>Lactobacillus plantarum</i>
<i>Erwinia rubrifaciens</i>	<i>Haemophilus paraphrophilus</i>	<i>Lactobacillus salivarius</i>
5 <i>Erwinia salicis</i>	<i>Haemophilus segnis</i>	<i>Lactobacillus salivarius</i> var. <i>salicinius</i>
<i>Erwinia species</i>	85 <i>Haemophilus somnus</i>	<i>Lactobacillus species</i>
<i>Erysipelothrix rhusiopathiae</i>	<i>Haemophilus species</i>	<i>Lactococcus diacetylactis</i>
<i>Erysipelothrix species</i>	<i>Hafnia alvei</i>	165 <i>Lactococcus garvieae</i>
<i>Escherichia blattae</i>	<i>Hanseniaspora guilliermondii</i>	<i>Lactococcus lactis</i> subsp. <i>cremoris</i>
10 <i>Escherichia coli</i>	<i>Hanseniaspora uvarum</i>	<i>Lactococcus lactis</i> subsp. <i>diacetylactis</i>
<i>Escherichia coli</i> A-D	90 <i>Hanseniaspora valbyensis</i>	<i>Lactococcus lactis</i> subsp. <i>hordniae</i>
<i>Escherichia coli</i> O157:H7	<i>Hansenula anomala</i>	<i>Lactococcus lactis</i> subsp. <i>lactis</i>
<i>Escherichia fergusonii</i>	<i>Hansenula holstii</i>	170 <i>Lactococcus plantarum</i>
<i>Escherichia hermannii</i>	<i>Hansenula polymorpha</i>	<i>Lactococcus raffinolactis</i>
15 <i>Escherichia species</i>	<i>Helicobacter (Campylobacter) cinaedi</i>	<i>Leclercia adecarboxylata</i>
<i>Escherichia vulnensis</i>	95 <i>Helicobacter (Campylobacter) fennelliae</i>	<i>Legionella species</i>
<i>Eubacterium aerofaciens</i>	<i>Helicobacter (Campylobacter) pylori</i>	<i>Leminorella species</i>
<i>Eubacterium alactolyticum</i>	175 <i>Issatchenkia orientalis</i>	<i>Leptospira species</i>
<i>Eubacterium lentum</i>	<i>Kingella denitrificans</i>	<i>Leptotrichia buccalis</i>
20 <i>Eubacterium limosum</i>	100 <i>Kingella indologenes</i>	<i>Leuconostoc (Weissella) paramesenteroides</i>
<i>Eubacterium species</i>	<i>Kingella kingae</i>	<i>Leuconostoc carnosum</i>
<i>Ewingella americana</i>	<i>Kingella species</i>	180 <i>Leuconostoc citreum</i>
<i>Filobasidiella neoformans</i>	<i>Klebsiella ornithinolytica</i>	<i>Leuconostoc gelidum</i>
<i>Filobasidium floriforme</i>	<i>Klebsiella oxytoca</i>	<i>Leuconostoc lactis</i>
25 <i>Filobasidium uniguttulatum</i>	105 <i>Klebsiella planticola</i>	<i>Leuconostoc mesenteroides</i>
<i>Flavimonas oryzae</i>	<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	185 <i>Leuconostoc mesenteroides</i> subsp. <i>cremoris</i>
<i>Flavobacterium gleum</i>	<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	<i>Leuconostoc mesenteroides</i> subsp. <i>dextranicum</i>
<i>Flavobacterium indologenes</i>	110 <i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	<i>Leuconostoc mesenteroides</i> subsp. <i>mesenteroides</i>
<i>Flavobacterium odoratum</i>	<i>Klebsiella species</i>	190 <i>Leuconostoc species</i>
30 <i>Flavobacterium species</i>	<i>Klebsiella terrigena</i>	<i>Listeria grayi</i>
<i>Francisella novicida</i>	<i>Kloeckera apiculata</i>	<i>Listeria innocua</i>
<i>Francisella philomiragia</i>	115 <i>Kloeckera apis</i>	<i>Listeria ivanovii</i>
<i>Francisella species</i>	<i>Kloeckera japonica</i>	<i>Listeria monocytogenes</i>
<i>Francisella tularensis</i>	<i>Kloeckera species</i>	195 <i>Listeria murrayi</i>
35 <i>Fusobacterium mortiferum</i>	<i>Kluyvera ascorbata</i>	<i>Listeria seeligeri</i>
<i>Fusobacterium necrogenes</i>	<i>Kluyvera cryocrescens</i>	<i>Listeria species</i>
<i>Fusobacterium necrophorum</i>	120 <i>Kluyvera species</i>	<i>Listeria welshimeri</i>
<i>Fusobacterium nucleatum</i>	<i>Kluyveromyces lactis</i>	<i>Megasphaera elsdenii</i>
<i>Fusobacterium species</i>	<i>Kluyveromyces marxianus</i>	200 <i>Methylobacterium mesophilicum</i>
40 <i>Fusobacterium varium</i>	<i>Kluyveromyces thermotolerans</i>	<i>Metschnikowia pulcherrima</i>
<i>Gaffkya species</i>	<i>Kocuria (Micrococcus) kristinae</i>	<i>Microbacterium species</i>
<i>Gardnerella vaginalis</i>	125 <i>Kocuria (Micrococcus) rosea</i>	<i>Micrococcus luteus</i>
<i>Gemella haemolysans</i>	<i>Kocuria (Micrococcus) varians</i>	<i>Micrococcus lylae</i>
<i>Gemella morbillorum</i>	<i>Koserella trabusii</i>	205 <i>Micrococcus species</i>
45 <i>Gemella species</i>	<i>Kytococcus (Micrococcus) sedentarius</i>	<i>Mobiluncus curtisii</i>
<i>Geotrichum candidum</i>	<i>Lactobacillus (Weissella) viridescens</i>	<i>Mobiluncus mulleris</i>
<i>Geotrichum fermentans</i>	130 <i>Lactobacillus A</i>	<i>Mobiluncus species</i>
<i>Geotrichum penicilliarum</i>	<i>Lactobacillus acidophilus</i>	<i>Moellerella wisconsinensis</i>
<i>Geotrichum penicillatum</i>	<i>Lactobacillus B</i>	210 <i>Moraxella (Branhamella) catarrhalis</i>
50 <i>Geotrichum species</i>	<i>Lactobacillus brevis</i>	<i>Moraxella atlantae</i>
<i>Gordona species</i>	<i>Lactobacillus buchneri</i>	<i>Moraxella bovis</i>
<i>Haemophilus aegyptius</i>	135 <i>Lactobacillus casei</i>	<i>Moraxella lacunata</i>
<i>Haemophilus aphrophilus</i>	<i>Lactobacillus casei</i> subsp. <i>casei</i>	<i>Moraxella nonliquefaciens</i>
<i>Haemophilus ducreyi</i>	<i>Lactobacillus casei</i> subsp. <i>lactosus</i>	215 <i>Moraxella osloensis</i>
55 <i>Haemophilus haemoglobinophilus</i>	<i>Lactobacillus casei</i> subsp. <i>rhannosus</i>	<i>Moraxella phenylpyruvica</i>
<i>Haemophilus haemolyticus</i>	<i>Lactobacillus catenaformis</i>	<i>Moraxella species</i>
<i>Haemophilus influenzae</i>	140 <i>Lactobacillus cellobiosus</i>	<i>Morganella morganii</i>
<i>Haemophilus influenzae</i> biotype I	<i>Lactobacillus collinoides</i>	<i>Morganella morganii</i> subsp. <i>morganii</i>
<i>Haemophilus influenzae</i> biotype II	<i>Lactobacillus coprophilus</i>	220 <i>Morganella morganii</i> subsp. <i>sibonii</i>
<i>Haemophilus influenzae</i> biotype III	<i>Lactobacillus crispatus</i>	<i>Mycobacterium africanum</i>
<i>Haemophilus influenzae</i> biotype IV	<i>Lactobacillus curvatus</i>	<i>Mycobacterium asiaticum</i>
<i>Haemophilus influenzae</i> biotype V	145 <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i>	<i>Mycobacterium avium</i>
<i>Haemophilus influenzae</i> biotype VI	<i>Lactobacillus delbrueckii</i> subsp. <i>delbrueckii</i>	<i>Mycobacterium bovis</i>
<i>Haemophilus influenzae</i> biotype VII	<i>Lactobacillus delbrueckii</i> subsp. <i>lactis</i>	225 <i>Mycobacterium chelonae</i>
<i>Haemophilus influenzae</i> biotype VIII	150 <i>Lactobacillus fermentum</i>	<i>Mycobacterium fortuitum</i>
<i>Haemophilus paragaillarum</i>	<i>Lactobacillus fructivorans</i>	<i>Mycobacterium gordonae</i>
<i>Haemophilus parahaemolyticus</i>	<i>Lactobacillus helveticus</i>	<i>Mycobacterium kansasii</i>
<i>Haemophilus parainfluenzae</i>	<i>Lactobacillus helveticus</i> subsp. <i>jugurti</i>	<i>Mycobacterium malmoense</i>
<i>Haemophilus parainfluenzae</i> biotype I	155 <i>Lactobacillus jensenii</i>	230 <i>Mycobacterium marinum</i>
<i>Haemophilus parainfluenzae</i> biotype II	<i>Lactobacillus lindneri</i>	<i>Mycobacterium phlei</i>
<i>Haemophilus parainfluenzae</i> biotype III	<i>Lactobacillus minutus</i>	<i>Mycobacterium scrofulaceum</i>
<i>Haemophilus parainfluenzae</i> biotype IV		<i>Mycobacterium smegmatis</i>
75 <i>Haemophilus parainfluenzae</i> biotype V		<i>Mycobacterium species</i>
<i>Haemophilus parainfluenzae</i> biotype VI		
<i>Haemophilus parainfluenzae</i> biotype		

Table 15. Microorganisms identified by commercial systems (continued)¹.

5	<i>Mycobacterium tuberculosis</i> <i>Mycobacterium ulcerans</i> <i>Mycobacterium xenopi</i> <i>Mycoplasma fermentans</i> <i>Mycoplasma hominis</i> <i>Mycoplasma orale</i> <i>Mycoplasma pneumoniae</i> <i>Mycoplasma species</i> <i>Myroides species</i>	80	<i>Pichia fermentans</i> <i>Pichia membranaefaciens</i> <i>Pichia norvegensis</i> <i>Pichia ohmeri</i> <i>Pichia spartinae</i> <i>Pichia species</i>	160	<i>Saccharomyces exiguus</i> <i>Saccharomyces kluyveri</i> <i>Saccharomyces species</i> <i>Sakaguchia dacryoides</i> (<i>Rhodospordium dacryoidum</i>) <i>Salmonella arizonae</i> <i>Salmonella choleraesuis</i> <i>Salmonella enteritidis</i>
10	<i>Neisseria cinerea</i> <i>Neisseria elongata</i> subsp. <i>elongata</i> <i>Neisseria flava</i> <i>Neisseria flavescens</i> <i>Neisseria gonorrhoeae</i> <i>Neisseria lactamica</i> <i>Neisseria meningitidis</i> <i>Neisseria mucosa</i> <i>Neisseria perflava</i> <i>Neisseria polysaccharea</i>	85	<i>Plasmonas shigelloides</i> <i>Porphyromonas asaccharolytica</i> <i>Porphyromonas endodontalis</i> <i>Porphyromonas gingivalis</i> <i>Porphyromonas levii</i>	165	<i>Salmonella gallinarum</i> <i>Salmonella paratyphi A</i> <i>Salmonella paratyphi B</i> <i>Salmonella pullorum</i> <i>Salmonella species</i> <i>Salmonella typhi</i> <i>Salmonella typhimurium</i> <i>Salmonella typhisuis</i> <i>Salmonella/Arizona</i>
15	<i>Neisseria saprophytes</i> <i>Neisseria sicca</i> <i>Neisseria subflava</i> <i>Neisseria weaveri</i> <i>Neisseria weaveri</i> (CDC group M5)	90	<i>Prevotella (Bacteroides) buccae</i> <i>Prevotella (Bacteroides) buccalis</i> <i>Prevotella (Bacteroides) corporis</i> <i>Prevotella (Bacteroides) denticola</i> <i>Prevotella (Bacteroides) loeschii</i>	170	<i>Serratia ficaria</i> <i>Serratia fonticola</i> <i>Serratia grimesii</i> <i>Serratia liquefaciens</i> <i>Serratia marcescens</i> <i>Serratia odorifera</i>
20	<i>Nocardia species</i> <i>Ochrobactrum anthropi</i> <i>Oerskovia species</i> <i>Oerskovia xanthineolytica</i> <i>Oligella (Moraxella) urethralis</i> <i>Oligella species</i> <i>Oligella ureolytica</i> <i>Paenibacillus alvei</i> <i>Paenibacillus macerans</i> <i>Paenibacillus polymyxa</i>	95	<i>Prevotella (Bacteroides) oralis</i> <i>Prevotella (Bacteroides) disiens</i> <i>Prevotella (Bacteroides) oris</i> <i>Prevotella bivia (Bacteroides bivius)</i> <i>Prevotella intermedia (Bacteroides intermedius)</i>	175	<i>Serratia odorifera</i> type 1 <i>Serratia odorifera</i> type 2 <i>Serratia plymuthica</i> <i>Serratia proteamaculans</i> <i>Serratia proteamaculans</i> subsp. <i>proteamaculans</i>
25	<i>Pantoea agglomerans</i> <i>Pantoea ananas</i> (<i>Erwinia uredovora</i>) <i>Pantoea dispersa</i> <i>Pantoea species</i> <i>Pantoea stewartii</i>	100	<i>Prevotella melaninogenica</i> (<i>Bacteroides melaninogenicus</i>) <i>Prevotella ruminicola</i> <i>Propionibacterium acnes</i> <i>Propionibacterium avidum</i> <i>Propionibacterium granulosum</i> <i>Propionibacterium propionicum</i> <i>Propionibacterium species</i>	180	<i>Serratia proteamaculans</i> subsp. <i>quinovora</i> <i>Serratia rubidaea</i> <i>Serratia species</i> <i>Shewanella (Pseudomonas, Altomonas) putrefaciens</i> <i>Shigella boydii</i> <i>Shigella dysenteriae</i> <i>Shigella flexneri</i>
30	<i>Pasteurella (Haemophilus) avium</i> <i>Pasteurella aerogenes</i> <i>Pasteurella gallinarum</i> <i>Pasteurella haemolytica</i> <i>Pasteurella haemolyticus</i> <i>Pasteurella multocida</i> <i>Pasteurella multocida</i> SF <i>Pasteurella multocida</i> subsp. <i>multocida</i> <i>Pasteurella multocida</i> subsp. <i>septica</i>	105	<i>Proteus mirabilis</i> <i>Proteus penneri</i> <i>Proteus species</i> <i>Proteus vulgaris</i> <i>Prototheca species</i> <i>Prototheca wickerhamii</i> <i>Prototheca zopfii</i> <i>Providencia alcalifaciens</i> <i>Providencia heimbachae</i> <i>Providencia rattergi</i> <i>Providencia rustigianii</i>	185	<i>Shigella sonnei</i> <i>Shigella species</i> <i>Sphingobacterium multivorum</i> <i>Sphingobacterium species</i> <i>Sphingobacterium spiritivorum</i> <i>Sphingobacterium thalpophilum</i> <i>Sphingomonas (Pseudomonas) paucimobilis</i> <i>Sporidiobolus salmonicolor</i> <i>Sporobolomyces roseus</i>
35	<i>Pasteurella pneumotropica</i> <i>Pasteurella species</i> <i>Pasteurella ureae</i> <i>Pediococcus acidilactici</i> <i>Pediococcus damnosus</i> <i>Pediococcus pentosaceus</i> <i>Pediococcus species</i> <i>Peptococcus niger</i> <i>Peptococcus species</i> <i>Peptostreptococcus anaerobius</i> <i>Peptostreptococcus asaccharolyticus</i> <i>Peptostreptococcus indolicus</i> <i>Peptostreptococcus magnus</i> <i>Peptostreptococcus micros</i> <i>Peptostreptococcus parvulus</i> <i>Peptostreptococcus prevotii</i> <i>Peptostreptococcus productus</i> <i>Peptostreptococcus species</i> <i>Peptostreptococcus tetradius</i> <i>Phaeococcomyces exophialae</i>	110	<i>Providencia stuartii</i> <i>Providencia stuartii</i> urea + <i>Pseudomonas (Chryseomonas) luteola</i>	190	<i>Sporobolomyces salmonicolor</i> <i>Sporobolomyces species</i> <i>Staphylococcus (Peptococcus) saccharolyticus</i> <i>Staphylococcus arlettae</i> <i>Staphylococcus aureus</i> <i>Staphylococcus aureus</i> (Coagulase-negative)
40	<i>Pediococcus damnosus</i> <i>Pediococcus pentosaceus</i> <i>Pediococcus species</i> <i>Peptococcus niger</i> <i>Peptococcus species</i> <i>Peptostreptococcus anaerobius</i> <i>Peptostreptococcus asaccharolyticus</i> <i>Peptostreptococcus indolicus</i> <i>Peptostreptococcus magnus</i> <i>Peptostreptococcus micros</i> <i>Peptostreptococcus parvulus</i> <i>Peptostreptococcus prevotii</i> <i>Peptostreptococcus productus</i> <i>Peptostreptococcus species</i> <i>Peptostreptococcus tetradius</i> <i>Photobacterium damsela</i>	115	<i>Pseudomonas fluorescens</i> <i>Pseudomonas fluorescens</i> group <i>Pseudomonas mendocina</i> <i>Pseudomonas pseudoalcaligenes</i>	195	<i>Staphylococcus auricularis</i> <i>Staphylococcus capitis</i> <i>Staphylococcus capitis</i> subsp. <i>capitis</i> <i>Staphylococcus capitis</i> subsp. <i>ureolyticus</i> <i>Staphylococcus caprae</i> <i>Staphylococcus carnosus</i> <i>Staphylococcus caseolyticus</i> <i>Staphylococcus chromogenes</i> <i>Staphylococcus cohnii</i> <i>Staphylococcus cohnii</i> subsp. <i>cohnii</i> <i>Staphylococcus cohnii</i> subsp. <i>urealyticum</i>
45	<i>Photobacterium damsela</i> <i>Pichia (Hansenula) anomala</i> <i>Pichia (Hansenula) jadinii</i> <i>Pichia (Hansenula) petersonii</i> <i>Pichia angusta</i> (<i>Hansenula polymorpha</i>) <i>Pichia carsonii</i> (<i>P. vini</i>) <i>Pichia etchellsii</i> <i>Pichia farinosa</i>	120	<i>Pseudomonas putida</i> <i>Pseudomonas species</i> <i>Pseudomonas stutzeri</i> <i>Pseudomonas testosteroni</i> <i>Pseudomonas vesicularis</i>	200	<i>Staphylococcus epidermidis</i> <i>Staphylococcus equorum</i> <i>Staphylococcus gallinarum</i> <i>Staphylococcus haemolyticus</i> <i>Staphylococcus hominis</i> <i>Staphylococcus hominis</i> subsp. <i>hominis</i> <i>Staphylococcus hominis</i> subsp. <i>novobioceticus</i>
50		125	<i>Pseudoramibacter (Eubacterium) alactolyticus</i> <i>Psychrobacter (Moraxella) phenylpyruvicus</i> <i>Rahnella aquatilis</i>	205	
55		130	<i>Ralstonia (Pseudomonas, Burkholderia) pickettii</i> <i>Rhodococcus (Corynebacterium) equi</i> <i>Rhodococcus species</i> <i>Rhodospiridium toruloides</i>	210	
60		135	<i>Rhodotorula glutinis</i> <i>Rhodotorula minuta</i> <i>Rhodotorula mucilaginosa</i> (<i>R. rubra</i>) <i>Rhodotorula species</i> <i>Rickettsia species</i> <i>Rothia dentocariosa</i> <i>Saccharomyces cerevisiae</i>	215	
65		140		220	
70		145		225	
75		150		230	

Table 15. Microorganisms identified by commercial systems (continued)¹.

5	<i>Staphylococcus hyicus</i> <i>Staphylococcus intermedius</i> <i>Staphylococcus kloosii</i> <i>Staphylococcus lentus</i> <i>Staphylococcus lugdunensis</i> <i>Staphylococcus saprophyticus</i> <i>Staphylococcus schleiferi</i> <i>Staphylococcus sciuri</i>	60	<i>Streptococcus Gamma</i> (non)- hemolytic <i>Streptococcus gordonii</i> <i>Streptococcus Group B</i> <i>Streptococcus Group C</i>	120	<i>Tetragenococcus (Pediococcus)</i> <i>halophilus</i> <i>Torulaspora delbrueckii</i> (<i>Saccharomyces rosei</i>) <i>Torulopsis candida</i> <i>Torulopsis haemulonii</i>
10	<i>Staphylococcus simulans</i> <i>Staphylococcus species</i> <i>Staphylococcus warneri</i> <i>Staphylococcus xylosum</i> <i>Stenotrophomonas (Xanthomonas)</i> <i>maltophilia</i>	65	<i>Streptococcus Group D</i> <i>Streptococcus Group E</i> <i>Streptococcus Group F</i> <i>Streptococcus Group G</i> <i>Streptococcus Group L</i>	125	<i>Torulopsis inconspicua</i> <i>Treponema species</i> <i>Trichosporon asahii</i> <i>Trichosporon asteroides</i> <i>Trichosporon belgelii</i>
15	<i>Stephanosaurus ciferrii</i> <i>Stomatococcus mucilaginosus</i> <i>Streptococcus acidominimus</i> <i>Streptococcus agalactiae</i>	70	<i>Streptococcus Group P</i> <i>Streptococcus Group U</i> <i>Streptococcus intermedius</i> <i>Streptococcus intermedius</i> (<i>Streptococcus milleri</i> II)	130	<i>Trichosporon cutaneum</i> <i>Trichosporon inkin</i> <i>Trichosporon mucoides</i> <i>Trichosporon ovoides</i> <i>Trichosporon pullulans</i>
20	<i>Streptococcus agalactiae</i> (Group B) <i>Streptococcus agalactiae</i> hemolytic <i>Streptococcus agalactiae</i> non- hemolytic <i>Streptococcus alactolyticus</i>	75	<i>Streptococcus intermedius</i> (viridans <i>Streptococcus</i>) <i>Streptococcus milleri</i> group <i>Streptococcus mitis</i> <i>Streptococcus mitis</i> (viridans <i>Streptococcus</i>)	135	<i>Trichosporon species</i> <i>Turicella otitidis</i> <i>Ureaplasma species</i> <i>Ureaplasma urealyticum</i> <i>Veillonella parvula</i> (<i>V. alcalescens</i>)
25	<i>Streptococcus anginosus</i> <i>Streptococcus anginosus</i> (Group D, nonenterococci) <i>Streptococcus beta-hemolytic group A</i> <i>Streptococcus beta-hemolytic non- group A or B</i>	80	<i>Streptococcus mitis</i> group <i>Streptococcus mutans</i> <i>Streptococcus mutans</i> (viridans <i>Streptococcus</i>)	140	<i>Veillonella species</i> <i>Vibrio alginolyticus</i> <i>Vibrio cholerae</i> <i>Vibrio damsela</i> <i>Vibrio fluvialis</i>
30	<i>Streptococcus beta-hemolytic non- group A</i> <i>Streptococcus beta-hemolytic</i> <i>Streptococcus bovis</i> (Group D, nonenterococci)	85	<i>Streptococcus oralis</i> <i>Streptococcus parasanguis</i> <i>Streptococcus pneumoniae</i> <i>Streptococcus porcinus</i> <i>Streptococcus pyogenes</i>	145	<i>Vibrio furnissii</i> <i>Vibrio harveyi</i> <i>Vibrio hollisae</i> <i>Vibrio metschnikovii</i> <i>Vibrio mimicus</i>
35	<i>Streptococcus bovis</i> I <i>Streptococcus bovis</i> II <i>Streptococcus canis</i> <i>Streptococcus constellatus</i> <i>Streptococcus constellatus</i> (<i>Streptococcus milleri</i> I)	90	<i>Streptococcus pyogenes</i> (Group A) <i>Streptococcus salivarius</i> <i>Streptococcus salivarius</i> (viridans <i>Streptococcus</i>)	150	<i>Vibrio parahaemolyticus</i> <i>Vibrio species</i> <i>Vibrio species SF</i> <i>Vibrio vulnificus</i> <i>Weeksella (Bergeyella) virosa</i>
40	<i>Streptococcus constellatus</i> (viridans <i>Streptococcus</i>) <i>Streptococcus downei</i>	95	<i>Streptococcus salivarius</i> subsp. <i>salivarius</i> <i>Streptococcus salivarius</i> subsp. <i>thermophilus</i> <i>Streptococcus sanguis</i> <i>Streptococcus sanguis</i> I (viridans <i>Streptococcus</i>)	155	<i>Weeksella species</i> <i>Weeksella virosa</i> <i>Williopsis (Hansenula) satumus</i> <i>Xanthomonas campestris</i> <i>Xanthomonas species</i>
45	<i>Streptococcus dysgalactiae</i> subsp. <i>dysgalactiae</i> <i>Streptococcus dysgalactiae</i> subsp. <i>equisimilis</i>	100	<i>Streptococcus sanguis</i> II (viridans <i>Streptococcus</i>) <i>Streptococcus sanguis</i> II (viridans <i>Streptococcus</i>)	160	<i>Yarrowia (Candida) lipolytica</i> <i>Yersinia aldovae</i> <i>Yersinia enterocolitica</i> <i>Yersinia enterocolitica</i> group
50	<i>Streptococcus equi</i> (Group C/Group G <i>Streptococcus</i>) <i>Streptococcus equi</i> subsp. <i>equi</i> <i>Streptococcus equi</i> subsp. <i>zooepidemicus</i>	105	<i>Streptococcus sobrinus</i> <i>Streptococcus species</i> <i>Streptococcus suis</i> I <i>Streptococcus suis</i> II <i>Streptococcus uberis</i> <i>Streptococcus uberis</i> (viridans <i>Streptococcus</i>)	165	<i>Yersinia frederiksenii</i> <i>Yersinia intermedia</i> <i>Yersinia intermedius</i> <i>Yersinia kristensenii</i> <i>Yersinia pestis</i>
55	<i>Streptococcus equinus</i> <i>Streptococcus equinus</i> (Group D, nonenterococci) <i>Streptococcus equisimilis</i> <i>Streptococcus equisimilis</i> (Group C/Group G <i>Streptococcus</i>)	110	<i>Streptococcus vestibularis</i> <i>Streptococcus zooepidemicus</i> <i>Streptococcus zooepidemicus</i> (Group C)	170	<i>Yersinia pseudotuberculosis</i> <i>Yersinia pseudotuberculosis</i> SF <i>Yersinia ruckeri</i> <i>Yersinia species</i> <i>Yokenella regensburgi</i> <i>Yokenella regensburgi</i> (<i>Koserella</i> <i>trabulsi</i>)
		115	<i>Streptomyces somaliensis</i> <i>Streptomyces species</i> <i>Suttonella (Kingella) indologenes</i> <i>Tatumella phycos</i>	175	<i>Zygoascus hellenicus</i> <i>Zygosaccharomyces species</i>

¹ The list includes microorganisms that may be identified by API identification test systems and VITEK[®] automated identification system from bioMérieux Inc., or by the MicroScan[®] - WalkAway[®] automated systems from Dade Behring. Identification relies on classical identification methods using batteries of biochemical and other phenotypical tests.

Table 16. *tuf* gene sequences obtained in our laboratory (Example 42).

Species	Strain no.	Gene	GenBank Accession no.*
<i>Abiotrophia adiacens</i>	ATCC49175	<i>tuf</i>	AF124224
<i>Enterococcus avium</i>	ATCC14025	<i>tufA</i>	AF124220
		<i>tufB</i>	AF274715
<i>Enterococcus casseliflavus</i>	ATCC25788	<i>tufA</i>	AF274716
		<i>tufB</i>	AF274717
<i>Enterococcus cecorum</i>	ATCC43198	<i>tuf</i>	AF274718
<i>Enterococcus columbae</i>	ATCC51263	<i>tuf</i>	AF274719
<i>Enterococcus dispar</i>	ATCC51266	<i>tufA</i>	AF274720
		<i>tufB</i>	AF274721
<i>Enterococcus durans</i>	ATCC19432	<i>tufA</i>	AF274722
		<i>tufB</i>	AF274723
<i>Enterococcus faecalis</i>	ATCC29212	<i>tuf</i>	AF124221
<i>Enterococcus faecium</i>	ATCC 19434	<i>tufA</i>	AF124222
		<i>tufB</i>	AF274724
<i>Enterococcus gallinarum</i>	ATCC49573	<i>tufA</i>	AF124223
		<i>tufB</i>	AF274725
<i>Enterococcus hirae</i>	ATCC8043	<i>tufA</i>	AF274726
		<i>tufB</i>	AF274727
<i>Enterococcus malodoratus</i>	ATCC43197	<i>tufA</i>	AF274728
		<i>tufB</i>	AF274729
<i>Enterococcus mundtii</i>	ATCC43186	<i>tufA</i>	AF274730
		<i>tufB</i>	AF274731
<i>Enterococcus pseudoavium</i>	ATCC49372	<i>tufA</i>	AF274732
		<i>tufB</i>	AF274733
<i>Enterococcus raffinosus</i>	ATCC49427	<i>tufA</i>	AF274734
		<i>tufB</i>	AF274735
<i>Enterococcus saccharolyticus</i>	ATCC43076	<i>tuf</i>	AF274736
<i>Enterococcus solitarius</i>	ATCC49428	<i>tuf</i>	AF274737
<i>Enterococcus sulfureus</i>	ATCC49903	<i>tuf</i>	AF274738
<i>Lactococcus lactis</i>	ATCC11154	<i>tuf</i>	AF274745
<i>Listeria monocytogenes</i>	ATCC15313	<i>tuf</i>	AF274746
<i>Listeria seeligeri</i>	ATCC35967	<i>tuf</i>	AF274747
<i>Staphylococcus aureus</i>	ATCC25923	<i>tuf</i>	AF274739
<i>Staphylococcus epidermidis</i>	ATCC14990	<i>tuf</i>	AF274740
<i>Streptococcus mutans</i>	ATCC25175	<i>tuf</i>	AF274741
<i>Streptococcus pneumoniae</i>	ATCC6303	<i>tuf</i>	AF274742
<i>Streptococcus pyogenes</i>	ATCC19615	<i>tuf</i>	AF274743
<i>Streptococcus suis</i>	ATCC43765	<i>tuf</i>	AF274744

*Corresponding sequence ID NO. for the above ATCC strains are given in table 7.

Table 17. *tuf* gene sequences selected from databases for Example 42.

Species	Gene	Accession no.*
<i>Agrobacterium tumefaciens</i>	<i>tufA</i>	X99673
	<i>tufB</i>	X99674
<i>Anacystis nidulans</i>	<i>tuf</i>	X17442
<i>Aquifex aeolicus</i>	<i>tufA</i>	AE000657
	<i>tufB</i>	AE000657
<i>Bacillus stearothermophilus</i>	<i>tuf</i>	AJ000260
<i>Bacillus subtilis</i>	<i>tuf</i>	AL009126
<i>Bacteroides fragilis</i>	<i>tuf</i>	P33165
<i>Borrelia burgdorferi</i>	<i>tuf</i>	AE000783
<i>Brevibacterium linens</i>	<i>tuf</i>	X76863
<i>Bulkholderia cepacia</i>	<i>tuf</i>	P33167
<i>Campylobacter jejuni</i>	<i>tufB</i>	Y17167
<i>Chlamydia pneumoniae</i>	<i>tuf</i>	AE001363
<i>Chlamydia trachomatis</i>	<i>tuf</i>	M74221
<i>Corynebacterium glutamicum</i>	<i>tuf</i>	X77034
<i>Cytophaga lytica</i>	<i>tuf</i>	X77035
<i>Deinococcus radiodurans</i>	<i>tuf</i>	AE000513
<i>Escherichia coli</i>	<i>tufA</i>	J01690
	<i>tufB</i>	J01717
<i>Fervidobacterium islandicum</i>	<i>tuf</i>	Y15788
<i>Haemophilus influenzae</i>	<i>tufA</i>	L42023
	<i>tufB</i>	L42023
<i>Helicobacter pylori</i>	<i>tuf</i>	AE000511
<i>Homo sapiens</i> (Human)	<i>EF-1α</i>	X03558
<i>Methanococcus jannaschii</i>	<i>EF-1α</i>	U67486
<i>Mycobacterium leprae</i>	<i>tuf</i>	D13869
<i>Mycobacterium tuberculosis</i>	<i>tuf</i>	X63539
<i>Mycoplasma genitalium</i>	<i>tuf</i>	L43967
<i>Mycoplasma pneumoniae</i>	<i>tuf</i>	U00089
<i>Neisseria gonorrhoeae</i>	<i>tufA</i>	L36380
<i>Nicotiana tabacum</i> (Tobacco)	<i>EF-1α</i>	U04632
<i>Peptococcus niger</i>	<i>tuf</i>	X76869
<i>Planobispora rosea</i>	<i>tuf1</i>	U67308
<i>Saccharomyces cerevisiae</i> (Yeast)	<i>EF-1α</i>	X00779
<i>Salmonella typhimurium</i>	<i>tufA</i>	X55116
	<i>tufB</i>	X55117
<i>Shewanella putrefaciens</i>	<i>tuf</i>	P33169
<i>Spirochaeta aurantia</i>	<i>tuf</i>	X76874
<i>Spirulina platensis</i>	<i>tufA</i>	X15646
<i>Streptomyces aureofaciens</i>	<i>tuf1</i>	AF007125
<i>Streptomyces cinnamomeus</i>	<i>tuf1</i>	X98831
<i>Streptomyces coelicolor</i>	<i>tuf1</i>	X77039
	<i>tuf3</i>	X77040
<i>Streptomyces collinus</i>	<i>tuf1</i>	S79408
<i>Streptomyces ramocissimus</i>	<i>tuf1</i>	X67057
	<i>tuf2</i>	X67058
	<i>tuf3</i>	X67059
<i>Synechocystis</i> sp.	<i>tuf</i>	AB001339
<i>Taxobacter ocellatus</i>	<i>tuf</i>	X77036
<i>Thermotoga maritima</i>	<i>tuf</i>	AE000512
<i>Thermus aquaticus</i>	<i>tuf</i>	X66322
<i>Thermus thermophilus</i>	<i>tuf</i>	X06657
<i>Thiobacillus cuprinus</i>	<i>tuf</i>	U78300
<i>Treponema pallidum</i>	<i>tuf</i>	AE000520
<i>Wolinella succinogenes</i>	<i>tuf</i>	X76872

* Sequence data were obtained from GenBank, EMBL, and SWISSPROT databases. Genes were designated as appeared in the references.

Table 18. Nucleotide and amino acid sequence identities of EF-Tu between different enterococci and other low G+C gram-positive bacteria.

5 The upper right triangle represents the deduced amino acid sequence identities of gram-positive bacterial EF-Tu, while the lower left triangle represents the DNA sequence identities of the corresponding *tuf* genes. The sequence identities between different enterococcal *tufA* genes are boxed while those between enterococcal *tufB* genes are shaded.

Bacterial <i>tuf</i> gene	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	
1. <i>E. avium</i> <i>tufA</i>		96	98	96	96	96	96	97	95	98	99	95	95	96	94	96	93	86	87	85	88	88	88	86	85	86	87	86	92	91	90	90	90	92	84	85	84	82	83	
2. <i>E. casseliflavus</i> <i>tufA</i>	90		97	96	96	99	96	95	96	96	96	95	95	96	96	94	93	87	88	86	87	87	86	87	87	87	88	88	94	91	90	91	91	92	86	87	85	85	83	
3. <i>E. dispar</i> <i>tufA</i>	93	90		95	95	96	95	96	95	97	97	91	90	95	95	95	93	86	87	85	87	87	86	87	86	87	87	87	93	90	89	90	90	92	85	86	84	85	84	
4. <i>E. durans</i> <i>tufA</i>	90	89	90		98	96	99	93	99	95	96	90	91	94	95	94	92	87	87	88	88	88	85	86	87	87	88	87	94	90	90	90	90	91	85	86	84	84	84	
5. <i>E. faecium</i> <i>tufA</i>	88	90	89	96		96	98	93	98	95	96	89	91	88	94	93	92	87	88	88	88	87	87	88	87	87	88	87	94	92	91	91	91	93	85	86	84	84	84	
6. <i>E. gallinarum</i> <i>tufA</i>	90	97	89	89	89		96	93	95	96	96	88	89	89	96	93	92	87	87	88	87	87	86	87	87	88	87	93	92	90	90	90	93	85	86	84	83	84		
7. <i>E. hirae</i> <i>tufA</i>	90	90	89	89	96	89		93	99	95	96	91	91	89	95	94	92	88	87	88	88	86	85	86	86	86	87	87	94	90	90	90	90	91	85	86	84	84	84	
8. <i>E. malodoratus</i> <i>tufA</i>	96	91	94	90	89	90	89		92	97	97	89	89	90	93	96	92	86	85	82	85	85	85	85	83	85	86	86	92	90	88	88	89	91	83	84	83	83	82	
9. <i>E. mundtii</i> <i>tufA</i>	89	89	88	86	93	89	96	88		94	95	88	90	88	94	94	92	87	87	88	88	86	85	86	87	87	88	87	94	90	89	90	89	91	85	86	84	84	84	
10. <i>E. pseudovarum</i> <i>tufA</i>	97	92	93	90	89	91	89	97	89		96	90	90	91	95	96	94	87	87	88	87	87	86	87	86	87	88	88	93	90	89	90	90	91	85	86	85	85	84	
11. <i>E. raffinosus</i> <i>tufA</i>	97	91	93	90	89	89	89	97	88	97		91	90	90	94	96	93	88	87	85	86	86	85	86	85	87	87	87	93	89	89	90	89	91	84	85	84	84	83	
12. <i>E. oecorum</i> <i>tufA</i>	90	90	95	96	96	95	96	92	95	95	95		96	95	93	93	93	88	88	87	87	87	86	88	89	87	89	89	93	90	90	91	91	93	86	88	84	85	84	
13. <i>E. columbae</i> <i>tufA</i>	90	90	95	96	97	96	96	93	95	95	95	97		95	94	92	92	89	88	86	87	88	88	87	87	87	89	89	94	92	91	91	92	86	86	85	86	85		
14. <i>E. laecobis</i> <i>tufA</i>	91	91	90	89	96	97	94	94	94	95	96	90	89		94	94	93	87	87	88	87	87	86	88	87	87	88	87	93	91	89	90	91	93	86	86	85	85	85	
15. <i>E. aschoerolycus</i> <i>tufA</i>	91	91	91	90	87	90	89	91	89	92	91	89	89	92		94	92	86	87	85	87	86	84	86	85	87	87	92	90	89	89	89	90	84	85	84	84	84		
16. <i>E. sulfureus</i> <i>tufA</i>	91	89	90	91	88	88	90	91	89	92	91	88	89	91	94		91	85	84	81	84	85	84	84	81	84	85	85	91	90	87	88	89	91	82	83	83	82	82	
17. <i>E. solitarius</i> <i>tuf</i>	83	84	83	83	84	83	82	84	83	84	84	84	83	84	83	83		88	87	88	87	87	86	87	88	88	88	88	89	92	91	89	90	90	91	86	85	85	85	84
18. <i>E. avium</i> <i>tufB</i>	77	77	78	78	78	77	78	78	77	78	77	78	78	78	77	76	77		93	93	94	94	94	92	98	93	99	97	87	86	87	86	85	86	89	88	87	85	86	
19. <i>E. casseliflavus</i> <i>tufB</i>	71	72	72	72	70	72	72	70	71	72	72	72	70	72	72	68	72	79		93	95	95	96	95	93	93	94	94	87	86	88	88	84	85	90	90	89	88	86	
20. <i>E. dispar</i> <i>tufB</i>	76	78	77	77	77	77	77	76	77	76	77	77	77	77	78	75	78	82	79		91	91	92	91	94	92	93	93	86	83	85	85	82	84	89	89	87	87	86	
21. <i>E. durans</i> <i>tufB</i>	77	78	78	78	78	77	78	77	78	77	78	77	77	78	78	75	83	80	82		98	95	97	94	97	95	94	87	86	88	88	84	85	90	91	89	88	89		
22. <i>E. faecium</i> <i>tufB</i>	76	75	76	76	75	77	76	76	75	78	77	77	77	76	74	80	78	79	86		96	97	95	97	95	94	87	87	88	88	84	86	90	90	89	87	87			
23. <i>E. gallinarum</i> <i>tufB</i>	72	73	72	73	72	74	72	71	72	72	72	72	72	73	72	72	78	81	77	81		82	94	94	95	95	94	85	87	89	89	84	86	90	90	89	87	88		
24. <i>E. hirae</i> <i>tufB</i>	75	74	75	75	75	75	75	75	75	75	75	74	74	74	75	72	74	80	79	79	84		83	79	93	87	93	94	87	85	86	88	83	85	89	90	88	88	87	
25. <i>E. malodoratus</i> <i>tufB</i>	78	76	76	77	77	77	77	74	77	76	76	77	75	77	77	73	78	90	79	83	81	80		77	79	93	98	97	87	86	87	87	85	86	88	89	87	85	88	
26. <i>E. mundtii</i> <i>tufB</i>	74	74	74	75	73	74	74	74	74	74	74	74	74	74	75	74	71	73	80	80	78	85	85	80	84	80		94	87	86	88	88	84	86	90	90	89	88	89	
27. <i>E. pseudovarum</i> <i>tufB</i>	77	77	78	77	78	77	77	77	76	78	78	77	77	78	78	77	77	78	91	80	85	84	81	79	80	91	80		96	88	87	88	87	85	87	90	89	88	86	87
28. <i>E. raffinosus</i> <i>tufB</i>	78	79	79	78	77	77	78	78	77	79	79	78	78	78	79	77	79	90	79	84	84	81	77	80	90	81	92		87	85	87	88	84	86	90	89	88	88	87	
29. <i>E. adiacens</i> <i>tuf</i>	88	87	87	86	88	86	86	89	88	88	87	88	88	88	88	90	82	77	70	76	77	76	71	73	77	73	78	78		90	88	89	90	91	85	86	84	85	83	
30. <i>B. subtilis</i> <i>tuf</i>	81	80	79	79	80	80	79	79	79	80	81	80	81	81	80	78	78	73	69	73	73	71	70	71	72	71	74	74		78	91	82	90	90	82	82	83	82	84	
31. <i>L. monocytogenes</i> <i>tuf</i>	82	81	82	82	82	82	82	81	81	81	82	81	81	81	81	79	79	76	71	75	75	73	74	75	73	79	76	79		82	99	88	90	84	84	84	84	84	84	
32. <i>L. seeligen</i> <i>tuf</i>	82	81	82	82	82	81	82	81	82	81	82	81	82	80	81	78	79	78	71	76	75	74	73	75	75	73	77	76		79	82	99	88	91	84	85	85	84	85	
33. <i>S. aureus</i> <i>tuf</i>	84	84	83	83	83	84	84	82	84	83	84	86	88	84	82	81	79	75	69	75	75	73	69	72	74	72	74	74		74	83	79	81	81	96	81	82	82	80	82
34. <i>S. epidermidis</i> <i>tuf</i>	83	85	83	84	83	84	84	82	84	83	83	86	87	85	83	82	79	75	69	75	75	73	68	72	74	72	74	75		81	79	82	81	94	83	83	83	83	83	
35. <i>S. mutans</i> <i>tuf</i>	76	77	78	76	78	77	76	75	76	76	76	77	76	76	76	74	78	79	72	77	78	77	74	75	78	75	78	81		77	75	76	77	74	73	97	96	94	88	
36. <i>S. pneumoniae</i> <i>tuf</i>	78	77	76	77	77	77	77	75	78	76	76	77	76	77	75	74	75	78	72	76	78	76	73	74	77	75	75	78	75		76	77	76	74	74	87	96	96	89	
37. <i>S. pyogenes</i> <i>tuf</i>	78	77	76	77	76	75	77	74	77	76	75	78	75	77	75	73	75	74	71	75	78	75	73	74	75	75	75	77		76	77	76	76	73	72	87	93	94	89	
38. <i>S. suis</i> <i>tuf</i>	74	78	76	76	74	75	76	74	78	76	77	77	75	78	76	73	75	74	71	75	78	74	70	74	75	73	73	77		77	77	77								

Table 19. Strains analyzed in Example 43.

Taxon	Strain*	Strain†	16S rDNA sequence accession number
<i>Cedecea</i>	ATCC 33431 ^T		
<i>Cedecea lapagei</i>	ATCC 33432 ^T		
<i>Cedecea neteri</i>	ATCC 33855 ^T		
<i>Citrobacter amalonaticus</i>	ATCC 25405 ^T	CDC 9020-77 ^T	AF025370
<i>Citrobacter braakii</i>	ATCC 43162		
		CDC 080-58 ^T	AF025368
<i>Citrobacter farmeri</i>	ATCC 51112 ^T	CDC 2991-81 ^T	AF025371
<i>Citrobacter freundii</i>	ATCC 8090 ^T	DSM 30039 ^T	AJ233408
<i>Citrobacter koseri</i>	ATCC 27156 ^T		
<i>Citrobacter sedlakii</i>	ATCC 51115 ^T	CDC 4696-86 ^T	AF025364
<i>Citrobacter werkmanii</i>	ATCC 51114 ^T	CDC 0876-58 ^T	AF025373
<i>Citrobacter youngae</i>	ATCC 29935 ^T		
<i>Edwardsiella hoshinae</i>	ATCC 33379 ^T		
<i>Edwardsiella tarda</i>	ATCC 15947 ^T		
		CDC 4411-68	AF015259
<i>Enterobacter aerogenes</i>	ATCC 13048 ^T	JCM 1235 ^T	AB004750
<i>Enterobacter agglomerans</i>	ATCC 27989		
<i>Enterobacter amnigenus</i>	ATCC 33072 ^T	JCM 1237 ^T	AB004749
<i>Enterobacter asburiae</i>	ATCC 35953 ^T	JCM 6051 ^T	AB004744
<i>Enterobacter cancerogenus</i>	ATCC 35317 ^T		
<i>Enterobacter cloacae</i>	ATCC 13047 ^T		
<i>Enterobacter gergoviae</i>	ATCC 33028 ^T	JCM 1234 ^T	AB004748
<i>Enterobacter hormaechei</i>	ATCC 49162 ^T		
<i>Enterobacter sakazakii</i>	ATCC 29544 ^T	JCM 1233 ^T	AB004746
<i>Escherichia coli</i>	ATCC 11775 ^T	ATCC 11775 ^T	X80725
<i>Escherichia coli</i>	ATCC 25922	ATCC 25922	X80724
<i>Escherichia coli</i> (ETEC)	ATCC 35401		
<i>Escherichia coli</i> (O157:H7)	ATCC 43895	ATCC 43895	Z83205
<i>Escherichia fergusonii</i>	ATCC 35469 ^T		
<i>Escherichia hermanii</i>	ATCC 33650 ^T		
<i>Escherichia vulneris</i>	ATCC 33821 ^T	ATCC 33821 ^T	X80734
<i>Ewingella americana</i>	ATCC 33852 ^T		
		NCPPB 3905	X88848
<i>Hafnia alvei</i>	ATCC 13337 ^T	ATCC 13337 ^T	M59155
<i>Klebsiella ornithinolytica</i>	ATCC 31898		
		CIP 103.364	U78182
<i>Klebsiella oxytoca</i>	ATCC 33496		
		ATCC 13182 ^T	U78183
<i>Klebsiella planticola</i>	ATCC 33531 ^T	JCM 7251 ^T	AB004755
<i>Klebsiella pneumoniae</i>			
subsp. <i>pneumoniae</i>	ATCC 13883 ^T	DSM 30104 ^T	AJ233420
subsp. <i>ozaenae</i>	ATCC 11296 ^T	ATCC 11296 ^T	Y17654
subsp. <i>rhinoscleromatis</i>	ATCC 13884 ^T		

Table 19. Strains analyzed in Example 43 (continued).

Taxon	Strain*	Strain†	16S rDNA sequence accession number
<i>Kluyvera ascorbata</i>	ATCC 33433 ^T	ATCC 14236	Y07650
<i>Kluyvera cryocrescens</i>	ATCC 33435 ^T		
<i>Kluyvera georgiana</i>	ATCC 51603 ^T		
<i>Leclercia adecarboxylata</i>	ATCC 23216 ^T		
<i>Leminorella grimontii</i>	ATCC 33999 ^T	DSM 5078 ^T	AJ233421
<i>Moellerella wisconsensis</i>	ATCC 35017 ^T		
<i>Morganella morganii</i>	ATCC 25830 ^T		
<i>Pantoea agglomerans</i>	ATCC 27155 ^T	DSM 3493 ^T	AJ233423
<i>Pantoea dispersa</i>	ATCC 14589 ^T		
<i>Plesiomonas shigelloides</i>	ATCC 14029 ^T		
<i>Pragia fontium</i>	ATCC 49100 ^T	DSM 5563 ^T	AJ233424
<i>Proteus mirabilis</i>	ATCC 25933		
<i>Proteus penneri</i>	ATCC 33519 ^T		
<i>Proteus vulgaris</i>	ATCC 13315 ^T	DSM 30118 ^T	AJ233425
<i>Providencia alcalifaciens</i>	ATCC 9886 ^T		
<i>Providencia rettgeri</i>	ATCC 9250		
<i>Providencia rustigianii</i>	ATCC 33673 ^T		
<i>Providencia stuartii</i>	ATCC 33672		
<i>Rahnella aquatilis</i>	ATCC 33071 ^T	DSM 4594 ^T	AJ233426
<i>Salmonella choleraesuis</i>			
subsp. <i>arizonae</i>	ATCC 13314 ^T		
subsp. <i>choleraesuis</i>			
serotype Choleraesuis	ATCC 7001		
serotype Enteritidis‡	ATCC 13076 ^T	SE22	SE22
serotype Gallinarum	ATCC 9184		
serotype Heidelberg	ATCC 8326		
serotype Paratyphi A	ATCC 9150		
serotype Paratyphi B	ATCC 8759		
serotype Typhi‡	ATCC 10749	St111	U88545
serotype Typhimurium‡	ATCC 14028		
serotype Virchow	ATCC 51955		
subsp. <i>dianzonae</i>	ATCC 43973 ^T		
subsp. <i>houtenae</i>	ATCC 43974 ^T		
subsp. <i>indica</i>	ATCC 43976 ^T		
subsp. <i>salamae</i>	ATCC 43972 ^T		
<i>Serratia fonticola</i>	DSM 4576 ^T	DSM 4576 ^T	AJ233429
<i>Serratia grimesii</i>	ATCC 14460 ^T	DSM 30063 ^T	AJ233430
<i>Serratia liquefaciens</i>	ATCC 27592 ^T		
<i>Serratia marcescens</i>	ATCC 13880 ^T	DSM 30121 ^T	AJ233431
<i>Serratia odorifera</i>	ATCC 33077 ^T	DSM 4582 ^T	AJ233432
<i>Serratia plymuthica</i>	DSM 4540 ^T	DSM 4540 ^T	AJ233433
<i>Serratia rubidaea</i>	DSM 4480 ^T	DSM 4480 ^T	AJ233436
<i>Shigella boydii</i>	ATCC 9207	ATCC 9207	X96965
<i>Shigella dysenteriae</i>	ATCC 11835	ATCC 13313 ^T	X96966
		ATCC 25931	X96964

Table 19. Strains analyzed in Example 43 (continued).

Taxon	Strain*	Strain†	16S rDNA sequence accession number
<i>Shigella flexneri</i>	ATCC 12022	ATCC 12022	X96963
<i>Shigella sonnei</i>	ATCC 29930 ^T		
<i>Tatumella pyseos</i>	ATCC 33301 ^T	DSM 5000 ^T	AJ233437
<i>Trabulsiella guamensis</i>	ATCC 49490 ^T		
<i>Yersinia enterocolitica</i>	ATCC 9610 ^T	ATCC 9610 ^T	M59292
<i>Yersinia frederiksenii</i>	ATCC 33641 ^T		
<i>Yersinia intermedia</i>	ATCC 29909 ^T		
<i>Yersinia pestis</i>	RRB KIMD27		
		ATCC 19428 ^T	X75274
<i>Yersinia pseudotuberculosis</i>	ATCC 29833 ^T		
<i>Yersinia rohdei</i>	ATCC 43380 ^T	ER-2935 ^T	X75276
<i>Shewanella putrefaciens</i>	ATCC 8071 ^T		
<i>Vibrio cholerae</i>	ATCC 25870		
		ATCC.14035 ^T	X74695

T Type strain

5 *Strains used in this study for sequencing of partial *tuf* and *atpD* genes. SEQ ID NOs. for *tuf* and *atpD* sequences corresponding to the above reference strains are given in table 7.

†Strains used in other studies for sequencing of 16S rDNA gene. When both strain numbers are on the same row, both strains are considered to be the same although strain numbers may be different.

‡Phylogenetic serotypes considered species by the Bacteriological Code (1990 Revision).

Table 20. PCR primer pairs used in this study

Primer SEQ ID NO.	Sequence	Nucleotide positions*	Amplicon length (bp)
<i>tuf</i>			
664	5'-AAYATGATACIGGIGCIGCICARATGGA- 3'	271-299	884
697	5'-CCIACIGTICKICCRCCYTCRCG-3'	1132-1156	
<i>atpD</i>			
568	5'-RTIATIGGIGCIGTIRTIGAYGT-3'	25-47	884
567	5'-TCRTCIGCIGGIACRTAIAYIGCYTG-3'	883-908	
700	5'-TIRTIGAYGTCGARTTCCCTCARG-3'	38-61	871
567	5'-TCRTCIGCIGGIACRTAIAYIGCYTG-3'	883-908	

- 5 *The nucleotide positions given are for *E. coli tuf* and *atpD* sequences (GenBank accession no. AE000410 and V00267, respectively). Numbering starts from the first base of the initiation codon.

Table 21. Selection of *M. catarrhalis*-specific primer pairs from SEQ ID NO: 29¹ (466 pb DNA fragment) other than those previously tested².

Primer	Sequence	Amplicon size (bp)	<i>Moraxella catarrhalis</i> ATCC 43628	<i>Moraxella catarrhalis</i> ATCC 53879	<i>Moraxella nonliquefaciens</i>	<i>Moraxella lacunata</i>	<i>Moraxella osloensis</i>	<i>Moraxella atlantae</i>	<i>Moraxella phenylpyruvica</i>	<i>Kingella indologenes</i>	<i>Kingella kingae</i>	<i>Neisseria meningitidis</i>	<i>Neisseria gonorrhoeae</i>	<i>Escherichia coli</i>	<i>Staphylococcus aureus</i>
SEQ ID NO:118	CGCTGACGGCTTGTGTGACCA	118	+	+	-	-	-	-	-	-	-	-	-	-	-
SEQ ID NO:119	TGTTTTGAGCTTTTATTTTGA														
VBmcat1	TGCTTAAGATTACCTCTGCCATTTT	93	+	+	-	-	-	-	-	-	-	-	-	-	-
VBmcat2	TAAGTCGCTGACGGCTTGT														
VBmcat3	CCTGCACCACAAAGTCATCAT	140	+	+	-	-	-	-	-	-	-	-	-	-	-
VBmcat4	AATTCACCAACAATGTCAAAGC														
VBmcat5	AATGATAACCAGTCAAGCAAGC	219	+	+	-	-	-	-	-	-	-	-	-	-	-
VBmcat6	GGTGCAATGGTGATTGTAAAA														
VBmcat7	GTGTGCCGTTCACTTTTACAAAT	160	+	+	-	-	-	-	-	-	-	-	-	-	-
VBmcat8	GGTGTAAAGCTGATGATGAGAG														
VBmcat9	TGACCATGCACACCCCTTATT	167	+	+	-	-	-	-	-	-	-	-	-	-	-
VBmcat10	TCATTGGGATGAAAGTATCGTT														

¹ SEQ ID NO. from US patent 6,001,564.

² All PCR assays were performed with 1 ng of purified genomic DNA by using an annealing temperature of 55°C and 30 cycles of amplification. The genomic DNA from the various bacterial species above was always isolated from reference strains obtained from ATCC.

³ All positive results showed a strong amplification signal with genomic DNA from the target species *M. catarrhalis*.

Table 22. Selection of *S. epidermidis*-specific primer pairs from SEQ ID NO: 36¹ (705 pb DNA fragment) other than those previously tested.

Primer	Sequence (all 25 nucleotides)	Amplicon size (bp)	<i>Staphylococcus epidermidis</i> ATCC 14990	<i>Staphylococcus epidermidis</i> ATCC 12228	<i>Staphylococcus capitis</i>	<i>Staphylococcus cohnii</i>	<i>Staphylococcus aureus</i>	<i>Staphylococcus auricularis</i>	<i>Staphylococcus</i>	<i>Staphylococcus hominis</i>	<i>Staphylococcus</i>	<i>Staphylococcus simulans</i>	<i>Staphylococcus warneri</i>	<i>Bacillus subtilis</i>	<i>Enterococcus faecalis</i>	<i>Enterococcus faecium</i>	<i>Enterococcus gallinarum</i>	<i>Listeria monocytogenes</i>	<i>Streptococcus agalactiae</i>	<i>Streptococcus pneumoniae</i>	<i>Streptococcus pyogenes</i>	Annealing temperature ² (°C)
SEQ ID NO:145	ATCAAAAAGTTGGCAACCTTTTCA	125	3	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	55
SEQ ID NO:146	CAAAAGAGCGTGGAGAAAAGTATCA				-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	55
VBsep3	CATAGTCTGATTGCTCAAAAGTCTTG	208	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	60
VBsep4	GCGAATAGTGAACATACATTCTGTG				-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	55
VBsep5	CACGCTCTTTTGCAATTTCATTTGA	208	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	55
VBsep6	GAAGCAAAATATTCAAAATGCACAG				-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	65
VBsep7	AAAGTCTTTTGCTTCTTCAGATTCA	177	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	55
VBsep8	GTGTTTCACAGGTATGGATGCTCTTA				-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	60
VBsep9	GAGCATCCATACCTGTGAACACAGA	153	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	65
VBsep10	TTTTTCCAATTACAAAGAGACATCAGT				-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	55
VBsep11	TTTGAATTTCGCATGTACTTTGTTTG	135	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	60
VBsep12	CCCCGGGTTTCGAAATCGATAAAAAG				-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	65
			+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	55

¹ SEQ ID NO. from US patent 6,001,564.

² All PCR assays were performed with 1 ng of purified genomic DNA by using an annealing temperature of 55 to 65°C and 30 cycles of amplification. The genomic DNA from the various bacterial species above was always isolated from reference strains obtained from ATCC.

³ All positive results showed a strong amplification signal with genomic DNA from the target species *S. epidermidis*. The intensity of the positive amplification signal with species other than *S. epidermidis* was variable.

NT = not tested.

Table 23. Influence of nucleotide variation(s) on the efficiency of the PCR amplification: Example with SEQ ID NO: 146 from *S. epidermidis*.

Primer ¹	Sequence (all 25 nucleotides)	Number of mutation	Staphylococcus epidermidis ² ATCC 14990					Staphylococcus aureus ³	
			50°C		55°C				
			1	1	0,1	0,01	1		
SEQ ID NO:145	ATCAAAAAGTTGCCGAACCTTTTCA	0						50°C	1
SEQ ID NO:146	CAAAAGAGCGTGGAGAAAAGTATCA	0	3 ⁴		2+	+			-
VBmut1	CAAAAGAGCGTGGAGAAAAGTA ⁵ CA	1	3+	3+	2+	+			-
VBmut2	CAAAAGAGCGTGGAGAAA ⁶ ATATCA	1	3+	3+	2+	+			-
VBmut3	CAAAAGAGCGTGGAGA ⁷ AAAGTATCA	1	3+	3+	2+	+			-
VBmut4	CAAAAGAGCGTGG ⁸ GAAAAAGTATCA	1	3+	3+	2+	+			-
VBmut5	CAAAAGAGCG ⁹ GGAGAAAAGTATCA	1	3+	3+	2+	+			-
VBmut6	CAAAAGA ¹⁰ CGTGGAGAAAAGTATCA	1	3+	3+	2+	+			-
VBmut7	CAAAGGAGCGTGGAGAAAAGTATCA	1	3+	3+	2+	+			-
VBmut8	C ¹¹ TAAAGAGCGTGGAGAAAAGTATCA	1	3+	3+	2+	+			-
VBmut9	CAAAAGAGCGTGGAGA ¹² AAAGTA ¹³ CA	2	3+	3+	2+	+			-
VBmut10	CAAAAGAGCG ¹⁴ GGAGA ¹⁵ GAAGTATCA	2	3+	3+	2+	+			-
VBmut11	CAAAGGAGCG ¹⁶ GGAGAAAAGTATCA	2	3+	3+	2+	+			-
VBmut12	CAAAGGAGCGTGG ¹⁷ GAAAAAGTA ¹⁸ CA	3	3+	3+	2+	+			-
VBmut13	CAAAGGAGCG ¹⁹ GGAGA ²⁰ GAAGTA ²¹ CA	4	3+	2+	+	-			-

¹ All PCR tests were performed with SEQ ID NO:145 without modification combined with SEQ ID NO:146 or 13 modified versions of SEQ ID NO:146. Boxed nucleotides indicate changes in SEQ ID NO:146. All SEQ ID NOs. are from US patent 6,001,564.

² The tests with *S. epidermidis* were performed by using an annealing temperature of 55°C with 1, 0,1 and 0,01 ng of purified genomic DNA or at 50°C with 1 ng of purified genomic DNA.

³ The tests with *S. aureus* were performed only at 50°C with 1 ng of genomic DNA.

⁴ The intensity of the positive amplification signal was quantified as follows: 3+ = strong signal, 2+ = intermediate signal and + = weak signal.

Table 24. Effect of the primer length on the efficiency of the PCR amplification¹: Example with the AT-rich SEQ ID NO: 145² and SEQ ID NO: 146² from *S. epidermidis*.

Primer	Sequence	Length (nt)	45°C						Staphylococcus aureus ³			Staphylococcus haemolyticus			Staphylococcus capitis			Staphylococcus warneri		
			55°C			45°C			1	0,1	0,01	1	0,1	0,01	45	55	45	55	45	55
			1	0,1	0,01	1	0,1	0,01												
VBsep301	ATATCATCAAAAAGTTGGCGAACCTTTTCA	30	NT	NT	NT	4+	3+	2+	NT	NT	NT	45	55	45	55	45	55	NT	NT	-
VBsep302	AATGCAAAAAGAGCGTGGAGAAAAGTATCA	30	4+ ⁵	3+	2+	4+	3+	2+	4+	3+	2+	45	55	45	55	45	55	NT	NT	-
SEQ ID NO:145	ATCAAAAAGTTGGCGAACCTTTTCA	25	4+ ⁵	3+	2+	4+	3+	2+	4+	3+	2+	45	55	45	55	45	55	NT	NT	-
SEQ ID NO:146	CAAAAAGAGCGTGGAGAAAAGTATCA	25	4+ ⁵	3+	2+	4+	3+	2+	4+	3+	2+	45	55	45	55	45	55	NT	NT	-
VBsep201	AAAGTTGGCGAACCTTTTCA	20	NT	NT	NT	4+	3+	2+	NT	NT	NT	45	55	45	55	45	55	NT	NT	-
VBsep202	GAGCGTGGAGAAAAGTATCA	20	4+	3+	2+	4+	3+	2+	4+	3+	2+	45	55	45	55	45	55	NT	NT	-
VBsep171	GTGGCGAACCTTTTCA	17	4+	3+	2+	4+	3+	2+	4+	3+	2+	45	55	45	55	45	55	NT	NT	-
VBsep172	CGTGGAGAAAAGTATCA	17	4+	3+	2+	4+	3+	2+	4+	3+	2+	45	55	45	55	45	55	NT	NT	-
VBsep151	TGGCGAACCTTTTCA	15	3+	2+	+	-	-	-	3+	2+	+	45	55	45	55	45	55	NT	NT	-
VBsep152	TGGAGAAAAGTATCA	15	3+	2+	+	-	-	-	3+	2+	+	45	55	45	55	45	55	NT	NT	-

¹ All PCR tests were performed using an annealing temperature of 45 or 55°C and 30 cycles of amplification.
² All SEQ ID NOs. in this Table are from US patent 6,001,546.
³ The tests with *S. epidermidis* were made with 1, 0,1 and 0,01 ng of purified genomic DNA.
⁴ The tests with all other bacterial species were made only with 1 ng of purified genomic DNA.
⁵ The intensity of the positive amplification signal was quantified as follows: 4+ = very strong signal, 3+ = strong signal, 2+ = intermediate signal and + = weak signal.
NT = not tested.

Table 25. Effect of the primer length on the efficiency of the PCR amplification¹: Example with the GC-rich SEQ ID NO: 83² and SEQ ID NO: 84² from *P. aeruginosa*.

Primer	Sequence	Length (nt)	<i>Pseudomonas aeruginosa</i> ³ ATCC 35554				<i>Pseudomonas fluorescens</i> ⁴	<i>Burkholderia cepacia</i>	<i>Shewanella putida</i>	<i>Stenotrophomonas maltophilia</i>	<i>Neisseria meningitidis</i>	<i>Haemophilus parahaemolyticus</i>
			1	0,1	0,01							
SEQ ID NO 83	CGAGCGGGTGGTGTTCATC	19	2+ ⁵	+	-							
SEQ ID NO 84	CAAGTCGTCGTCGGAGGGA	19										
Pse554-16a	CGAGCGGGTGGTGTTC	16	2+	+	-							
Pse674-16a	GTCGTCGTCGGAGGGA	16										
Pse554-13b	GCGGGTGGTGTTC	13	2+	+	-							
Pse674-13a	GTCGTCGGAGGGA	13										

¹ All PCR tests were performed using an annealing temperature of 55°C and 30 cycles of amplification.

² All SEQ ID NOs. in this Table are from US patent 6,001,546.

³ The tests with *P. aeruginosa* were made with 1, 0,1 and 0,01 ng of purified genomic DNA.

⁴ The tests with all other bacterial species were made only with 1 ng of purified genomic DNA.

⁵ The intensity of the positive amplification signal was quantified as follows: 2+ = strong signal and + = moderately strong signal.

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences).

		Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO. Nucleotide position
10	Bacterial species: <i>Acinetobacter baumannii</i>		
	1692	5'-GGT GAG AAC TGT GGT ATC TTA CTT	1 478-501
	1693 ^a	5'-CAT TTC AAC GCC TTC TTT CAA CTG	1 691-714
15	Bacterial species: <i>Chlamydia pneumoniae</i>		
	630	5'-CGG AGC TAT CCT AGT CGT TTC A	20 2-23
	629 ^a	5'-AAG TTC CAT CTC AAC AAG GTC AAT A	20 146-170
20	2085	5'-CAA ACT AAA GAA CAT ATC TTG CTA	20 45-68
	2086 ^a	5'-ATA TAA TTT GCA TCA CCT TCA AG	20 237-259
	2087	5'-TCA GCT CGT GGG ATT AGG AGA G	20 431-452
	2088 ^a	5'-AGG CTT CAC GCT GTT AGG CTG A	20 584-605
25	Bacterial species: <i>Chlamydia trachomatis</i>		
	554	5'-GTT CCT TAC ATC GTT GTT TTT CTC	22 82-105
	555 ^a	5'-TCT CGA ACT TTC TCT ATG TAT GCA	22 249-272
30	Parasitical species: <i>Cryptosporidium parvum</i>		
	798	5'-TGG TTG TCC CAG CCG ATC GTT T	865 158-179
	804 ^a	5'-CCT GGG ACG GCC TCT GGC AT	865 664-683
35	799	5'-ACC TGT GAA TAC AAG CAA TCT	865 280-300
	805 ^a	5'-CTC TTG TCC ATC TTA GCA GT	865 895-914
	800	5'-GAT GAA ATC TTC AAC GAA GTT GAT	865 307-330
40	806 ^a	5'-AGC ATC ACC AGA CTT GAT AAG	865 946-966
	801	5'-ACA ACA CCG AGA AGA TCC CA	865 353-372
	803 ^a	5'-ACT TCA GTG GTA ACA CCA GC	865 616-635
45	802	5'-TTG CCA TTT CTG GTT TCG TT	865 377-396
	807 ^a	5'-AAA GTG GCT TCA AAG GTT GC	865 981-1000
	Bacterial species: <i>Enterococcus faecium</i>		
50	1696	5'-ATG TTC CTG TAG TTG CTG GA	64 189-208
	1697 ^a	5'-TTT CTT CAG CAA TAC CAA CAA C	64 422-443
	Bacterial species: <i>Klebsiella pneumoniae</i>		
55	1329	5'-TGT AGA GCG CGG TAT CAT CAA AGT A	103 352-377
	1330 ^a	5'-AGA TTC GAA CTT GGT GTG CGG G	103 559-571

^a These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex I: Specific and ubiquitous primers for nucleic acid amplification (*tuf* sequences) (continued).

		Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO. Nucleotide position
10	<u>Bacterial species:</u> <i>Mycoplasma pneumoniae</i>		
	2093	5'-TGT TGG CAA TCG AAG ACA CC	2097 ^a 635-654
	2094 ^b	5'-TTC AAT TTC TTG ACC TAC TTT CAA	2097 ^a 709-732
15	<u>Bacterial species:</u> <i>Neisseria gonorrhoeae</i>		
	551	5'-GAA GAA AAA ATC TTC GAA CTG GCT A	126 256-280
	552 ^b	5'-TAC ACG GCC GGT GAC TAC G	126 378-396
20	2173	5'-AAG AAA AAA TCT TCG AAC TGG CTA	126 257-280
	2174 ^b	5'-TCT ACA CGG CCG GTG	126 384-398
	2175	5'-CCG CCA TAC CCC GTT T	126 654-669
	2176 ^b	5'-CGG CAT TAC CAT TTC CAC ACC TTT	126 736-759
25	<u>Bacterial species:</u> <i>Pseudomonas aeruginosa</i>		
	1694	5'-AAG GCA AGG ATG ACA ACG GC	153 231-250
	1695 ^b	5'-ACG ATT TCC ACT TCT TCC TGG	153 418-438
30	<u>Bacterial species:</u> <i>Streptococcus agalactiae</i>		
	549	5'-GAA CGT GAT ACT GAC AAA CCT TTA	207-210 ^c 308-331 ^d
	550 ^b	5'-GAA GAA GAA CAC CAA CGT TG	207-210 ^c 520-539 ^d
35	<u>Bacterial species:</u> <i>Streptococcus pyogenes</i>		
	999	5'-TTG ACC TTG TTG ATG ACG AAG AG	1002 143-165
	1000 ^b	5'-TTA GTG TGT GGG TTG ATT GAA CT	1002 622-644
40	1001	5'-AAG AGT TGC TTG AAT TAG TTG AG	1002 161-183
	1000 ^b	5'-TTA GTG TGT GGG TTG ATT GAA CT	1002 622-644
45	<u>Parasitical species:</u> <i>Trypanosoma brucei</i>		
	820	5'-GAA GGA GGT GTC TGC TTA CAC	864 513-533
	821 ^b	5'-GGC GCA AAC GTC ACC ACA TCA	864 789-809
	820	5'-GAA GGA GGT GTC TGC TTA CAC	864 513-533
50	822 ^b	5'-CGG CGG ATG TCC TTA ACA GAA	864 909-929

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^c These sequences were aligned to derive the corresponding primer.

^d The nucleotide positions refer to the *S. agalactiae* *tuf* sequence fragment (SEQ ID NO. 209).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Parasitical species:</u> <i>Trypanosoma cruzi</i>			
	794	5'-GAC GAC AAG TCG GTG AAC TT	840-842 ^a	281-300 ^c
	795 ^b	5'-ACT TGC ACG CGA TGT GGC AG	840-842 ^a	874-893 ^c
15	<u>Bacterial genus:</u> <i>Clostridium</i> sp.			
	796	5'-GGT CCA ATG CCW CAA ACW AGA	32,719-724,736 ^a	32-52 ^d
	797 ^b	5'-CAT TAA GAA TGG YTT ATC TGT SKC TCT	32,719-724,736 ^a	320-346 ^d
20	808	5'-GCI TTA IWR GCA TTA GAA RAY CCA	32,719-724,736 ^a	224-247 ^d
	809 ^b	5'-TCT TCC TGT WGC AAC TGT TCC TCT	32,719-724,736 ^a	337-360 ^d
25	810	5'-AGA GMW ACA GAT AAR SCA TTC TTA	32,719-724,736 ^a	320-343 ^d
	811 ^b	5'-TRA ART AGA ATT GTG GTC TRT ATC C	32,719-724,736 ^a	686-710 ^d
30	<u>Bacterial genus:</u> <i>Corynebacterium</i> sp.			
	545	5'-TAC ATC CTB GTY GCI CTI AAC AAG TG	34-44,662 ^a	89-114 ^e
	546 ^b	5'-CCR CGI CCG GTR ATG GTG AAG AT	34-44,662 ^a	350-372 ^e
35	<u>Bacterial genus:</u> <i>Enterococcus</i> sp.			
	656	5'-AAT TAA TGG CTG CAG TTG AYG A	58-72 ^a	273-294 ^f
	657 ^b	5'-TTG TCC ACG TTC GAT RTC TTC A	58-72 ^a	556-577 ^f
40	656	5'-AAT TAA TGG CTG CAG TTG AYG A	58-72 ^a	273-294 ^f
	271 ^b	5'-TTG TCC ACG TTG GAT RTC TTC A	58-72 ^a	556-577 ^f
	1137	5'-AAT TAA TGG CTG CWG TTG AYG AA	58-72 ^a	273-295 ^f
45	1136 ^b	5'-ACT TGT CCA CGT TSG ATR TCT	58-72 ^a	559-579 ^f

^a These sequences were aligned to derive the corresponding primer.

^b These sequences are from the complementary DNA strand of the sequence of the
50 originating fragment given in the Sequence Listing.

^c The nucleotide positions refer to the *T. cruzi* tuf sequence fragment (SEQ ID NO. 842).

^d The nucleotide positions refer to the *C. perfringens* tuf sequence fragment (SEQ ID NO. 32).

^e The nucleotide positions refer to the *C. diphtheriae* tuf sequence fragment (SEQ ID NO. 662).
55

^f The nucleotide positions refer to the *E. durans* tuf sequence fragment (SEQ ID NO. 61).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial genus:</u> <i>Legionella</i> sp.			
	2081	5'-GRA TYR TYA AAG TTG GTG AGG AAG	111-112 ^a	411-434 ^b
	2082 ^c	5'-CMA CTT CAT CYC GCT TCG TAC C	111-112 ^a	548-569 ^b
15	<u>Bacterial genus:</u> <i>Staphylococcus</i> sp.			
	553	5'-GGC CGT GTT GAA CGT GGT CAA ATC A	176-203 ^a	313-337 ^d
	575 ^c	5'-TIA CCA TTT CAG TAC CTT CTG GTA A	176-203 ^a	653-677 ^d
20	553	5'-GGC CGT GTT GAA CGT GGT CAA ATC A	176-203 ^a	313-337 ^d
	707 ^c	5'-TWA CCA TTT CAG TAC CTT CTG GTA A	176-203 ^a	653-677 ^d
	<u>Bacterial genus:</u> <i>Streptococcus</i> sp.			
25	547	5'-GTA CAG TTG CTT CAG GAC GTA TC	206-231 ^a	372-394 ^e
	548 ^c	5'-ACG TTC GAT TTC ATC ACG TTG	206-231 ^a	548-568 ^e
	<u>Fungal genus:</u> <i>Candida</i> sp.			
30	576	5'-AAC TTC RTC AAG AAG GTY GGT TAC AA	407-426, 428-432 ^a	332-357 ^f
	632 ^c	5'-CCC TTT GGT GGR TCS TKC TTG GA	407-426, 428-432 ^a	791-813 ^f
35	631	5'-CAG ACC AAC YGA IAA RCC ATT RAG AT	407-426, 428-432 ^a	523-548 ^f
	632 ^c	5'-CCC TTT GGT GGR TCS TKC TTG GA	407-426, 428-432 ^a	791-813 ^f
40	633	5'-CAG ACC AAC YGA IAA RCC ITT RAG AT	407-426, 428-432 ^a	523-548 ^f
	632 ^c	5'-CCC TTT GGT GGR TCS TKC TTG GA	407-426, 428-432 ^a	791-813 ^f

45

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *L. pneumophila* tuf sequence fragment (SEQ ID NO. 112).

50 ^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d The nucleotide positions refer to the *S. aureus* tuf sequence fragment (SEQ ID NO. 179).

^e The nucleotide positions refer to the *S. agalactiae* tuf sequence fragment (SEQ ID NO. 209).

55 ^f The nucleotide positions refer to the *C. albicans* tuf(EF-1) sequence fragment (SEQ ID NO. 408).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
5				
10	<u>Fungal genus:</u> <i>Cryptococcus sp.</i>			
	1971	5'-CYG ACT GYG CCA TCC TYA TCA	434,623,1281, 1985,1986 ^a	150-170 ^b
	1973 ^c	5'-RAC ACC RGI YTT GGW ITC CTT	434,623,1281, 1985,1986 ^a	464-484 ^b
15				
	1972	5'-MGI CAG CTC ATY ITT GCW KSC	434,623,1281, 1985,1986 ^a	260-280 ^b
	1973 ^c	5'-RAC ACC RGI YTT GGW ITC CTT	434,623,1281, 1985,1986 ^a	464-484 ^b
20				
	<u>Parasitical genus:</u> <i>Entamoeba sp.</i>			
	703	5'-TAT GGA AAT TCG AAA CAT CT	512	38-57
25	704 ^c	5'-AGT GCT CCA ATT AAT GTT GG	512	442-461
	703	5'-TAT GGA AAT TCG AAA CAT CT	512	38-57
	705 ^c	5'-GTA CAG TTC CAA TAC CTG AA	512	534-553
30	703	5'-TAT GGA AAT TCG AAA CAT CT	512	38-57
	706 ^c	5'-TGA AAT CTT CAC ATC CAA CA	512	768-787
	793	5'-TTA TTG TTG CTG CTG GTA CT	512	149-168
	704 ^c	5'-AGT GCT CCA ATT AAT GTT GG	512	442-461
35				
	<u>Parasitical genus:</u> <i>Giardia sp.</i>			
	816	5'-GCT ACG ACG AGA TCA AGG GC	513	305-324
	819 ^c	5'-TCG AGC TTC TGG AGG AAG AG	513	895-914
40				
	817	5'-TGG AAG AAG GCC GAG GAG TT	513	355-374
	818 ^c	5'-AGC CGG GCT GGA TCT TCT TC	513	825-844
	<u>Parasitical genus:</u> <i>Leishmania sp.</i>			
45				
	701	5'-GTG TTC ACG ATC ATC GAT GCG	514-526 ^a	94-114 ^d
	702 ^c	5'-CTC TCG ATA TCC GCG AAG CG	514-526 ^a	913-932 ^d

- 50 ^a These sequences were aligned to derive the corresponding primer.
- ^b The nucleotide positions refer to the *C. neoformans tuf* (EF-1) sequence fragment (SEQ ID NO. 623).
- ^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.
- 55 ^d The nucleotide positions refer to the *L. tropica tuf*(EF-1) sequence fragment (SEQ ID NO. 526).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (*tuf* sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Parasitical genus:</u> <i>Trypanosoma</i> sp.			
	823	5'-GAG CGG TAT GAY GAG ATT GT	529,840- 842,864 ^a	493-512 ^b
	824 ^c	5'-GGC TTC TGC GGC ACC ATG CG	529,840- 842,864 ^a	1171-1190 ^b
15	<u>Bacterial family:</u> <i>Enterobacteriaceae</i>			
	933	5'-CAT CAT CGT ITT CMT GAA CAA RTG	78,103,146, 168,238,698 ^a	390-413 ^d
20	934 ^c	5'-TCA CGY TTR RTA CCA CGC AGI AGA	78,103,146, 168,238,698 ^a	831-854 ^d
25	<u>Bacterial family:</u> <i>Mycobacteriaceae</i>			
	539	5'-CCI TAC ATC CTB GTY GCI CTI AAC AAG	122	85-111
	540 ^c	5'-GGD GCI TCY TCR TCG WAI TCC TG	122	181-203
30	<u>Bacterial group:</u> <i>Escherichia coli</i> and <i>Shigella</i>			
	1661	5'-TGG GAA GCG AAA ATC CTG	1668 ^e	283-300
	1665 ^c	5'-CAG TAC AGG TAG ACT TCT G	1668 ^e	484-502
35	<u>Bacterial group:</u> <i>Pseudomonads</i> group			
	541	5'-GTK GAA ATG TTC CGC AAG CTG CT	153-155 ^a	476-498 ^f
	542 ^c	5'-CGG AAR TAG AAC TGS GGA CGG TAG	153-155 ^a	679-702 ^f
	541	5'-GTK GAA ATG TTC CGC AAG CTG CT	153-155 ^a	476-498 ^f
40	544 ^c	5'-AYG TTG TCG CCM GGC ATT MCC AT	153-155 ^a	749-771 ^f

^a These sequences were aligned to derive the corresponding primer.

45 ^b The nucleotide positions refer to the *T. brucei tuf* (EF-1) sequence fragment (SEQ ID NO. 864).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

50 ^d The nucleotide positions refer to the *E. coli tuf* sequence fragment (SEQ ID NO. 698).

^e Sequence from databases.

^f The nucleotide positions refer to the *P. aeruginosa tuf* sequence fragment (SEQ ID NO. 153).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Parasitical group:</u> <i>Trypanosomatidae</i> family			
	923	5'-GAC GCI GCC ATC CTG ATG ATC	511,514-526, 529,840-842, 864 ^a	166-188 ^b
15	924 ^c	5'-ACC TCA GTC GTC ACG TTG GCG	511,514-526, 529,840-842, 864 ^a	648-668 ^b
20	925	5'-AAG CAG ATG GTT GTG TGC TG	511,514-526, 529,840-842, 864 ^a	274-293 ^b
	926 ^c	5'-CAG CTG CTC GTG GTG CAT CTC GAT	511,514-526, 529,840-842, 864 ^a	676-699 ^b
25	927	5'-ACG CGG AGA AGG TGC GCT T	511,514-526, 529,840-842, 864 ^a	389-407 ^b
30	928 ^c	5'-GGT CGT TCT TCG AGT CAC CGC A	511,514-526, 529,840-842, 864 ^a	778-799 ^b
Universal primers (bacteria)				
35	636	5'-ACT GGY GTT GAI ATG TTC CGY AA	7,54,78, 100,103,159, 209,224,227 ^b	470-492 ^d
	637 ^c	5'-ACG TCA GTI GTA CGG AAR TAG AA	7,54,78, 100,103,159, 209,224,227 ^b	692-714 ^d
40	638	5'-CCA ATG CCA CAA ACI CGT GAR CAC AT	7,54,78, 100,103,159, 209,224,227 ^b	35-60 ^e
45	639 ^c	5'-TTT ACG GAA CAT TTC WAC ACC WGT IAC A	7,54,78, 100,103,159, 209,224,227 ^b	469-496 ^e

- 50 ^a These sequences were aligned to derive the corresponding primer.
- ^b The nucleotide positions refer to the *L. tropica* tuf (EF-1) sequence fragment (SEQ ID NO. 526).
- ^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.
- 55 ^d The nucleotide positions refer to the *E. coli* tuf sequence fragment (SEQ ID NO. 78).
- ^e The nucleotide positions refer to the *B. cereus* tuf sequence fragment (SEQ ID NO. 7).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Universal primers (bacteria) (continued)			
	643	5'-ACT GGI GTI GAR ATG TTC CGY AA	1,3,4,7,12,13,16,49,54,72,78,85,88,91,94,98,103,108,112,115,116,120,121,126,128,134,136,146,154,159,179,186,205,209,212,224,238 ^a	470-492 ^b
15				
20	644 ^c	5'-ACG TCI GTI GTI CKG AAR TAG AA	same as SEQ ID NO. 643	692-714 ^b
25				
	643	5'-ACT GGI GTI GAR ATG TTC CGY AA	1,3,4,7,12,13,16,49,54,72,78,85,88,91,94,98,103,108,112,115,116,120,121,126,128,134,136,146,154,159,179,186,205,209,212,224,238 ^a	470-492 ^b
30				
35				
	645 ^c	5'-ACG TCI GTI GTI CKG AAR TAR AA	same as SEQ ID NO. 643	692-714 ^b
40	646	5'-ATC GAC AAG CCI TTC YTI ATG SC	2,13,82,122,145 ^a	317-339 ^d
	647 ^c	5'-ACG TCC GTS GTR CGG AAG TAG AAC TG	2,13,82,122,145 ^a	686-711 ^d
45	646	5'-ATC GAC AAG CCI TTC YTI ATG SC	2,13,82,122,145 ^a	317-339 ^d
	648 ^c	5'-ACG TCS GTS GTR CGG AAG TAG AAC TG	2,13,82,122,145 ^a	686-711 ^d

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *E. coli* tuf sequence fragment (SEQ ID NO. 78).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d The nucleotide positions refer to the *A. meyeri* tuf sequence fragment (SEQ ID NO. 2)

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Universal primers (bacteria) (continued)			
	649	5'-GTC CTA TGC CTC ARA CWC GIG AGC AC	8,86,141,143 ^a	33-58 ^b
	650 ^c	5'-TTA CGG AAC ATY TCA ACA CCI GT	8,86,141,143 ^a	473-495 ^b
15	636	5'-ACT GGY GTT GAI ATG TTC CGY AA	8,86,141,143 ^a	473-495 ^b
	651 ^c	5'-TGA CGA CCA CCI TCY TCY TTY TTC A	8,86,141,143 ^a	639-663 ^b
	Universal primers (fungi)			
20	1974	5'-ACA AGG GIT GGR MSA AGG AGA C	404,405,433, 445,898,1268, 1276,1986 ^a	443-464 ^d
	1975 ^c	5'-TGR CCR GGG TGG TTR AGG ACG	404,405,433, 445,898,1268, 1276,1986 ^a	846-866 ^d
25				
	1976	5'-GAT GGA YTC YGT YAA ITG GGA	407-412, 414-426,428- 431,439,443,447, 448,622,624,665, 1685,1987-1990 ^a	286-306 ^e
30				
	1978 ^c	5'-CAT CIT GYA ATG GYA ATC TYA AT	same as SEQ ID NO. 1976	553-575 ^e
35	1977	5'-GAT GGA YTC YGT YAA RTG GGA	same as SEQ ID NO. 1976	286-306 ^e
	1979 ^c	5'-CAT CYT GYA ATG GYA ASC TYA AT	same as SEQ ID NO. 1976	553-575 ^e
40	1981	5'-TGG ACA CCI SCA AGI GGK CYG	401-405, 433,435,436, 438,444,445,449, 453,455,457,779, 781-783,785,786, 788-790,897-903, 1267-1272,1274-1280, 1282-1287,1991-1998 ^a	281-301 ^d
45				
	1980 ^c	5'-TCR ATG GCI TCI AIR AGR GTY T	same as SEQ ID NO. 1981	488-509 ^d
50				

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *B. distasonis* tuf sequence fragment (SEQ ID NO. 8).

55 ^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d The nucleotide positions refer to the *A. fumigatus* tuf (EF-1) sequence fragment (SEQ ID NO. 404).

60 ^e The nucleotide positions refer to the *C. albicans* tuf (EF-1) sequence fragment (SEQ ID NO. 407).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (*tuf* sequences) (continued).

			Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position	
Universal primers (fungi) (continued)				
1982	5'-TGG ACA CYI SCA AGI GGK CYG	same as SEQ ID NO. 1981	281-301 ^a	
1980 ^b	5'-TCR ATG GCI TCI AIR AGR GTY T	same as SEQ ID NO. 1981	488-509 ^a	
1983	5'-CYG AYT GCG CYA TIC TCA TCA	same as SEQ ID NO. 1981	143-163 ^a	
1980 ^b	5'-TCR ATG GCI TCI AIR AGR GTY T	same as SEQ ID NO. 1981	488-509 ^a	
1984	5'-CYG AYT GYG CYA TYC TSA TCA	same as SEQ ID NO. 1981	143-163 ^a	
1980 ^b	5'-TCR ATG GCI TCI AIR AGR GTY T	same as SEQ ID NO. 1981	488-509 ^a	
Sequencing primers				
556	5'-CGG CGC NAT CYT SGT TGT TGC	668 ^c	306-326	
557 ^b	5'-CCM AGG CAT RAC CAT CTC GGT G	668 ^c	1047-1068	
694	5'-CGG CGC IAT CYT SGT TGT TGC	668 ^c	306-326	
557 ^b	5'-CCM AGG CAT RAC CAT CTC GGT G	668 ^c	1047-1068	
664	5'-AAY ATG ATI ACI GGI GCI GCI CAR ATG GA	619 ^c	604-632	
652 ^b	5'-CCW AYA GTI YKI CCI CCY TCY CTI ATA	619 ^c	1482-1508	
664	5'-AAY ATG ATI ACI GGI GCI GCI CAR ATG GA	619 ^c	604-632	
561 ^b	5'-ACI GTI CGG CCR CCC TCA CGG AT	619 ^c	1483-1505	
543	5'-ATC TTA GTA GTT TCT GCT GCT GA	607	8-30	
660 ^b	5'-GTA GAA TTG AGG ACG GTA GTT AG	607	678-700	
658	5'-GAT YTA GTC GAT GAT GAA GAA TT	621	116-138	
659 ^b	5'-GCT TTT TGI GTT TCW GGT TTR AT	621	443-465	
658	5'-GAT YTA GTC GAT GAT GAA GAA TT	621	116-138	
661 ^b	5'-GTA GAA YTG TGG WCG ATA RTT RT	621	678-700	
558	5'-TCI TTY AAR TAY GCI TGG GT	665 ^c	157-176	
559 ^b	5'-CCG ACR GCR AYI GTY TGI CKC AT	665 ^c	1279-1301	
813	5'-AAT CYG TYG AAA TGC AYC ACG A	665 ^c	687-708	
559 ^b	5'-CCG ACR GCR AYI GTY TGI CKC AT	665 ^c	1279-1301	

^a The nucleotide positions refer to the *A. fumigatus tuf* (EF-1) sequence fragment (SEQ ID NO. 404).

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^c Sequences from databases.

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

		Originating DNA fragment		
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Sequencing primers (continued)			
	558	5'-TCI TTY AAR TAY GCI TGG GT	665 ^a	157-176
	815 ^b	5'-TGG TGC ATY TCK ACR GAC TT	665 ^a	686-705
15	560	5'-GAY TTC ATY AAR AAY ATG ATY AC	665 ^a	289-311
	559 ^b	5'-CCG ACR GCR AYI GTY TGI CKC AT	665 ^a	1279-1301
	653	5'-GAY TTC ATI AAR AAY ATG AT	665 ^a	289-308
	559 ^b	5'-CCG ACR GCR AYI GTY TGI CKC AT	665 ^a	1279-1301
20	558	5'-TCI TTY AAR TAY GCI TGG GT	665 ^a	157-176
	655 ^b	5'-CCR ATA CCI CMR ATY TTG TA	665 ^a	754-773
	654	5'-TAC AAR ATY KGI GGT ATY GG	665 ^a	754-773
25	559 ^b	5'-CCG ACR GCR AYI GTY TGI CKC AT	665 ^a	1279-1301
	696	5'-ATI GGI CAY RTI GAY CAY GGI AAR AC	698 ^a	52-77
	697 ^b	5'-CCI ACI GTI CKI CCR CCY TCR CG	698 ^a	1132-1154
30	911	5'-GAC GGM KKC ATG CCG CAR AC	853	22-41
	914 ^b	5'-GAA RAG CTG CGG RCG RTA GTG	853	700-720
	912	5'-GAC GGC GKC ATG CCG CAR AC	846	20-39
	914 ^b	5'-GAA RAG CTG CGG RCG RTA GTG	846	692-712
35	913	5'-GAC GGY SYC ATG CCK CAG AC	843	251-270
	915 ^b	5'-AAA CGC CTG AGG RCG GTA GTT	843	905-925
	916	5'-GCC GAG CTG GCC GGC TTC AG	846	422-441
40	561 ^b	5'-ACI GTI CGG CCR CCC TCA CGG AT	619 ^a	1483-1505
	664	5'-AAY ATG ATI ACI GGI GCI GCI CAR ATG GA	619 ^a	604-632
	917 ^b	5'-TCG TGC TAC CCG TYG CCG CCA T	846	593-614
45				

^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Sequencing primers (continued)			
	1221	5'-GAY ACI CCI GGI CAY GTI GAY TT	1230 ^a	292-314
	1226 ^b	5'-GTI RMR TAI CCR AAC ATY TC	1230 ^a	2014-2033
15	1222	5'-ATY GAY ACI CCI GGI CAY GTI GAY TT	1230 ^a	289-314
	1223 ^b	5'-AYI TCI ARR TGI ARY TCR CCC ATI CC	1230 ^a	1408-1433
	1224	5'-CCI GYI HTI YTI GAR CCI ATI ATG	1230 ^a	1858-1881
	1225 ^b	5'-TAI CCR AAC ATY TCI SMI ARI GGI AC	1230 ^a	2002-2027
20	1227	5'-GTI CCI YTI KCI GAR ATG TTY GGI TA	1230 ^a	2002-2027
	1229 ^b	5'-TCC ATY TGI GCI GCI CCI GTI ATC AT	698 ^a	4-29
	1228	5'-GTI CCI YTI KCI GAR ATG TTY GGI TAY GC	1230 ^a	2002-2030
25	1229 ^b	5'-TCC ATY TGI GCI GCI CCI GTI ATC AT	698 ^a	4-29
	1999	5'-CAT GTC AAY ATT GGT ACT ATT GGT CAT GT	498-500, 502,505,506, 508,619,2004,2005 ^c	25-53 ^d
30	2000 ^b	5'-CCA CCY TCI CTC AMG TTG AAR CGT T	same as SEQ ID NO. 1999	1133-1157 ^d
	2001	5'-ACY ACI TTR ACI GCY GCY ATY AC	same as SEQ ID NO. 1999	67-89 ^d
35	2003 ^b	5'-CAT YTC RAI RTT GTC ACC TGG	same as SEQ ID NO. 1999	1072-1092 ^d
	2002	5'-CCI GAR GAR AGA GCI MGW GGT	same as SEQ ID NO. 1999	151-171 ^d
40	2003 ^b	5'-CAT YTC RAI RTT GTC ACC TGG	same as SEQ ID NO. 1999	1072-1092 ^d

^a Sequences from databases.

45 ^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^c These sequences were aligned to derive the corresponding primer.

^d The nucleotide positions refer to the *C. albicans* tuf sequence fragment (SEQ ID NO. 2004).

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Annex II: Specific and ubiquitous primers for nucleic acid amplification (atpD sequences).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial species:</u> <i>Acinetobacter baumannii</i>			
	1690	5'-CAG GTC CTG TTG CGA CTG AAG AA	243	186-208
	1691 ^b	5'-CAC AGA TAA ACC TGA GTG TGC TTT C	243	394-418
15	<u>Bacterial species:</u> <i>Bacteroides fragilis</i>			
	2134	5'-CGC GTG AAG CTT CTG TG	929	184-200
	2135 ^b	5'-TCT CGC CGT TAT TCA GTT TC	929	395-414
20	<u>Bacterial species:</u> <i>Bordetella pertussis</i>			
	2180	5'-TTC GCC GGC GTG GGC	1672 ^C	544-558
	2181 ^b	5'-AGC GCC ACG CGC AGG	1672 ^C	666-680
25	<u>Bacterial species:</u> <i>Enterococcus faecium</i>			
	1698	5'-GGA ATC AAC AGA TGG TTT ACA AA	292	131-153
	1699 ^b	5'-GCA TCT TCT GGG AAA GGT GT	292	258-277
30	1700	5'-AAG ATG CGG AAA GAA GCG AA	292	271-290
	1701 ^b	5'-ATT ATG GAT CAG TTC TTG GAT CA	292	439-461
	<u>Bacterial species:</u> <i>Klebsiella pneumoniae</i>			
35	1331	5'-GCC CTT GAG GTA CAG AAT GGT AAT GAA GTT	317	88-118
	1332 ^b	5'-GAC CGC GGC GCA GAC CAT CA	317	183-203

^a These sequences were aligned to derive the corresponding primer.

40 ^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^c Sequence from databases.

Annex II: Specific and ubiquitous primers for nucleic acid amplification (atpD sequences).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial species:</u> <i>Streptococcus agalactiae</i>			
	627	5'-ATT GTC TAT AAA AAT GGC GAT AAG TC	379-383 ^a	42-67 ^b
	625 ^c	5'-CGT TGA AGA CAC GAC CCA AAG TAT CC	379-383 ^a	206-231 ^b
15	628	5'-AAA ATG GCG ATA AGT CAC AAA AAG TA	379-383 ^a	52-77 ^b
	625 ^c	5'-CGT TGA AGA CAC GAC CCA AAG TAT CC	379-383 ^a	206-231 ^b
	627	5'-ATT GTC TAT AAA AAT GGC GAT AAG TC	379-383 ^a	42-67 ^b
	626 ^c	5'-TAC CAC CTT TTA AGT AAG GTG CTA AT	379-383 ^a	371-396 ^b
20	628	5'-AAA ATG GCG ATA AGT CAC AAA AAG TA	379-383 ^a	52-77 ^b
	626 ^c	5'-TAC CAC CTT TTA AGT AAG GTG CTA AT	379-383 ^a	371-396 ^b
	<u>Bacterial group:</u> <i>Campylobacter jejuni</i> and <i>C. coli</i>			
25	2131	5'-AAG CMA TTG TTG TAA ATT TTG AAA G	1576,1600, 1849,1863,2139 ^{d, a}	7-31 ^e
	2132 ^c	5'-TCA TAT CCA TAG CAA TAG TTC TA	1576,1600, 1849,1863,2139 ^{d, a}	92-114 ^e
30	<u>Bacterial genus:</u> <i>Bordetella</i> sp.			
	825	5'-ATG AGC ARC GSA ACC ATC GTT CAG TG	1672 ^d	1-26
	826 ^c	5'-TCG ATC GTG CCG ACC ATG TAG AAC GC	1672 ^d	1342-1367
35	<u>Fungal genus:</u> <i>Candida</i> sp.			
	634	5'-AAC ACY GTC AGR RCI ATT GCY ATG GA	460-472, 474-478 ^a	101-126 ^f
40	635 ^c	5'-AAA CCR GTI ARR GCR ACT CTI GCT CT	460-472, 474-478 ^a	617-642 ^f

^a These sequences were aligned to derive the corresponding primer.

45 ^b The nucleotide positions refer to the *S. agalactiae* atpD sequence fragment (SEQ ID NO. 380).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d Sequence from databases.

50 ^e The nucleotide positions refer to the *C. jejuni* atpD sequence fragment (SEQ ID NO. 1576).

^f The nucleotide positions refer to the *C. albicans* atpD sequence fragment (SEQ ID NO. 460).

Annex II: Specific and ubiquitous primers for nucleic acid amplification (atpD sequences) (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Universal primers			
15	562	5'-CAR ATG RAY GAR CCI CCI GGI GYI MGI ATG	243,244,262, 264,280,284, 291,297,309, 311,315,317, 324,329,332, 334-336,339, 342,343,351, 356,357,364- 366,370,375, 379,393 ^a	528-557 ^b
20	563 ^c	5'-GGY TGR TAI CCI ACI GCI GAI GGC AT	243,244,262, 264,280,284, 291,297,309, 311,315,317, 324,329,332, 334-336,339, 342,343,351, 356,357,364- 366,370,375, 379,393 ^a	687-712 ^b
25	564	5'-TAY GGI CAR ATG AAY GAR CCI CCI GGI AA	243,244,262, 264,280,284, 291,297,309, 311,315,317, 324,329,332, 334-336,339, 342,343,351, 356,357,364- 366,370,375, 379,393 ^a	522-550 ^b
30	565 ^c	5'-GGY TGR TAI CCI ACI GCI GAI GGD AT	243,244,262, 264,280,284, 291,297,309, 311,315,317, 324,329,332, 334-336,339, 342,343,351, 356,357,364- 366,370,375, 379,393 ^a	687-712 ^b
35				
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55 ^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *K. pneumoniae* atpD sequence fragment (SEQ ID NO. 317).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex II: Specific and ubiquitous primers for nucleic acid amplification (atpD sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Universal primers (continued)			
	640	5'-TCC ATG GTI TWY GGI CAR ATG AA	248,284,315, 317,343,357, 366,370,379,393 ^a	513-535 ^b
15	641 ^c	5'-TGA TAA CCW ACI GCI GAI GGC ATA CG	248,284,315, 317,343,357, 366,370,379,393 ^a	684-709 ^b
20	642	5'-GGC GTI GGI GAR CGI ACI CGT GA	248,284,315, 317,343,357, 366,370,379,393 ^a	438-460 ^b
	641 ^c	5'-TGA TAA CCW ACI GCI GAI GGC ATA CG	248,284,315, 317,343,357, 366,370,379,393 ^a	684-709 ^b
25	Sequencing primers			
	566	5'-TTY GGI GGI GCI GGI GTI GGI AAR AC	669 ^d	445-470
30	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908
	566	5'-TTY GGI GGI GCI GGI GTI GGI AAR AC	669 ^d	445-470
	814	5'-GCI GGC ACG TAC ACI GCC TG	666 ^d	901-920
35	568	5'-RTI ATI GGI GCI GTI RTI GAY GT	669 ^d	25-47
	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908
	570	5'-RTI RYI GGI CCI GTI RTI GAY GT	672 ^d	31-53
	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908
40	572	5'-RTI RTI GGI SCI GTI RTI GA	669 ^d	25-44
	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908
	569	5'-RTI RTI GGI SCI GTI RTI GAT AT	671 ^d	31-53
45	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908
	571	5'-RTI RTI GGI CCI GTI RTI GAT GT	670 ^d	31-53
	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908

- 50 ^a These sequences were aligned to derive the corresponding primer.
- ^b The nucleotide positions refer to the *K. pneumoniae* atpD sequence fragment (SEQ ID NO. 317).
- ^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.
- 55 ^d Sequences from databases.

Annex II: Specific and ubiquitous primers for nucleic acid amplification (atpD sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Sequencing primers (continued)			
	700	5'-TIR TIG AYG TCG ART TCC CTC ARG	669 ^a	38-61
	567 ^b	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^a	883-908
15	568	5'-RTI ATI GGI GCI GTI RTI GAY GT	669 ^a	25-47
	573 ^b	5'-CCI CCI ACC ATR TAR AAI GC	666 ^a	1465-1484
	574	5'-ATI GCI ATG GAY GGI ACI GAR GG	666 ^a	283-305
	573 ^b	5'-CCI CCI ACC ATR TAR AAI GC	666 ^a	1465-1484
20	574	5'-ATI GCI ATG GAY GGI ACI GAR GG	666 ^a	283-305
	708 ^b	5'-TCR TCC ATI CCI ARI ATI GCI ATI AT	666 ^a	1258-1283
	681	5'-GGI SSI TTY GGI ISI GGI AAR AC	685	694-716
25	682 ^b	5'-GTI ACI GGY TCY TCR AAR TTI CCI CC	686	1177-1202
	681	5'-GGI SSI TTY GGI ISI GGI AAR AC	685	694-716
	683 ^b	5'-GTI ACI GGI TCI SWI AWR TCI CCI CC	685	1180-1205
30	681	5'-GGI SSI TTY GGI ISI GGI AAR AC	685	694-716
	699	5'-GTI ACI GGY TCY TYR ARR TTI CCI CC	686	1177-1202
	681	5'-GGI SSI TTY GGI ISI GGI AAR AC	685	694-716
	812 ^b	5'-GTI ACI GGI TCY TYR ARR TTI CCI CC	685	1180-1205
35	1213	5'-AAR GGI GGI ACI GCI GCI ATH CCI GG	714 ^a	697-722
	1212 ^b	5'-CCI CCI RGI GGI GAI ACI GCW CC	714 ^a	1189-1211
	1203	5'-GGI GAR MGI GGI AAY GAR ATG	709 ^a	724-744
40	1207 ^b	5'-CCI TCI TCW CCI GGC ATY TC	709 ^a	985-1004
	1204	5'-GCI AAY AAC ITC IWM YAT GCC	709 ^a	822-842
	1206 ^b	5'-CKI SRI GTI GAR TCI GCC A	709 ^a	926-944
45	1205	5'-AAY ACI TCI AWY ATG CCI GT	709 ^a	826-845
	1207 ^b	5'-CCI TCI TCW CCI GGC ATY TC	709 ^a	985-1004
	2282	5'-AGR RGC IMA RAT GTA TGA	714 ^a	84-101
	2284 ^b	5'-TCT GWG TRA CIG GYT CKG AGA	714 ^a	1217-1237
50	2283	5'-ATI TAT GAY GGK ITT CAG AGG C	714 ^a	271-292
	2285 ^b	5'-CMC CIC CWG GTG GWG AWA C	714 ^a	1195-1213

55 ^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex III: Internal hybridization probes for specific detection of tuf sequences.

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial species:</u> <i>Abiotrophia adiacens</i>			
	2170	5'-ACG TGA CGT TGA CAA ACC A	1715	313-331
15	<u>Bacterial species:</u> <i>Chlamydia pneumoniae</i>			
	2089	5'-ATG CTG AAC TTA TTG ACC TT	20	136-155
	2090	5'-CGT TAC TGG AGT CGA AAT G	20	467-485
20	<u>Bacterial species:</u> <i>Enterococcus faecalis</i>			
	580	5'-GCT AAA CCA GCT ACA ATC ACT CCA C	62-63,607 ^a	584-608 ^b
	603	5'-GGT ATT AAA GAC GAA ACA TC	62-63,607 ^a	440-459 ^b
	1174	5'-GAA CGT GGT GAA GTT CGC	62-63,607 ^a	398-415 ^b
25	<u>Bacterial species:</u> <i>Enterococcus faecium</i>			
	602	5'-AAG TTG AAG TTG TTG GTA TT	64,608 ^a	426-445 ^c
30	<u>Bacterial species:</u> <i>Enterococcus gallinarum</i>			
	604	5'-GGT GAT GAA GTA GAA ATC GT	66,609 ^a	419-438 ^d
35	<u>Bacterial species:</u> <i>Escherichia coli</i>			
	579	5'-GAA GGC CGT GCT GGT GAG AA	78	503-522
	2168	5'-CAT CAA AGT TGG TGA AGA AGT TG	78	409-431
40	<u>Bacterial species:</u> <i>Neisseria gonorrhoeae</i>			
	2166	5'-GAC AAA CCA TTC CTG CTG	126	322-339 ^e
45	<u>Fungal species:</u> <i>Candida albicans</i>			
	577	5'-CAT GAT TGA ACC ATC CAC CA	407-411 ^a	406-425 ^f
50	<u>Fungal species:</u> <i>Candida dubliniensis</i>			
	578	5'-CAT GAT TGA AGC TTC CAC CA	412,414-415 ^a	418-437 ^g

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *E. faecalis* tuf sequence fragment (SEQ ID NO. 607).

^c The nucleotide positions refer to the *E. faecium* tuf sequence fragment (SEQ ID NO. 608).

^d The nucleotide positions refer to the *E. gallinarum* tuf sequence fragment (SEQ ID NO. 609).

^e The nucleotide positions refer to the *N. gonorrhoeae* tuf sequence fragment (SEQ ID NO. 126).

^f The nucleotide positions refer to the *C. albicans* tuf(EF-1) sequence fragment (SEQ ID NO. 408).

^g The nucleotide positions refer to the *C. dubliniensis* tuf(EF-1) sequence fragment (SEQ ID NO. 414).

**Annex III: Internal hybridization probes for specific detection of
tuf sequences (continued).**

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial species:</u> <i>Haemophilus influenzae</i>			
	581	5'-ACA TCG GTG CAT TAT TAC GTG G	610 ^a	551-572
15	<u>Bacterial species:</u> <i>Mycoplasma pneumoniae</i>			
	2095	5'-CGG TCG GGT TGA ACG TGG	2097 ^a	687-704
	<u>Bacterial species:</u> <i>Staphylococcus aureus</i>			
20	584	5'-ACA TGA CAC ATC TAA AAC AA	176-180 ^b	369-388 ^c
	585	5'-ACC ACA TAC TGA ATT CAA AG	176-180 ^b	525-544 ^c
	586	5'-CAG AAG TAT ACG TAT TAT CA	176-180 ^b	545-564 ^c
	587	5'-CGT ATT ATC AAA AGA CGA AG	176-180 ^b	555-574 ^c
	588	5'-TCT TCT CAA ACT ATC GTC CA	176-180 ^b	593-612 ^c
25	<u>Bacterial species:</u> <i>Staphylococcus epidermidis</i>			
	589	5'-GCA CGA AAC TTC TAA AAC AA	185,611 ^b	445-464 ^d
	590	5'-TAT ACG TAT TAT CTA AAG AT	185,611 ^b	627-646 ^d
30	591	5'-TCC TGG TTC TAT TAC ACC AC	185,611 ^b	586-605 ^d
	592	5'-CAA AGC TGA AGT ATA CGT AT	185,611 ^b	616-635 ^d
	593	5'-TTC ACT AAC TAT CGC CCA CA	185,611 ^b	671-690 ^d
	<u>Bacterial species:</u> <i>Staphylococcus haemolyticus</i>			
35	594	5'-ATT GGT ATC CAT GAC ACT TC	186,188-190 ^b	437-456 ^e
	595	5'-TTA AAG CAG ACG TAT ACG TT	186,188-190 ^b	615-634 ^e
	<u>Bacterial species:</u> <i>Staphylococcus hominis</i>			
40	596	5'-GAA ATT ATT GGT ATC AAA GA	191,193-196 ^b	431-450 ^f
	597	5'-ATT GGT ATC AAA GAA ACT TC	191,193-196 ^b	437-456 ^f
	598	5'-AAT TAC ACC TCA CAC AAA AT	191,193-196 ^b	595-614 ^f

^a Sequences from databases.

^b These sequences were aligned to derive the corresponding probe.

^c The nucleotide positions refer to the *S. aureus* tuf sequence fragment (SEQ ID NO. 179).

^d The nucleotide positions refer to the *S. epidermidis* tuf sequence fragment (SEQ ID NO. 611).

^e The nucleotide positions refer to the *S. haemolyticus* tuf sequence fragment (SEQ ID NO. 186).

^f The nucleotide positions refer to the *S. hominis* tuf sequence fragment (SEQ ID NO. 191).

Annex III: Internal hybridization probes for specific detection of tuf sequences (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial species:</u> <i>Staphylococcus saprophyticus</i>			
	599	5'-CGG TGA AGA AAT CGA AAT CA	198-200 ^a	406-425 ^b
	600	5'-ATG CAA GAA GAA TCA AGC AA	198-200 ^a	431-450 ^b
	601	5'-GTT TCA CGT GAT GAT GTA CA	198-200 ^a	536-555 ^b
15	695	5'-GTT TCA CGT GAT GAC GTA CA	198-200 ^a	563-582 ^b
	<u>Bacterial species:</u> <i>Streptococcus agalactiae</i>			
	582 ^c	5'-TTT CAA CTT CGT CGT TGA CAC GAA CAG T	207-210 ^a	404-431 ^d
20	583 ^c	5'-CAA CTG CTT TTT GGA TAT CTT CTT TAA TAC CAA CG	207-210 ^a	433-467 ^d
	1199	5'-GTA TTA AAG AAG ATA TCC AAA AAG C	207-210 ^a	438-462 ^d
	<u>Bacterial species:</u> <i>Streptococcus pneumoniae</i>			
25	1201	5'-TCA AAG AAG AAA CTA AAA AAG CTG T	971,977, 979,986 ^a	513-537 ^e
	<u>Bacterial species:</u> <i>Streptococcus pyogenes</i>			
30	1200	5'-TCA AAG AAG AAA CTA AAA AAG CTG T	1002	473-497
	<u>Bacterial group:</u> <i>Enterococcus casseliflavus-flavescens-gallinarum</i> group			
35	620	5'-ATT GGT GCA TTG CTA CGT	58,65,66 ^a	527-544 ^f
	1122	5'-TGG TGC ATT GCT ACG TGG	58,65,66 ^a	529-546 ^f
	<u>Bacterial group:</u> <i>Enterococcus</i> sp., <i>Gemella</i> sp., <i>A. adiacens</i>			
40	2172	5'-GTG TTG AAA TGT TCC GTA AA	58-62,67-71, 87-88,607-609, 727,871 1715,1722 ^a	477-496 ^g

- 45 ^a These sequences were aligned to derive the corresponding primer.
- ^b The nucleotide positions refer to the *S. saprophyticus* tuf sequence fragment (SEQ ID NO. 198).
- ^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.
- 50 ^d The nucleotide positions refer to the *S. agalactiae* tuf sequence fragment (SEQ ID NO. 209).
- ^e The nucleotide positions refer to the *S. pneumoniae* tuf sequence fragment (SEQ ID NO. 986).
- ^f The nucleotide positions refer to the *E. flavescens* tuf sequence fragment (SEQ ID NO. 65).
- 55 ^g The nucleotide positions refer to the *E. faecium* tuf sequence fragment (SEQ ID NO. 608).

Annex III: Internal hybridization probes for specific detection of tuf sequences (continued).

			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
5				
10	<u>Bacterial genus:</u>	<i>Gemella</i>		
	2171	5'-TCG TTG GAT TAA CTG AAG AA	87,88 ^a	430-449 ^b
	<u>Bacterial genus:</u>	<i>Staphylococcus</i> sp.		
15				
	605	5'-GAA ATG TTC CGT AAA TTA TT	176-203 ^a	403-422 ^c
	606	5'-ATT AGA CTA CGC TGA AGC TG	176-203 ^a	420-439 ^c
	1175	5'-GTT ACT GGT GTA GAA ATG TTC	176-203 ^a	391-411 ^c
	1176	5'-TAC TGG TGT AGA AAT GTT C	176-203 ^a	393-411 ^c
20	<u>Bacterial genus:</u>	<i>Streptococcus</i> sp.		
	1202	5'-GTG TTG AAA TGT TCC GTA AAC A	206-231,971, 977,979,982-986 ^a	466-487 ^d
25	<u>Fungal species:</u>	<i>Candida albicans</i>		
	1156	5'-GTT GAA ATG CAT CAC GAA CAA TT	407-412,624 ^a	680-702 ^e
30	<u>Fungal group:</u>	<i>Candida albicans</i> and <i>C. tropicalis</i>		
	1160	5'-CGT TTC TGT TAA AGA AAT TAG AAG	407-412, 429,624 ^a	748-771 ^e
35	<u>Fungal species:</u>	<i>Candida dubliniensis</i>		
	1166	5'-ACG TTA AGA ATG TTT CTG TCA A	414-415 ^a	750-771 ^f
	1168	5'-GAA CAA TTG GTT GAA GGT GT	414-415 ^a	707-726 ^f
40	<u>Fungal species:</u>	<i>Candida glabrata</i>		
	1158	5'-AAG AGG TAA TGT CTG TGG T	417	781-799
	1159	5'-TGA AGG TTT GCC AGG TGA	417	718-735
45	<u>Fungal species:</u>	<i>Candida krusei</i>		
	1161	5'-TCC AGG TGA TAA CGT TGG	422	720-737
50				

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *G. haemolysans* tuf sequence fragment (SEQ ID NO. 87).

^c The nucleotide positions refer to the *S. aureus* tuf sequence fragment (SEQ ID NO. 179).

^d The nucleotide positions refer to the *S. pneumoniae* tuf sequence fragment (SEQ ID NO. 986).

^e The nucleotide positions refer to the *C. albicans* tuf(EF-1) sequence fragment (SEQ ID NO. 408).

^f The nucleotide positions refer to the *C. dubliniensis* tuf(EF-1) sequence fragment (SEQ ID NO. 414).

Annex III: Internal hybridization probes for specific detection of tuf sequences (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Fungal group:</u> <i>Candida lusitaniae</i> and <i>C. guilliermondii</i>			
	1162	5'-CAA GTC CGT GGA AAT GCA	418,424 ^a	682-699 ^b
	<u>Fungal species:</u> <i>Candida parapsilosis</i>			
15	1157	5'-AAG AAC GTT TCA GTT AAG GAA AT	426	749-771
	<u>Fungal species:</u> <i>Candida zeylanoides</i>			
20	1165	5'-GGT TTC AAC GTG AAG AAC	432	713-730
	<u>Fungal genus:</u> <i>Candida</i> sp.			
25	1163	5'-GTT GGT TTC AAC GTT AAG AAC	407-412,414-415,417,418,422,429 ^a	728-748 ^c
	1164	5'-GGT TTC AAC GTC AAG AAC	413,416,420,421,424,425,426,428,431 ^a	740-757 ^b
30	1167	5'-GTT GGT TTC AAC GT	406-426, 428-432, 624 ^a	728-741 ^c

^a These sequences were aligned to derive the corresponding primer.

35 ^b The nucleotide positions refer to the *C. lusitaniae* tuf(EF-1) sequence fragment (SEQ ID NO. 424).

^c The nucleotide positions refer to the *C. albicans* tuf(EF-1) sequence fragment (SEQ ID NO. 408).

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Annex IV: Strategy for the selection of amplification/sequencing primers from atpD (F-type) sequences.

SEQ ID	Accession #	910 NO.:
5	B. cepacia	23
10	B. pertussis	49
15	P. aeruginosa	443
20	E. coli	472
	N. gonorrhoeae	881
	M. thermoacetica	
	S. aurantiaca	
	M. tuberculosis	
	B. fragilis	
	C. lytica	
	A. woodii	
	C. acetobutylicum	
	M. pneumoniae	
	H. pylori	
25	Selected sequences for universal primers	
30	Selected sequence for universal primer	

The sequence numbering refers to the *Escherichia coli* atpD gene fragment (SEQ ID NO. 669). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

"R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

This sequence is the reverse-complement of the selected primer.

5

272

"R" "y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a These sequences are the reverse-complement of the selected primers.

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Annex VII: Strategy for the selection of eukaryotic sequencing primers from tuf (EF-1) sequences.

5		154	179	286	314	SEQ ID NO.:	Accession #:
	S. cerevisiae	GG TTCCTTCAAG TACGCTTGGG TTTT...AGAGA TTTCATCAAG AACATGATTA CTGG...				665	X00779
	B. hominis	GG CTCCTTCAAG TACGCGTGGG TGCT...CGTGA CTTTCATCAAG AACATGATTA CCGG...				-	D64080
	C. albicans	GG TTCCTTCAAG TACGCGTGGG TCCT...AGAGA TTTCATCAAG AACATGATTA CCGG...				-	M29934
10	C. neoformans	TC TTCCTTCAAG TACGCGTGGG TTCT...CGAGA CTTTCATCAAG AACATGATTA CCGG...				-	U81803
	E. histolytica	GG ATCATTCAAA TATGCTTGGG TCCT...AGAGA TTTCATCAAG AACATGATTA CCGG...				-	M92073
	G. lamblia	GG CTCCTTCAAG TACGCGTGGG TCCT...CGCGA CTTTCATCAAG AACATGATTA CCGG...				-	D14342
	H. capsulatum	AA ATCCTTCAAA TATGCGTGGG TCCT...CGTGA CTTTCATCAAG AACATGATTA CCGG...				-	U14100
	Human	GG CTCCTTCAAG TATGCGTGGG TCCT...AGAGA CTTTCATCAAG AACATGATTA CCGG...				-	X03558
15	L. braziliensis	GC GTCCTTCAAG TACGCGTGGG TGCT...CGCGA CTTTCATCAAG AACATGATTA CCGG...				-	U72244
	O. volvulus	GG CTCATTTAAA TATGCTTGGG TATT...CGTGA TTTCATCAAG AACATGATTA CCGG...				-	M64333
	P. berghei	GG TagTTTCAAA TATGCTTGGG TTTT...AAACA TTTCATCAAG AACATGATTA CCGG...				-	AJ224150
	P. knowlesi	GG AagTTTAAAG TACGCGTGGG TGTT...AAGGA TTTCATCAAG AACATGATTA CCGG...				-	AJ224153
20	S. pombe	GG TTCCTTCAAG TACGCGTGGG TTTT...CGTGA TTTCATCAAG AACATGATTA CCGG...				-	U42189
	T. cruzi	TC TTCCTTCAAG TACGCGTGGG TCCT...CGCGA CTTTCATCAAG AACATGATTA CCGG...				-	L76077
	Y. lipolytica	GG TTCCTTCAAG TACGCGTGGG TTCT...CGAGA TTTCATCAAG AACATGATTA CCGG...				-	AF054510
	Selected sequences for amplification primers	TCITTYAAR TAYGCITGGG T				558	
25				GA YTTTCATYAAR AAYATGATYA C		560	
				GA YTTTCATIAAR AAYATGAT		653	

30 The sequence numbering refers to the *Saccharomyces cerevisiae* tuf (EF-1) gene fragment (SEQ ID NO. 665). Nucleotides in capitals are identical to the selected sequences SEQ ID NOS. 558, 560 or 653, or match those sequences. Mismatches for SEQ ID no. 558 and 560 are indicated by lower-case letters. Mismatches for SEQ ID NO. 653 are indicated by underlined nucleotides. Dots indicate gaps in the sequences displayed.

35 "R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

Annex VII: Strategy for the selection of eukaryotic sequencing primers from tuf (EF-1) sequences (continued).

5		751	776	1276	1304	SEQ ID Accession NO.: #:	
	S. cerevisiae	...GTTTACAA	GATCGGTGGT	ATTGGTAC...	GACATG	AGACAAACTG TCGCTGTCCG TGT	665 X00779
	B. hominis	...GTGTACAA	GATTGGCGGT	ATTGGTAC...	GATATG	AGACAGACTG TCGCTGTCCG TAT	- D64080
	C. albicans	...GTTTACAA	GATCGGTGGT	ATTGGTAC...	GATATG	AGACAAACCG TTGCTGTtGG TGT	- M29934
	C. neoformans	...GTCTACAA	GATCGGTGGT	ATCGGCAC...	GACATG	CGACAGACCG TTGCCGTtGG TGT	- U81803
10	E. histolytica	...GTTTACAA	GATTTCAGGT	ATTGGAAC...	GATATG	AaACAAACCG TTGCTGTtGG AGT	- M92073
	G. lamblia	...GTCTACAA	GATCTcGGGc	gTCGGGAC...	~~~~~	~~~~~	- D14342
	H. capsulatum	...GTGTACAA	AATCTctGGT	ATTGGCAC...	GACATG	AGACAAACCG TCGCTGTCCG TGT	- U14100
	Human	...GTCTACAA	AATTGGTGGT	ATTGGTAC...	GATATG	AGACAGACAG TTGCGGTgGG TGT	- X03558
15	L. braziliensis	...GTGTACAA	GATCGGCGGT	ATCGGCAC...	GACATG	CGCagAACCG TCGCCGTCCG CAT	- U72244
	O. volvulus	...GTTTACAA	AATTGGAGGT	ATTGGAAC...	GATATG	AGACAAACAG TTGCTGTtGG CGT	- M64333
	P. berghei	...GTATACAA	AATTGGTGGT	ATTGGTAC...	GATATG	AGACAAACAA TTGCTGTCCG TAT	- AJ224150
	P. knowlesi	...GTATACAA	AATCGGTGGT	ATTGGTAC...	GATATG	AGACAAACCA TTGCTGTCCG TAT	- AJ224153
20	S. pombe	...GTTTACAA	GATCGGTGGT	ATTGGTAC...	GACATG	CGTCAAACCG TCGCTGTCCG TGT	- U42189
	T. cruzi	...GTGTACAA	GATCGGCGGT	ATCGGCAC...	GACATG	CGCCAGACGG TCGCCGTCCG CAT	- L76077
	Y. lipolytica	...GTCTACAA	GATCGGTGGT	ATCGGCAC...	GACATG	CGACAGACCG TTGCTGTCCG TGT	- AF054510
	Selected sequence for amplification primer	TACAA	RATYKGIGGT	ATYGG			654
25	Selected sequences for amplification primers ^a	TACAA	RATYKGIGGT	ATYGG	ATG MGICARACIR	TYGCYGTCCG	655 559

30 The sequence numbering refers to the *Saccharomyces cerevisiae* tuf (EF-1) gene fragment (SEQ ID NO. 665). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. "~" indicate incomplete sequence data. Dots indicate gaps in the sequences displayed.

35 "R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a This sequences are the reverse-complement of the selected primers.

Annex VIII: Strategy for the selection of Streptococcus agalactiae-specific amplification primers from tuf sequences.

5	S. agalactiae	305	334	517	542	SEQ ID NO.:	Accession #:
	S. agalactiae	CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTTCTTCG TG
	S. agalactiae	CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTTCTTCG TG
	S. agalactiae	CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTTCTTCG TG
	S. agalactiae	CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTTCTTCG TG
10	S. anginosus	CCAGAA	CGTGATACTG	ACAAACCTTT	gCTT...AGAT	AACGTTGGTG	TTCCTTCTTCG TG
	S. anginosus	CCAGAA	CGTGATACTG	ACAAACCTTT	gCTT...AGAT	AACGTTGGTG	TTCCTTCTTCG TG
	S. bovis	CCAGAA	CGTGATACTG	ACAAACCTTT	gCTT...GGAT	AACGTTGGTG	TTCCTTCTTCG TG
	S. gordonii	CCAGAA	CGTGATACTG	ACAAACCTTT	gCTT...AGAT	AACGTTGGTG	TTCCTTCTTCG TG
	S. mutans	CCAGAA	CGTGATACTG	ACAAACCTTT	cCTT...GGAT	AACGTTGGTG	TTCCTTCTTCG TG
15	S. pneumoniae	CCAGAA	CGTGATACTG	ACAAACCTTT	gCTT...AGAT	AACGTTGGTG	TTCCTTCTTCG TG
	S. sanguinis	CCAGAA	CGTGATACTG	ACAAACCTTT	gCTT...GGAT	AACGTTGGTG	TTCCTTCTTCG TG
	S. sobrinus	CCAGAA	CGTGATACTG	ACAAACCTTT	gCTT...AGAT	AACGTTGGTG	TTCCTTCTTCG TG
	B. cepacia	CCAGAA	CGTGATACTG	ACAAACCTTT	cCTG...CGAC	AACGTTGGTG	TTCCTTCTTCG TG
	B. fragilis	CCAGAA	CGTGATACTG	ACAAACCTTT	cCTG...TGAC	AACGTTGGTG	TTCCTTCTTCG TG
	B. subtilis	CCAGAA	CGTGATACTG	ACAAACCTTT	cCTG...TGAC	AACGTTGGTG	TTCCTTCTTCG TG
20	C. diphtheriae	CCAGAA	CGTGATACTG	ACAAACCTTT	cCTC...CGAC	AACGTTGGTG	TTCCTTCTTCG TG
	C. trachomatis	CCAGAA	CGTGATACTG	ACAAACCTTT	cCTA...AGAG	AACGTTGGTG	TTCCTTCTTCG TG
	E. coli	CCAGAA	CGTGATACTG	ACAAACCTTT	cCTg...TGAG	AACGTTGGTG	TTCCTTCTTCG TG
	G. vaginalis	CCAGAA	CGTGATACTG	ACAAACCTTT	cCTg...CGAT	AACGTTGGTG	TTCCTTCTTCG TG
25	S. aureus	CCAGAA	CGTGATACTG	ACAAACCTTT	cATg...TGAC	AACGTTGGTG	TTCCTTCTTCG TG
	Selected sequence for species-specific primer	GAA	CGTGATACTG	ACAAACCTTT	A		549
30	Selected sequence for species-specific primer ^b					C AACGTTGGTG	TTCCTTCTTC

The sequence numbering refers to the Streptococcus agalactiae tuf gene fragment (SEQ ID NO. 209). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

"R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a The SEQ ID NO. refers to previous patent publication WO98/20157.
^b This sequence is the reverse-complement of the selected primer.

Annex IX: Strategy for the selection of Streptococcus agalactiae-specific hybridization probes from tuf sequences.

		401	431	433	470	SEQ ID NO.: Accession #:				
5	S. acidominimus	GGTACTGT	TaaAGTCAAT	GACGAAGTTG	AAATCGTTGG	TATCAAGAC	GAAATCTCTA	AAGCAGTTGT	TA	206
	S. agalactiae	GGTACTGT	TCGTGTCAAC	GACGAAGTTG	AAATCGTTGG	TATTAAGAA	GATATCCAAA	AAGCAGTTGT	TA	209
	S. agalactiae	GGTACTGT	TCGTGTCAAC	GACGAAGTTG	AAATCGTTGG	TATTAAGAA	GATATCCAAA	AAGCAGTTGT	TA	144*
	S. agalactiae	GGTACTGT	TCGTGTCAAC	GACGAAGTTG	AAATCGTTGG	TATTAAGAA	GATATCCAAA	AAGCAGTTGT	TA	207
10	S. agalactiae	GGTACTGT	TCGTGTCAAC	GACGAAGTTG	AAATCGTTGG	TATTAAGAA	GATATCCAAA	AAGCAGTTGT	TA	210
	S. agalactiae	GGTACTGT	TCGTGTCAAC	GACGAAGTTG	AAATCGTTGG	TATTAAGAA	GATATCCAAA	AAGCAGTTGT	TA	208
	S. anginosus	GGTACTGT	TaaAGTCAAC	GACGAAGTTG	AAATCGTTGG	TATCGTGT	GAAATCCAAA	AAGCAGTTGT	TA	211
	S. anginosus	GGTACTGT	TaaAGTCAAC	GATGAAGTTG	AAATCGTTGG	TATCGTGT	GAAATCCAAA	AAGCAGTTGT	TA	212
15	S. bovis	GGTACTGT	TaaAGTCAAT	GACGAAGTTG	AAATCGTTGG	TATCGTGT	GAAATCCAAA	AAGCAGTTGT	TA	213
	S. anginosus	GGTACTGT	TaaAGTCAAT	GATGAAGTTG	AAATCGTTGG	TATCGTGT	GAAATCCAAA	AAGCAGTTGT	TA	214
	S. cricetus	GGTACTGT	TaaAGTCAAT	GACGAAGTTG	AAATCGTTGG	TATCAAGAC	GAAATCCAAA	AAGCAGTTGT	TA	215
	S. cristatus	GGTACTGT	TCGTGTCAAC	GATGAAGTGG	AAATCGTTGG	TATCAAGAA	GAAATCCAAA	AAGCAGTTGT	TA	216
20	S. downei	GGTACTGT	TaaAGTCAAC	GACGAAGTTG	AAATCGTTGG	TATCAAGAC	GAAATCCAAA	AAGCAGTTGT	TA	217
	S. dysgalactiae	GGTACTGT	TCGTGTCAAC	GACGAAGTGG	AAATCGTTGG	TATCAAGAA	GAAATCCAAA	AAGCAGTTGT	TA	218
	S. equi equi	GGTACTGT	TCGTGTCAAC	GACGAAGTGG	AAATCGTTGG	TATCAAGAC	GAAATCCAAA	AAGCAGTTGT	TA	219
	S. ferus	GGTACTGT	TaaAGTCAAC	GATGAAGTTG	AAATCGTTGG	TATCAAGAC	GAAATCCAAA	AAGCAGTTGT	TA	220
25	S. gordonii	GGTACTGT	TaaAGTCAAT	GACGAAGTGG	AAATCGTTGG	TATCAAGAA	GAAATCCAAA	AAGCAGTTGT	TA	222
	S. macacae	GGTACTGT	TaaAGTCAAT	GATGAAGTTG	AAATCGTTGG	TATCGTGT	GAAATCCAAA	AAGCAGTTGT	TA	223
	S. gordonii	GGTACTGT	TaaAGTCAAC	GACGAAGTGG	AAATCGTTGG	TATCAAGAA	GAAATCCAAA	AAGCAGTTGT	TA	224
	S. mutans	GGTACTGT	TaaAGTCAAC	GATGAAGTTG	AAATCGTTGG	TATCGTGT	GAAATCCAAA	AAGCAGTTGT	TA	-
30	S. oralis	GGTACTGT	TCGTGTCAAC	GACGAAGTGG	AAATCGTTGG	TATCAAGAA	GAAATCCAAA	AAGCAGTTGT	TA	P33170
	S. parasanguinis	GGTACTGT	TCGTGTCAAC	GATGAAGTGG	AAATCGTTGG	TATCAAGAA	GAAATCCAAA	AAGCAGTTGT	TA	225
	S. pneumoniae	GGTACTGT	TaaAGTCAAC	GACGAAGTGG	AAATCGTTGG	TATCAAGAA	GAAATCCAAA	AAGCAGTTGT	TA	145*
	S. pyogenes	GGTACTGT	TCGTGTCAAC	GACGAAGTGG	AAATCGTTGG	TATCAAGAA	GAAATCCAAA	AAGCAGTTGT	TA	-
35	S. ratti	GGTACTGT	TaaAGTCAAT	GACGAAGTGG	AAATCGTTGG	TATCGTGT	GAAATCCAAA	AAGCAGTTGT	TA	Genome project
	S. salivarius	GGTACTGT	TCGTGTCAAC	GACGAAGTGG	AAATCGTTGG	TATCGTGT	GAAATCCAAA	AAGCAGTTGT	TA	226
	S. sanguinis	GGTACTGT	TaaAGTCAAC	GATGAAGTGG	AAATCGTTGG	TATCGTGT	GAAATCCAAA	AAGCAGTTGT	TA	146*
	S. sobrinus	GGTACTGT	TaaAGTCAAC	GACGAAGTGG	AAATCGTTGG	TATCAAGAA	GAAATCCAAA	AAGCAGTTGT	TA	227
35	S. suis	GGTACTGT	TaaAGTCAAC	GACGAAGTGG	AAATCGTTGG	TATCAAGAA	GAAATCCAAA	AAGCAGTTGT	TA	228
	S. uberis	GGTACTGT	TCGTGTCAAC	GACGAAGTGG	AAATCGTTGG	TATCGTGT	GAAATCCAAA	AAGCAGTTGT	TA	229
	S. vestibularis	GGTACTGT	TCGTGTCAAC	GACGAAGTGG	AAATCGTTGG	TATCAAGAA	GAAATCCAAA	AAGCAGTTGT	TA	230
		GGTACTGT	TCGTGTCAAT	GACGAAGTGG	AAATCGTTGG	TCTTAAGAA	GAAATCCAAA	AAGCAGTTGT	TA	231

Selected sequences for species-specific hybridization probes^a

ACTGT TCGTGTCAAC GACGAAGTTG AAA CGTTGG TATTAAGAA GATATCCAAA AAGCAGTTG

582
583

The sequence numbering refers to the Streptococcus agalactiae tuf gene fragment (SEQ ID NO. 209). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^a The SEQ ID NO. refers to previous patent publication WO98/20157.
^b These sequences are the reverse-complement of the selected probes.

NO.:	39	80	203	234	368	SEQ ID 399
<i>S. agalactiae</i>	TT GATTGCTCTAT AAAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA CTTTGGGTGG TGTCTTCAAC GTTC..CTT ATTAGCACCT TACTTTAAAG GTGGTAAAG 380					
<i>S. agalactiae</i>	TT GATTGCTCTAT AAAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA CTTTGGGTGG TGTCTTCAAC GTTC..CTT ATTAGCACCT TACTTTAAAG GTGGTAAAG 379					
<i>S. agalactiae</i>	TT GATTGCTCTAT AAAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA CTTTGGGTGG TGTCTTCAAC GTTC..CTT ATTAGCACCT TACTTTAAAG GTGGTAAAG 381					
<i>S. agalactiae</i>	TT GATTGCTCTAT AAAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA CTTTGGGTGG TGTCTTCAAC GTTC..CTT ATTAGCACCT TACTTTAAAG GTGGTAAAG 382					
<i>S. agalactiae</i>	TT GATTGCTCTAT AAAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA CTTTGGGTGG TGTCTTCAAC GTTC..CTT ATTAGCACCT TACTTTAAAG GTGGTAAAG 383					
<i>S. bovis</i>	TT GATTGTTTAT AAAATGGCG ATAACTCTCA AAAAATGCTG..TAAAGAA CTTTGGGTGG TGTGTTTAAAT GTTC..CCT TATTGGCCCT TACCTTAAAG GTGGTAAAG - ^a					
<i>S. salivarius</i>	TT GGTGCTTAT ACTGATGAAC AAAAGTCTCA ACgTATGCTG..TAAAGATA CcCTtGGaCG TGTCTTTAAAC GTTC..CTT gCTAGCCCTT TACCTTAAAG GTGGTAAAG 387					
<i>S. pneumoniae</i>	CT TGTCGTCTAC AAAATGAAC AAAGAAATC GTTC..CCT TATTGGCCCT TACCTTAAAG GTGGTAAAG - ^b					
<i>S. pyogenes</i>	TT GATTGTTTAT AAAATGAAG ATAAATGCTC..TAAAGAA CTTTGGGaCG CGTCTTTAAAT GTaC..CCT TATTGGCCCT TACCTTAAAG GTGGTAAAG - ^c					
<i>S. anginosus</i>	CT TGTAAGTCTAT AAAATGAAG ATAAATGCTC..TAAAGAA CcCTtGGaCG GTTC..CCT TATTGGCCCT TACCTTAAAG GTGGTAAAG 386					
<i>S. sanguinis</i>	CT TGTAAGTCTAT AAAATGAAG ATAAATGCTC..TAAAGAA CcCTtGGaCG GTTC..CCT gCTAGCACCT TATCTGAAG GTGGTAAAG - ^d					
<i>S. mutans</i>	TT GGTGCTTAT AAAATGGCG ACAAGTCTCA AAAATGCTT..TAAAGAA CcCTtGGaCG TGTCTTTAAAT GTTC..CCT TATTGGCCCT TACTTTAAAG GTGGTAAAG - ^e					
<i>B. anthracis</i>	GT ABAACAGAGC AACGAAAACG GAACAGCAT TAACTTAAcA..TgATGcAA CcCTtGGaCG TGTATTTAAAC GTat..CTT ACTGCTCCTT TACATTTAAAG GTGGTAAAG 247					
<i>B. cereus</i>	GT ABAACAAAGC AACGAAAACG g...aagcat GAACTTAAcA..TgATGcAA CcCTtGGaCG TGTATTTAAAC GTat..CTT ACTGCTCCTT TACATTTAAAG GTGGTAAAG 248					
<i>E. faecium</i>	TT agTTGTTTAT AAAATGAAGC AGAAAaAaAc AAATaAaTc AAAAGTGTt..TAAAGAA CcCTtGGaCG CcCTaTTCAAC GTaC..TTT gCTGGCCCA TATTTAAAG GTGGTAAAG 292					
<i>E. gallinarum</i>	TT GATCGTTTAT AAAAAGGACG AGAAAaAaAc AAAAGTAGTA..TAAAGATA CcCTaGGTGG CcCTaTTCAAC GTaC..TTT ATTAGCTCCTT TACTTTAAAG GTGGTAAAG 293					
<i>E. faecalis</i>	TT agTCGTTTAT AAAAATGGCG AAGCAaAaCA AAAAGTAGTA..TAAAGATA CcCTaGGTGG CcCTaTTCAAC GTat..CCT gATgTgtCCg TtCgCTAAAG GcGGTAAAG - ^f					
<i>E. coli</i>	Ta cgaTGctcTt gAggtgcaaa ATggttaatgA ggttGTgTg..TAAAGGgA CcCTaGGTGG CcCTaTTCAAC GTaC..CCT gATgTgtCCg TtCgCTAAAG GcGGTAAAG - ^f					
<i>L. monocytogenes</i>	Ta TAAatctgAT gcAGAAAGaAG CcCcaAcTAg CcCAACTtact..TACaGtaa CcCTtGGTGG CcCTaTTCAAC GTat..CCT gCTAGCTCCTT TACTTTAAAG GTGGTAAAG 324					
<i>S. aureus</i>	GT TATTGatgtg cCTAAAGaAG AAggtacAAAT ACAACTAAcA..TgATGAA CcCTaGGTGG CcCTaTTCAAC GTaC..TTT ACCTAGCACCT TATaTTTAAAG GTGGTAAAG 366					
<i>S. epidermidis</i>	Ca CATCGaagtT cCTAAAGaAG ATggaGcGT tCAATTAAC..TgACGtaa CcCTaGGaAG aGTgTtTAAAC GTaC..CTT ATTAGCACCT TACATTTAAAG GTGGTAAAG 370					
Selected sequences for species-specific primer	ATTGTCTAT AAAAATGGCG ATAAGTC AAAATGGCG ATAAGTCACA AAAAGTA					627 628
Selected sequences for species-specific primers ^g	GGATA CTTTGGGTGG TGTCTTCAAC G					625 626

The sequence numbering refers to the *Streptococcus agalactiae* *tuf* gene fragment (SEQ ID NO. 380). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^{4,4,a,f} These sequences were obtained from Genbank and have accession #: a=AB009314, d=AF001955, e=U31170, and f=V00311.

^{b,c} These sequences were obtained from genome sequencing projects.

^g These sequences are the reverse-complement of the selected primers.

Annex XI: Strategy for the selection of Candida albicans/dubliniensis-specific primers, Candida albicans-specific hybridization probe and Candida dubliniensis-specific hybridization probe from tuf sequences.

	337	368	403	428	460	491	SEQ ID NO.:	Accession #:
5								
10	C. albicans	CGTC AAGAAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCGGTA AAGTTACTGG TAAGACCTTG T					624	-
	C. albicans	CGTC AAGAAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCGGTA AAGTTACTGG TAAGACCTTG T					409	-
	C. albicans	CGTC AAGAAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCGGTA AAGTTACTGG TAAGACCTTG T					410	-
	C. albicans	CGTC AAGAAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCGGTA AAGTTACTGG TAAGACCTTG T					407	-
	C. albicans	CGTC AAGAAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCGGTA AAGTTACTGG TAAGACCTTG T					408	-
	C. dubliniensis	CGTC AAGAAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCGGTA AAGTTACTGG TAAGACCTTG T					412	-
	C. dubliniensis	CGTC AAGAAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCGGTA AAGTTACTGG TAAGACCTTG T					414	-
	C. dubliniensis	CGTC AAGAAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCGGTA AAGTTACTGG TAAGACCTTG T					415	-
15	C. glabrata	CATC AAGAAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AAGGCTGGTg tCGTCAAGG TAAGACCTTG T					417	-
	C. guilliermondii	CGTC AAGAAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AAGGCTGGTg tCGTCAAGG TAAGACCTTG T					418	-
	C. kefyr	CATC AAGAAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AAGGCTGGTg tCGTCAAGG TAAGACCTTG T					421	-
	C. krusei	CATC AAGAAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AAGGCTGGTg tCGTCAAGG TAAGACCTTG T					422	-
	C. lusitaniae	CGTC AAGAAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AAGGCTGGTg tCGTCAAGG TAAGACCTTG T					424	-
20	C. neoformans	CATC AAGAAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AAGGCTGGTg tCGTCAAGG TAAGACCTTG T					623	-
	C. parapsilosis	CGTC AAGAAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AAGGCTGGTg tCGTCAAGG TAAGACCTTG T					426	-
	C. tropicalis	CGTC AAGAAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AAGGCTGGTg tCGTCAAGG TAAGACCTTG T					429	-
	A. fumigatus	CATC AAGAAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AAGGCTGGTg tCGTCAAGG TAAGACCTTG T					404	-
25	Human	CATt AAGAAaATTG GcTACAACCC cGAcACAG...CAACATGc TgGAGCCaAg tGcTAACA...T AAggatGGcA AtGccAGTgG aAccACgctG C					-	X03558
	P. anomala	TATC AAGAAaATTG GcTACAACCC cGAcACAG...CAACATGc TgGAGCCaAg tGcTAACA...T AAggatGGcA AtGccAGTgG aAccACgctG C					447	-
	S. cerevisiae	TATC AAGAAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AAGGCTGGTg tCGTCAAGG TAAGACCTTG T					622	-
	S. pombe	CATC AAGAAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AAGGCTGGTg tCGTCAAGG TAAGACCTTG T					-	U42189

30 Selected sequence
for species-specific
amplification primer^a C AAGAAGGTTG GTTACAACCC AAGA

35 Selected sequence
for species-specific
amplification primer^{a,b}

40 Selected sequences
for species-specific
hybridization probes

ATCCGGTA AAGTTACTGG TAAGACCT

CATGA TTGAACCATC CACCA (C. albicans) 577
CATGA TTGAAGCTTC CACCA (C. dubliniensis) 578

The sequence numbering refers to the Candida albicans tuf gene fragment (SEQ ID NO. 408). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches for SEQ ID NO. 577 are indicated by lower-case letters. Mismatches for SEQ ID NO. 578 are indicated by underlined nucleotides. Dots indicate gaps in the sequences displayed.
"R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a C. albicans primers have been described in a previous patent (publication WO98/20157, SEQ ID NOS. 11-12)

^b This sequence is the reverse-complement of the selected primer.

Annex XII: Strategy for the selection of *Staphylococcus*-specific amplification primers from *tuf* sequences.

	310	340	682	SEQ ID NO.:	Accession #:
5	<i>S. aureus</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...CACTTACCA GAAGGTACTG AAATGGTAAT GC	682	179	-
	<i>S. aureus</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...CACTTACC~		176	-
	<i>S. aureus</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...CACTTACCA GAAGGTACTG AAATGGTAAT GC		177	-
	<i>S. aureus aureus</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...CACTTACCA GAAGGTACTG AAATGGTAAT GC		180	-
10	<i>S. auricularis</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...ActTTACCA GAAGGTACTG AAATGGTAAT GC		181	-
	<i>S. capitis capitis</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...AACTTACCA GAAGGTACTG AAATGGTAAT GC		182	-
	<i>M. caseolyticus</i>	A CTGgaCGTGT TGAACGTGCT CAAATCAAAG...AACTTACCA GAAGGTACTG AAATGGTAAT GC		183	-
	<i>S. cohnii</i>	A CAGGcCGTGT TGAACGTGCT CAAATCAAAG...ActTTACCA GAAGGTACTG AAATGGTAAT GC		184	-
	<i>S. epidermidis</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...~		185	-
15	<i>S. epidermidis</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...AACTTACCA GAAGGTACTG AAATGGTAAT GC		141*	-
	<i>S. haemolyticus</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...AACTTACCA GAAGGTACTG AAATGGTAAT GC		186	-
	<i>S. haemolyticus</i>	A CAGGtCGTGT TGAACGTGCT CAAATCAAAG...AACTTACCA GAAG~		188	-
	<i>S. haemolyticus</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...AACTTACCA GAAGGTACTG AAATGG~		189	-
	<i>S. hominis hominis</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...AACTTACCA GAAGGTACTG AAATGGTAAT GC		191	-
	<i>S. hominis</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...AACTTACCA GAAGGTACTG AAATGGTAAT GC		193	-
20	<i>S. hominis</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...AACTTACCA GAAG~		194	-
	<i>S. hominis</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...AACTTACCA GAAGGTACTG AAATGGTAAT GC		195	-
	<i>S. hominis</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...AACTTACCA GAAGGTACTG AAATGGTAAT GC		196	-
	<i>S. lugdunensis</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...AACTTACCA GAAGGTACTG AAATGGTAAT GC		197	-
	<i>S. saprophyticus</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...~		198	-
25	<i>S. saprophyticus</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...AACTTACCA GAAGGTACTG AAATGGTAAT GC		199	-
	<i>S. saprophyticus</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...AACTTACCA GAAGGTACTG AAATGGTAAT GC		200	-
	<i>S. sciuri sciuri</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCACTG...AACTTACCA GAAGGTACTG AAATGGTAAT GC		201	-
	<i>S. warneri</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...CAaTTACCA GAAGGTACTG ~		187	-
30	<i>S. warneri</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...~		192	-
	<i>S. warneri</i>	A CAGGCCGCTGT TGAACGTGCT CAAATCAAAG...CAaTTACCA GAAGGTACTG AAATGGTAAT GC		202	-
	<i>B. subtilis</i>	A CTGGCCGCTGT aGAACGCGGa CAaGtTAAAG...CAtoTtCCA GAAGGcgtag AAATGGTAAT GC		-	299104
	<i>E. coli</i>	A CCGGtCGTGT aGAACGCGGT atcATCAAAG...GAaCTgCCg GAAGGcgtag AgATGGTAAT GC		78	-
	<i>L. monocytogenes</i>	A CTGgaCGTGT TGAACGTGCT CAAgTtAAAG...AcacTtCCA GAAGGTACTG AAATGGTAAY GC		138*	-
35	selected sequence for genus-specific primer	GGCCGCTGT TGAACGTGCT CAAATCA		553	
40	Selected sequences for genus-specific primers ^b	TTACCA GAAGGTACTG AAATGGTAA TTACCA GAAGGTACTG AAATGGTAA		575 707	

The sequence numbering refers to the *Staphylococcus aureus* *tuf* gene fragment (SEQ ID NO. 179). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. "~" indicate incomplete sequence data. Dots. indicate gaps in the sequences displayed.

"R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

* The SEQ ID NO. refers to previous patent publication WO98/20157.
b These sequences are the reverse-complement of the selected primers.

Annex XIII: Strategy for the selection of the *Staphylococcus*-specific hybridization probe from *tuf* sequences.

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		400	425	SEQ ID NO.:	Accession #:
	<i>S. aureus</i>	G TTGAAATGTT CCGTAAATTA TTAGA	179	-	
10	<i>S. aureus</i>	G TTGAAATGTT CCGTAAATTA TTAGA	176	-	
	<i>S. aureus</i>	G TTGAAATGTT CCGTAAATTA TTAGA	177	-	
	<i>S. aureus</i>	G TTGAAATGTT CCGTAAATTA TTAGA	178	-	
	<i>S. aureus aureus</i>	G TTGAAATGTT CCGTAAATTA TTAGA	180	-	
	<i>S. auricularis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	181	-	
15	<i>S. capitis capitis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	182	-	
	<i>M. caseolyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	183	-	
	<i>S. cohnii</i>	G TAGAAATGTT CCGTAAATTA TTAGA	184	-	
	<i>S. epidermidis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	185	-	
	<i>S. haemolyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	186	-	
20	<i>S. haemolyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	189	-	
	<i>S. haemolyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	190	-	
	<i>S. haemolyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	188	-	
	<i>S. hominis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	196	-	
	<i>S. hominis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	194	-	
25	<i>S. hominis hominis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	191	-	
	<i>S. hominis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	193	-	
	<i>S. hominis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	195	-	
	<i>S. lugdunensis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	197	-	
	<i>S. saprophyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	198	-	
30	<i>S. saprophyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	200	-	
	<i>S. saprophyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	199	-	
	<i>S. sciuri sciuri</i>	G TTGAAATGTT CCGTAAATTA TTAGA	201	-	
	<i>S. warneri</i>	G TAGAAATGTT CCGTAAgTTA TTAGA	187	-	
	<i>S. warneri</i>	G TAGAAATGTT CCGTAAgTTA TTAGA	192	-	
35	<i>S. warneri</i>	G TAGAAATGTT CCGTAAgTTA TTAGA	202	-	
	<i>S. warneri</i>	G TAGAAATGTT CCGTAAgTTA TTAGA	203	-	
	<i>B. subtilis</i>	G TTGAAATGTT CCGTAAgcTt cTTGA	-	299104	
	<i>E. coli</i>	G TTGAAATGTT CCGcAAAcTg cTGGA	78	-	
40	<i>L. monocytogenes</i>	G TAGAAATGTT CCGTAAATTA cTAGA	138 ^a	-	
	Selected sequence for genus-specific hybridization probe	GAAATGTT CCGTAAATTA TT	605		

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The sequence numbering refers to the *Staphylococcus aureus tuf* gene fragment (SEQ ID NO. 179). Nucleotides in capitals are identical to the selected sequence or match that sequence. Mismatches are indicated by lower-case letters.

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^a The SEQ ID NO. refers to previous patent publication WO98/20157.

Annex XIV: Strategy for the selection of *Staphylococcus saprophyticus*-specific and of *Staphylococcus haemolyticus*-specific hybridization probes from *tuf* sequences.

5

						SEQ ID
						NO.:
10		339			383	
	<i>S. aureus</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACaTC TAA				179
	<i>S. aureus</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACaTC TAA				176
	<i>S. aureus</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACaTC TAA				177
	<i>S. aureus</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACaTC TAA				178
15	<i>S. aureus aureus</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACaTC TAA				180
	<i>S. auricularis</i>	AG TCGGTGAAGA AgTtGAAATC ATcGGTATga AaGACggTTC AAA				181
	<i>S. capitis capitis</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTATCC AcGaaACTTC TAA				182
	<i>M. caseolyticus</i>	AG TtGGTGAAGA AgTtGAAATC ATTGGTtTaa cTGAagaacC AAA				183
	<i>S. cohnii</i>	AG TCGGTGAAGA AgTtGAAATC ATcGGTATgC AaGAagaTTC CAA				184
20	<i>S. epidermidis</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTATgC AcGaaACTTC TAA				185
	<i>S. haemolyticus</i>	AG TtGGTGAAGA AgTtGAAATC ATTGGTATCC ATGACACTTC TAA				186
	<i>S. haemolyticus</i>	AG TtGGTGAAGA AgTtGAAATC ATTGGTATCC ATGACACTTC TAA				189
	<i>S. haemolyticus</i>	AG TtGGTGAAGA AgTtGAAATC ATTGGTATCC ATGACACTTC TAA				190
	<i>S. haemolyticus</i>	AG TtGGTGAAGA AgTtGAAATt ATTGGTATCa AaGaaACTTC TAA				188
25	<i>S. hominis</i>	AG TtGGTGAAGA AgTtGAAATt ATTGGTATCa AaGaaACTTC TAA				194
	<i>S. hominis hominis</i>	AG TtGGTGAAGA AgTtGAAATt ATTGGTATCa AaGaaACTTC TAA				191
	<i>S. hominis</i>	AG TtGGTGAAGA AgTtGAAATt ATTGGTATCa AaGaaACTTC TAA				193
	<i>S. hominis</i>	AG TtGGTGAAGA AgTtGAAATt ATTGGTATCa AaGaaACTTC TAA				195
	<i>S. hominis</i>	AG TtGGTGAAGA AgTtGAAATt ATTGGTATCa AaGaaACTTC TAA				196
30	<i>S. lugdunensis</i>	AG TCGGTGAAGA AgTtGAAATt ATTGGTATCC AcGaaACTaC TAA				197
	<i>S. saprophyticus</i>	AG TCGGTGAAGA AATCGAAATC ATcGGTATgC AaGAagaaTC CAA				198
	<i>S. saprophyticus</i>	AG TCGGTGAAGA AATCGAAATC ATcGGTATgC AaGAagaaTC CAA				200
	<i>S. saprophyticus</i>	AG TCGGTGAAGA AATCGAAATC ATcGGTATgC AaGAagaaTC CAA				199
	<i>S. sciuri sciuri</i>	TG TtGGTGAAGA AgTtGAAATC ATcGGTtTaa cTGAagaaTC TAA				201
35	<i>S. warneri</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACTTC TAA				187
	<i>S. warneri</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACTTC TAA				192
	<i>S. warneri</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACTTC TAA				202
	<i>S. warneri</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACTTC TAA				203
	<i>B. subtilis</i>	AG TCGGTGAcGA AgTtGAAATC ATcGGTcTtC AaGAagagag AAA				- ^a
40	<i>E. coli</i>	AG TtGGTGAAGA AgTtGAAATC gTTGGTATCa AaGagACTca GAA				78
	<i>L. monocytogenes</i>	AG TtGGTGAcGA AgTaGAAGtT ATcGGTATCg AaGAagaaag AAA				138 ^b

Selected sequences for
species-specific

45	hybridization probes	CGGTGAAGA AATCGAAATC A (<i>S. saprophyticus</i>)	599
		(<i>S. haemolyticus</i>) ATTGGTATCC ATGACACTTC	594

The sequence numbering refers to the *Staphylococcus aureus tuf* gene fragment (SEQ ID NO. 179). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters.

^a This sequence was obtained from Genbank accession #Z99104.

^b The SEQ ID NO. refers to previous patent publication WO98/20157.

Annex XV: Strategy for the selection of *Staphylococcus aureus*-specific and of *Staphylococcus epidermidis*-specific hybridization probes from *tuf* sequences.

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		521	547	592	617	SEQ ID NO.:
10	<i>S. aureus</i>	TACACCACA TACTGAATTC	AAAGCAG...TTCTTCTCa	AACTATCGtC	CACAATT	179
	<i>S. aureus</i>	TACACCACA TACTGAATTC	AAAGCAG...TTCTTCTC-	-----	-----	178
	<i>S. aureus</i>	TACACCACA TACTGAATTC	AAAGCAG...TTCTTCTCa	AACTATCGtC	CACAATT	176
	<i>S. aureus</i>	TACACCACA TACTGAATTC	AAAGCAG...TTCTTCTCa	AACTATCGtC	CACAATT	177
	<i>S. aureus aureus</i>	TACACCACA TACTGAATTC	AAAGCAG...TTCTTCTCa	AACTATCGtC	CACAATT	180
15	<i>S. auricularis</i>	TACACCACA cACTaAATTC	ActGCAG...TTCTTCTCT	AACTAcCGtC	CACAATT	181
	<i>S. capitis capitis</i>	CACACCACA cACTaAATTC	AAAGCGG...TTCTTCAGT	AACTAcCGCC	CACAATT	182
	<i>M. caseolyticus</i>	TACTCCACA TACTaAATTC	AAAGCTG...TTCTTCACT	AACTAcCGCC	CtCAGTT	183
	<i>S. cohnii</i>	TACACCACA cACaaAcTTt	AAAGCGG...TTCTTCAGT	AACTATCGCC	CACAATT	184
	<i>S. epidermidis</i>	TACACCACA cACaaAATTC	AAAGCTG...TTCTTCACT	AACTATCGCC	CACAATT	185
20	<i>S. haemolyticus</i>	CACACCtCA cACaaAATTC	AAAGCAG...TTCTTCACa	AACTATCGtC	CACAATT	186
	<i>S. haemolyticus</i>	CACACCtCA cACaaAATTC	AAAGCAG...TTCTTCACa	AACTATCGtC	CACAATT	189
	<i>S. haemolyticus</i>	CACACCtCA cACaaAATTC	AAAGCAG...TTCTTCACa	AACTATCGtC	CACAATT	190
	<i>S. haemolyticus</i>	TACACCtCA cACaaAATTC	AAAGCAG...TTCTTCACT	AACTATCGtC	CACAATT	188
	<i>S. hominis</i>	CACACCtCA cACaaAATTC	AAAGCAG...TTCTTCACT	AACTATCGtC	CACAATT	195
25	<i>S. hominis</i>	TACACCtCA cACaaAATTC	AAAGCAG...TTCTTCACT	AACTATCGtC	CACAATT	196
	<i>S. hominis hominis</i>	TACACCtCA cACaaAATTC	AAAGCAG...TTCTTCTCT	AACTATCGtC	CACAATT	191
	<i>S. hominis</i>	TACACCtCA cACaaAATTC	AAAGCAG...TTCTTCTCT	AACTATCGtC	CACAATT	193
	<i>S. hominis</i>	TACACCtCA cACaaAATTC	AAAGCAG...TTCTTCTCT	AACTATCGtC	CACAATT	194
	<i>S. lugdunensis</i>	TACACCtCA cACTaAATTC	AAAGCTG...TTCTTCTCa	AACTAcCGCC	CACAATT	197
30	<i>S. saprophyticus</i>	TACACCACA TACaaAATTC	AAAGCGG...TTCTTCACT	AACTAcCGCC	CACAATT	198
	<i>S. saprophyticus</i>	TACACCACA TACaaAATTC	AAAGCGG...TTCTTCACT	AACTAcCGCC	CACAATT	199
	<i>S. saprophyticus</i>	TACACCACA TACaaAATTC	AAAGCGG...TTCTTCACT	AACTAcCGCC	CACAATT	200
	<i>S. sciuri sciuri</i>	CACACCtCA cACTaAATTC	AAAGCTG...TTCTTCACa	AACTAcCGCC	CACAATT	201
	<i>S. warneri</i>	TACACCACA TACaaAATTC	AAAGCGG...-----	-----	-----	192
35	<i>S. warneri</i>	TACACCACA TACaaAATTC	AAAGCGG...TTCTTCAGT	AACTAcCGCC	CACAATT	187
	<i>S. warneri</i>	TACACCACA TACaaAATTC	AAAGCGG...TTCTTCAGT	AACTAcCGCC	CACAATT	202
	<i>S. warneri</i>	TACACCACA TACaaAATTC	AAAGCGG...TTCTTCAGT	AACTAcCGCC	CACAATT	203
	<i>B. subtilis</i>	CACtCCACA cAgcaAATTC	AAAGCTG...TTCTTCTCT	AACTAcCGtC	CtCAGTT	- ^a
	<i>E. coli</i>	CAAgCCgCA cACcaAgTTC	gAAtCTG...TTCTTCaaa	ggCTAcCGtC	CgCAGTT	78
40	<i>L. monocytogenes</i>	TACTCCACA cACTaAcTTC	AAAGCTG...TTCTTCAac	AACTAcCGCC	CACAATT	138 ^b

Selected sequences
for species-specific
hybridization

45	probes	ACCACA TACTGAATTC AAAG (<i>S. aureus</i>)	585
		(<i>S. epidermidis</i>) TTCACT AACTATCGCC CACA	593

50 The sequence numbering refers to the *Staphylococcus aureus tuf* gene fragment (SEQ ID NO. 179). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. "-" indicate incomplete sequence data. Dots indicate gaps in the sequences displayed.

^a This sequence was obtained from Genbank accession #Z99104.

^b The SEQ ID NO. refers to previous patent publication WO98/20157.

Annex XVI: Strategy for the selection of the *Staphylococcus hominis*-specific hybridization probe from *tuf* sequences.

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	358	383	SEQ ID NO.:
<i>S. aureus</i>	ATC ATcGGTtTac AtGAcACaTC TAA		179
10 <i>S. aureus</i>	ATC ATcGGTtTac AtGAcACaTC TAA		176
<i>S. aureus</i>	ATC ATcGGTtTac AtGAcACaTC TAA		177
<i>S. aureus</i>	ATC ATcGGTtTac AtGAcACaTC TAA		178
<i>S. aureus aureus</i>	ATC ATcGGTtTac AtGAcACaTC TAA		180
<i>S. auricularis</i>	ATC ATcGGTATgA AAGAcggTTC AAA		181
15 <i>S. capitis capitis</i>	ATC ATcGGTATCc AcGAAACTTC TAA		182
<i>M. caseolyticus</i>	ATC ATTGGTtTaa ctGAAGAacC AAA		183
<i>S. cohnii</i>	ATC ATcGGTATgc AAGAAGaTTC CAA		184
<i>S. epidermidis</i>	ATC ATcGGTATgc AcGAAACTTC TAA		185
<i>S. haemolyticus</i>	ATC ATTGGTATCc AtGAcACTTC TAA		186
20 <i>S. haemolyticus</i>	ATC ATTGGTATCc AtGAcACTTC TAA		189
<i>S. haemolyticus</i>	ATC ATTGGTATCc AtGAcACTTC TAA		190
<i>S. haemolyticus</i>	ATT ATTGGTATCA AAGAACTTC TAA		188
<i>S. hominis</i>	ATT ATTGGTATCA AAGAtACTTC TAA		196
<i>S. hominis</i>	ATT ATTGGTATCA AAGAACTTC TAA		194
25 <i>S. hominis hominis</i>	ATT ATTGGTATCA AAGAACTTC TAA		191
<i>S. hominis</i>	ATT ATTGGTATCA AAGAACTTC TAA		193
<i>S. hominis</i>	ATT ATTGGTATCA AAGAACTTC TAA		195
<i>S. lugdunensis</i>	ATT ATTGGTATCc AcGAtACTaC TAA		197
<i>S. saprophyticus</i>	ATC ATcGGTATgc AAGAAGaaTC CAA		198
30 <i>S. saprophyticus</i>	ATC ATcGGTATgc AAGAAGaaTC CAA		200
<i>S. saprophyticus</i>	ATC ATcGGTATgc AAGAAGaaTC CAA		199
<i>S. sciuri sciuri</i>	ATC ATcGGTtTaa ctGAAGaaTC TAA		201
<i>S. warneri</i>	ATC ATcGGTtTac AtGAcACTTC TAA		187
<i>S. warneri</i>	ATC ATcGGTtTac AtGAcACTTC TAA		192
35 <i>S. warneri</i>	ATC ATcGGTtTac AtGAcACTTC TAA		202
<i>S. warneri</i>	ATC ATcGGTtTac AtGAcACTTC TAA		203
<i>B. subtilis</i>	ATC ATcGGTcTtc AAGAAGagag AAA		- ^a
<i>E. coli</i>	ATC gTTGGTATCA AAGAGACTca GAA		78
<i>L. monocytogenes</i>	GTT ATcGGTATCg AAGAAGaaag AAA		138 ^b
40	Selected sequence for species-specific hybridization probe		
	ATTGGTATCA AAGAACTTC		597

45

The sequence numbering refers to the *Staphylococcus aureus tuf* gene fragment (SEQ ID NO. 179). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

50

^a This sequence was obtained from Genbank accession #Z99104.

^b The SEQ ID NO. refers to previous patent publication WO98/20157.

Annex XVII: Strategy for the selection of the *Enterococcus*-specific amplification primers from *tuf* sequences.

		270	298	556	582	SEQ ID NO.:	Accession #:
5	<i>E. avium</i>	TAGAAATTAAT	GGCTGCTGTT	GACGAATAT...TGAA	GATATCCAAC	131 ^a	-
	<i>E. casseliflavus</i>	TGGAAATTAAT	GGCTGCAGTT	GACGAATAT...TGAA	GATATCCAAC	58	-
	<i>E. cecorum</i>	TAGAATTAAT	GGCTGCAGTT	GACGAATAT...TGAA	GATATCCAAC	59	-
	<i>E. dispar</i>	TAGAATTAAT	GGCTGCAGTT	GACGAATAT...TGAA	GATATCCAAC	60	-
	<i>E. durans</i>	TTGAATTAAT	GGCTGCAGTT	GACGAATAT...TGAA	GATATCCAAC	61	-
10	<i>E. flavescens</i>	TGGAATTAAT	GGCTGCAGTT	GACGAATAT...TGAA	GATATCCAAC	65	-
	<i>E. faecium</i>	TTGAATTAAT	GGCTGCAGTT	GACGAATAT...TGAA	GATATCCAAC	608	-
	<i>E. faecalis</i>	TAGAATTAAT	GGCTGCAGTT	GACGAATAT...TGAA	GATATCCAAC	607	-
	<i>E. gallinarum</i>	TGGAATTAAT	GGCTGCAGTT	GACGAATAT...TGAA	GATATCCAAC	609	-
	<i>E. hirae</i>	TTGAATTAAT	GGCTGCAGTT	GACGAATAT...TGAA	GATATCCAAC	67	-
15	<i>E. mundtii</i>	TTGAATTAAT	GGCTGCAGTT	GACGAATAT...TGAA	GATATCCAAC	68	-
	<i>E. pseudoavium</i>	TAGAATTAAT	GGCTGCAGTT	GACGAATAT...TGAA	GATATCCAAC	69	-
	<i>E. raffinosus</i>	TAGAATTAAT	GGCTGCAGTT	GACGAATAT...TGAA	GATATCCAAC	70	-
	<i>E. saccharolyticus</i>	TCGAATTAAT	GGCTGCAGTT	GACGAATAT...TGAA	GATATCCAAC	71	-
	<i>E. solitarius</i>	TGGAATTAAT	GGCTGCAGTT	GACGAATAT...TGAA	GATATCCAAC	72	-
20	<i>E. coli</i>	TGGAATTAAT	GGCTGCAGTT	GACGAATAT...TGAA	GATATCCAAC	78	-
	<i>B. cepacia</i>	TCGAGCTGgg	CGAGGCTgg	GACGCTGg	GACGCTGg	16	-
	<i>B. fragilis</i>	TCGAGCTGgg	CGAGGCTgg	GACGCTGg	GACGCTGg	-	M22247
	<i>B. subtilis</i>	TCGAGCTGgg	CGAGGCTgg	GACGCTGg	GACGCTGg	-	Z99104
	<i>C. diphtheriae</i>	TCGAGCTGgg	CGAGGCTgg	GACGCTGg	GACGCTGg	662	-
25	<i>C. trachomatis</i>	GAGAGCTAAT	GCAAGGCTGg	GATGATAT...GAAG	GATGATAT...GAAG	22	-
	<i>G. vaginalis</i>	AGGAATTAAT	GCAAGGCTGg	GATGATAT...GAAG	GATGATAT...GAAG	135 ^a	-
	<i>S. aureus</i>	TAGAATTAAT	GCAAGGCTGg	GATGATAT...GAAG	GATGATAT...GAAG	179	-
	<i>S. pneumoniae</i>	TGGAATTAAT	GCAAGGCTGg	GATGATAT...GAAG	GATGATAT...GAAG	145 ^a	-
	<i>A. adiacens</i>	TAGAATTAAT	GGCTGCTGTT	GACGAATAT...TGAA	GATATCCAAC	118 ^a	-
30	<i>G. haemolysans</i>	TCGAATTAAT	GGAAACAGTT	GACGAATAT...TGAA	GATATCCAAC	87	-
	<i>G. morbillorum</i>	TCGAATTAAT	GGAAACAGTT	GACGAATAT...TGAA	GATATCCAAC	88	-

Selected sequence for amplification primer AATTAAT GGCTGCTGTT GAYGAA 1137

Selected sequence for amplification primer^b A GAYATCSEAAC GTGGACAAGT 1136

The sequence numbering refers to the *Enterococcus* *tuf* gene fragment (SEQ ID NO. 61). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed. 'y' 'w' and 's' designate nucleotide positions which are degenerated. 'y' stands for C or T; 'w' stands for A or T; 's' stands for C or G. 'I' stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a The SEQ ID NO. refers to previous patent publication WO98/20157.

^b This sequence is the reverse-complement of the selected primer.

Annex XVIII: Strategy for the selection of the *Enterococcus faecalis*-specific hybridization probe, of the *Enterococcus faecium*-specific hybridization probe and of the *Enterococcus casseliflavus*-*flavescens*-*gallinarum* group-specific hybridization probe from tuf sequences.

5

		448...526	549 SEQ ID NO.: Accession #:
395	<i>E. avium</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	131 ^a
	<i>E. casseliflavus</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	58
10	<i>E. cecorum</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	59
	<i>E. dispar</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	60
	<i>E. durans</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	61
	<i>E. faecalis</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	62
15	<i>E. faecium</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	608
	<i>E. flavescens</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	65
	<i>E. gallinarum</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	609
	<i>E. hirae</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	67
	<i>E. mundtii</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	68
	<i>E. pseudoavium</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	69
20	<i>E. raffinosus</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	70
20	<i>E. saccharolyticus</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	71
20	<i>E. solitarius</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	72
	<i>C. diphtheriae</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	662
	<i>G. vaginalis</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	135 ^a
25	<i>B. cepacia</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	16
	<i>S. aureus</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	179
	<i>B. subtilis</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	299104
	<i>S. pneumoniae</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	145 ^a
30	<i>E. coli</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	78
	<i>B. fragilis</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	M22247
	<i>C. trachomatis</i>	GTGGA ACGTGGACAA GTTCGCGTTC GTGACGAACT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	22
	Selected sequences for species-specific or group-specific hybridization probes	GA ACGTGGTGA GTTCGC (<i>E. faecalis</i>) AAGT TGAAGTTGTT GGTATT (<i>E. faecium</i>) T GGTGCATTGC TACGTGG	1174 602 1122

The sequence numbering refers to the *Enterococcus faecium* tuf gene fragments (SEQ ID NO. 608). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^a The SEQ ID NO. refers to previous patent publication WO98/20157.

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Annex XIX: Strategy for the selection of primers for the identification of platelets contaminants from tuf sequences.

		467	495	689	717	SEQ ID NO.:	Accession #:
5						7	-
	<i>B. cereus</i>	GTA ACTGGGTGTAAG AGATGTTCCG TAAACT...C AGTTCTACTT CCGTACAACT GACGTAAC				-	Z99104
	<i>B. subtilis</i>	GTT ACaGGTGTG AAATGTTCCG TAAGCT...C AGTTCTACTT CCGTACAACT GACGTAAC				54	-
	<i>E. cloacae</i>	TGT ACTGGCGGTG AAATGTTCCG CAAACT...C AGTTCTACTT CCGTACAACT GACGTGAC				78	-
	<i>E. coli</i>	TGT ACTGGCGGTG AAATGTTCCG CAAACT...C AGTTCTACTT CCGTACAACT GACGTGAC				100	-
10	<i>K. oxytoca</i>	TGT ACTGGCGGTG AAATGTTCCG CAAACT...C AGTTCTACTT CCGTACAACT GACGTGAC				103	-
	<i>K. pneumoniae</i>	TGT ACTGGCGGTG AAATGTTCCG CAAACT...C AGTTCTACTT CCGTACAACT GACGTGAC				153	-
	<i>P. aeruginosa</i>	TGC ACcGGCGGTG AAATGTTCCG CAAAGCT...C AGTTCTACTT CCGTACCACT GACGTGAC				209	-
	<i>S. agalactiae</i>	GTT ACTGGGTGTTG AAATGTTCCG TAAACA...C AATTCTACTT CCGTACAACT GACGTAAC				140 ^a	-
	<i>S. aureus</i>	GTT ACaGGTGTG AAATGTTCCG TAAATT...C AATTCTACTT CCGTACAACT GACGTAAC				159	-
15	<i>S. choleraesuis</i>	TGT ACTGGCGGTG AAATGTTCCG CAAACT...C AGTTCTACTT CCGTACAACT GACGTAAC				611	-
	<i>S. epidermidis</i>	GTT ACTGGGTGTAAG AAATGTTCCG TAAATT...C AATTCTACTT CCGTACAACT GACGTAAC				168	-
	<i>S. marcescens</i>	TGT ACTGGCGGTG AAATGTTCCG CAAACT...C AGTTCTACTT CCGTACCACT GACGTGAC				224	-
	<i>S. mutans</i>	GTT ACTGGGTGTTG AAATGTTCCG TAAACA...C AATTCTACTT CCGTACAACT GACGTAAC				-	U40453
	<i>S. pyogenes</i>	GTT ACTGGGTGTTG AAATGTTCCG TAAACA...C AATTCTACTT CCGTACAACT GACGTAAC				146 ^a	-
20	<i>S. salivarius</i>	GTT ACTGGGTGTTG AAATGTTCCG TAAACA...C AGTTCTACTT CCGTACAACT GACGTTAC				227	-
	<i>S. sanguinis</i>	GTT ACTGGGTGTTG AAATGTTCCG TAAACA...C AGTTCTACTT CCGTACAACT GACGTTAC				235	-
	<i>Y. enterocolitica</i>	TGT ACTGGCGGTG AAATGTTCCG CAAACT...C AGTTCTACTT CCGTACAACT GACGTAAC					

Selected sequence for amplification primer

ACTGGYGTG ALATGTTCCG YAA

636

Selected sequence for amplification primer^b

TTCTAYTT CCGTACIACT GACGT

637

The sequence numbering refers to the *E. coli* tuf gene fragment (SEQ ID NO. 78). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

"R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a The SEQ ID NO. refers to previous patent publication WO98/20157.

^b This sequence is the reverse-complement of the selected primer.

Annex XX: Strategy for the selection of the universal amplification primers from *atpD* sequences.

[illegible]

35 The sequence numbering refers to the *Escherichia coli atpD* gene fragment (SEQ ID NO. 669). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches for SEQ ID NOs. 562 and 565 are indicated by lower-case letters. Mismatches for SEQ ID NOs. 564 and 563 are indicated by underlined nucleotides. Dots indicate gaps in the sequences displayed.

"R" "Y" "M" "K" "W" and "S" letters designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "H" stands for A, C or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

* These sequences are the reverse-complement of the selected primers.

Annex XXI: Specific and ubiquitous primers for nucleic acid amplification (recA sequences).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
Universal primers (recA)			
919	5'-GGI CCI GAR TCI TMI GGI AAR AC	918 ^a	437-459
920 ^b	5'-TCI CCV ATI TCI CCI TCI AIY TC	918 ^a	701-723
921	5'-TIY RTI GAY GCI GAR CAI GC	918 ^a	515-534
922 ^b	5'-TAR AAY TTI ARI GCI YKI CCI CC	918 ^a	872-894
Sequencing primers (recA)			
1605	5'-ATY ATY GAA RTI TAY GCI CC	1704 ^a	220-239
1606	5'-CCR AAC ATI AYI CCI ACT TTT TC	1704 ^a	628-650
Universal primers (rad51)			
935	5'-GGI AAR WSI CAR YTI TGY CAY AC	939 ^a	568-590
936 ^b	5'-TCI SIY TCI GGI ARR CAI GG	939 ^a	1126-1145
Universal primers (dmc1)			
937	5'-ATI ACI GAR GYI TTY GGI GAR TT	940 ^a	1038-1060
938 ^b	5'-CYI GTI GYI SWI GCR TGI GC	940 ^a	1554-1573

^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex XXII: Specific and ubiquitous primers for nucleic acid amplification (*speA* sequences).

5	Originating DNA fragment			
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial species: <i>Streptococcus pyogenes</i></u>			
15	994	5'-TGG ACT AAC AAT CTC GCA AGA GG	993 ^a	60-82
	995 ^b	5'-ACA TTC TCG TGA GTA ACA GGG T	993 ^a	173-194
	996	5'-ACA AAT CAT GAA GGG AAT CAT TTA G	993 ^a	400-424
	997 ^b	5'-CTA ATT CTT GAG CAG TTA CCA TT	993 ^a	504-526
20	998	5'-GGA GGG GTA ACA AAT CAT GAA GG	993 ^a	391-413
	997 ^b	5'-CTA ATT CTT GAG CAG TTA CCA TT	993 ^a	504-526

^a Sequence from databases.

25 ^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex XXIII: First strategy for the selection of *Streptococcus pyogenes*-specific amplification primers from *speA* sequences.

	Accession #	57	85	170	197	SEQ ID NO.:
5	<i>speA</i> X61573	CCTT GGGCTAAACAA	CCTCaCAAGA	AGTAT...GTGATCCTT.GT	CGTTCATGAG AATGTAAA	-
	<i>speA</i> AF029051	-----	GGGCTAAACAA	CCTCaCAAGA	AGTAT...GTGATCCTT.GT	CGTTCATGAG AATGTAAA
	<i>speA</i> X61571	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA	-
	<i>speA</i> X61570	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA	-
	<i>speA</i> X61568	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA	-
10	<i>speA</i> X61569	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA	-
	<i>speA</i> X61572	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA	-
	<i>speA</i> X61560	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA	-
	<i>speA</i> U40453	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA	993
15	<i>speA</i> X61554	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA	-
	<i>speA</i> X61557	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA	-
	<i>speA</i> X61559	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA	-
	<i>speA</i> X61558	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA	-
	<i>speA</i> X61556	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA	-
	<i>speA</i> X61555	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA	-
20	<i>speA</i> X61560	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA	-
	<i>speA</i> X61561	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA	-
	<i>speA</i> X61566	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA	-
	<i>speA</i> X61567	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA	-
	<i>speA</i> X61562	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA	-
25	<i>speA</i> X61563	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA	-
	<i>speA</i> X61564	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA	-
	<i>speA</i> X61565	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA	-
	<i>speA</i> AF055698	-----	GGACTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACCAG AATGTGAA
30	<i>speA</i> X03929 ^a	TCCTT GGGCTAAACAA	TCTCGCAAGA	GGTAT...GTGACCCCTGGT	TACTCACCAG AATGTGAA	-
	Selected sequence for species-specific primer	T	GGACTAAACAA	TCTCGCAAGA	GG	994
35	Selected sequence for species-specific primer ^b			ACCCTT.GT	TACTCACCAG AATGT	995

The sequence numbering refers to the *Streptococcus pyogenes speA* gene fragment (SEQ ID NO. 993). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. "-" indicate incomplete sequence data. Dots indicate gaps in the sequences displayed.

^a The extra G nucleotide introducing a gap in the sequence is probably a sequencing error.

^b This sequence is the reverse-complement of the selected primer.

Annex XXIV: Second strategy for the selection of *Streptococcus pyogenes*-specific amplification primers from *speA* sequences.

5	speA	Accession #	388	427	501	529	SEQ ID NO.		
	speA	AF029051	TA TGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
	speA	X61571	TA TGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
	speA	X61570	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
	speA	X61568	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
10	speA	X61569	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
	speA	X61572	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
	speA	X61560	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
	speA	U40453	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
	speA	X61554	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	993
15	speA	X61557	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
	speA	X61559	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
	speA	X61558	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
	speA	X61556	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
	speA	X61555	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
20	speA	X61560	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
20	speA	X61561	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
	speA	X61566	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
	speA	X61567	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
25	speA	X61562	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
	speA	X61563	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
	speA	X61564	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
	speA	X61565	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
	speA	AF055698	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
30	speA	X03929	TA CGGAGGGGTA	ACAAATCATG	AAGGGAAATCA	TTTAGAAA...AAAAATGGT	AACTGCTCAA	GAATTAGACT	-
	Selected sequences for species-specific primers		CGAGGGGTA	ACAAATCATG	AAGG				998
			ACAAATCATG	AAGGGAAATCA	TTTAG				996
35	Selected sequence for species-specific primer ^a					AATGGT	AACTGCTCAA	GAATTAG	997

The sequence numbering refers to the *Streptococcus pyogenes speA* gene fragment (SEQ ID NO. 993). Dots indicate gaps in the sequences displayed.

^a This sequence is the reverse-complement of the selected primer.

Annex XXV: Strategy for the selection of Streptococcus pyogenes-specific amplification primers from tuf sequences.

		140	186	619	647	SEQ ID NO.:
5	<i>S. anginosus</i>	A AGTTGACTTg GTTGACGATg AAGAATTGCT TGAATTgGTT GAAATG...CC AGTTTCAATc cAtCCACACa CTAAATTT				211
	<i>S. bovis</i>	A AGTTGACCTT GTTGACGATg AAGAATTGCT TGAATTgGTT GAAATG...CC AGTTTCAATc cAtCCACACa CTAAATTT				212
	<i>S. dysgalactiae</i>	A AATTGACCTT GTTGACGATg AAGAATTGCT TGAATTgGTT GAAATG...CC AGTTTCAATc AAtCCACACa CTAAATTT				217
	<i>S. pyogenes</i>	A AGTTGACCTT GTTGACGATg AAGAATTGCT TGAATTgGTT GAAATG...CC AGTTTCAATc AAtCCACACa CTAAATTT				1002
	<i>S. agalactiae</i>	A AGTTGACCTT GTTGACGATg AAGAATTGCT TGAATTgGTT GAAATG...CC AGTTTCAATc AAtCCACACa CTAAATTT				144 ^a
10	<i>S. oralis</i>	A AATTGACTTg GTTGACGATg AAGAATTGCT TGAATTgGTT GAAATG...CC AGTTTCAATc AAtCCACACa CTAAATTT				985
	<i>S. pneumoniae</i>	A AGTTGACTTg GTTGACGATg AAGAATTGCT TGAATTgGTT GAAATG...CC AGTTTCAATc AAtCCACACa CTAAATTT				145 ^a
	<i>S. cristatus</i>	A GATCGACTTg GTTGACGATg AAGAATTGCT TGAATTgGTT GAAATG...CC AGTTTCAATc AAtCCACACa CTAAATTT				215
	<i>S. mitis</i>	A GATCGACTTg GTTGACGATg AAGAATTGCT TGAATTgGTT GAAATG...CC AGTTTCAATc AAtCCACACa CTAAATTT				982
	<i>S. gordonii</i>	A AGTTGACTTg GTTGACGATg AAGAATTGCT TGAATTgGTT GAAATG...CC AGTTTCAATc AAtCCACACa CTAAATTT				200
15	<i>S. sanguinis</i>	A AGTTGACTTg GTTGACGATg AAGAATTGCT TGAATTgGTT GAAATG...CC AGTTTCAATc AAtCCACACa CTAAATTT				227
	<i>S. parasanguinis</i>	A AGTTGACTTg GTTGACGATg AAGAATTGCT TGAATTgGTT GAAATG...CC AGTTTCAATc AAtCCACACa CTAAATTT				225
	<i>S. salivarius</i>	A AGTTGACTTg GTTGACGATg AAGAATTGCT TGAATTgGTT GAAATG...CC AGTTTCAATc AAtCCACACa CTAAATTT				146 ^a
	<i>S. vestibularis</i>	A AGTTGACTTg GTTGACGATg AAGAATTGCT TGAATTgGTT GAAATG...CC AGTTTCAATc AAtCCACACa CTAAATTT				231
	<i>S. suis</i>	A AGTTGACTTg GTTGACGATg AAGAATTGCT TGAATTgGTT GAAATG...CC AGTTTCAATc AAtCCACACa CTAAATTT				229
20	<i>S. mutans</i>	A AGTTGACTTg GTTGACGATg AAGAATTGCT TGAATTgGTT GAAATG...CC AGTTTCAATc AAtCCACACa CTAAATTT				224
2020	<i>S. ratti</i>	A GGTGACTTg GTTGACGATg AAGAATTGCT TGAATTgGTT GAAATG...CC AGTTTCAATc AAtCCACACa CTAAATTT				226
	<i>S. macacae</i>	A AGTTGACTTg GTTGACGATg AAGAATTGCT TGAATTgGTT GAAATG...CC AGTTTCAATc AAtCCACACa CTAAATTT				222
	<i>S. cricetus</i>	A GGTGACTTg GTTGACGATg AAGAATTGCT TGAATTgGTT GAAATG...CC AGTTTCAATc AAtCCACACa CTAAATTT				214
	<i>E. faecalis</i>	A AATGGATATg GTTGACGATg AAGAATTATt aGAATTAGTa GAAATG...CC AGTTTCAATc AAtCCACACa CaAAATTT				607
25	<i>S. aureus</i>	A AGTTGACATg GTTGACGATg AAGAATTATt aGAATTAGTa GAAATG...CC AGTTTCAATc AAtCCACACa CTgAAATTT				176
	<i>B. cereus</i>	A ATgCGACATg GTaGATGACg AAGAATTATt aGAATTAGTa GAAATG...AG CgGTTCTgTa AAgCtCACg CTAAATTT				7
	<i>E. coli</i>	A ATgCGACATg GTTGATGACg AAGAGCTGCT gGAACtGTT GAAATG...CC GgGCaCCATc AAgCCgCACa CgAAGTTT				78

Selected sequences for species-specific primers TTGACCTT GTTGATGACg AAGAG AAGAGTTGCT TGAATTAGTT GAG

Selected sequence for species-specific primer^b AGTTTCAATc AAtCCACACa CTAA 1000

35 The sequence numbering refers to the Streptococcus pyogenes tuf gene fragment (SEQ ID NO. 1002). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^a The SEQ ID NO. refers to previous patent publication WO98/20157.

^b This sequence is the reverse-complement of the selected primer.

Annex XXVI: Strategy for the selection *stx*₁-specific amplification primers and hybridization probe.

5	stx ₁	Accession #	230	263	343	375	391	421	SEQ ID NO.:					
	stx ₁	M19473a	TTGATGTC	AGAGGGATAG	ATCCAGAGGA	AGGGCG...TATCG	CTTTGCTGAT	TTTTCACATG	TTACCTTT...GTTACAT	TGTCCTGGTGA	CAGTAGCTAT	ACCA	421	
	stx ₁	M16625	TTGATGTC	AGAGGGATAG	ATCCAGAGGA	AGGGCG...TATCG	CTTTGCTGAT	TTTTCACATG	TTACCTTT...GTTACAT	TGTCCTGGTGA	CAGTAGCTAT	ACCA	-	
	stx ₁	M17358	TTGATGTC	AGAGGGATAG	ATCCAGAGGA	AGGGCG...TATCG	CTTTGCTGAT	TTTTCACATG	TTACCTTT...GTTACAT	TGTCCTGGTGA	CAGTAGCTAT	ACCA	-	
	stx ₁	Z36900	TTGATGTC	AGAGGGATAG	ATCCAGAGGA	AGGGCG...TATCG	CTTTGCTGAT	TTTTCACATG	TTACCTTT...GTTACAT	TGTCCTGGTGA	CAGTAGCTAT	ACCA	-	
10	stx ₁	L04539	TTGATGTC	AGAGGGATAG	ATCCAGAGGA	AGGGCG...TATCG	CTTTGCTGAT	TTTTCACATG	TTACCTTT...GTTACAT	TGTCCTGGTGA	CAGTAGCTAT	ACCA	-	
	stx ₁	M19437	TTGATGTC	AGAGGGATAG	ATCCAGAGGA	AGGGCG...TATCG	CTTTGCTGAT	TTTTCACATG	TTACCTTT...GTTACAT	TGTCCTGGTGA	CAGTAGCTAT	ACCA	-	
	stx ₁	M24352	TTGATGTC	AGAGGGATAG	ATCCAGAGGA	AGGGCG...TATCG	CTTTGCTGAT	TTTTCACATG	TTACCTTT...GTTACAT	TGTCCTGGTGA	CAGTAGCTAT	ACCA	-	
	stx ₁	X07903	TTGATGTC	AGAGGGATAG	ATCCAGAGGA	AGGGCG...TATCG	CTTTGCTGAT	TTTTCACATG	TTACCTTT...GTTACAT	TGTCCTGGTGA	CAGTAGCTAT	ACCA	-	
	stx ₁	Z36899	TTGATGTC	AGAGGGATAG	ATCCAGAGGA	AGGGCG...TATCG	CTTTGCTGAT	TTTTCACATG	TTACCTTT...GTTACAT	TGTCCTGGTGA	CAGTAGCTAT	ACCA	-	
15	stx ₁	Z36901	TTGATGTC	AGAGGGATAG	ATCCAGAGGA	AGGGCG...TATCG	CTTTGCTGAT	TTTTCACATG	TTACCTTT...GTTACAT	TGTCCTGGTGA	CAGTAGCTAT	ACCA	1076	
	stx ₂	X61283	TGGATATA	CGAGGGCTTG	ATGtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTtCaCATa	TatCaGtG...GTTtCca	TGcCaacgGA	CAGcAGtTAT	ACCA	-	
	stx ₂	L11079	TGGATATA	CGAGGGCTTG	ATGtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTtCaCATa	TatCaGtG...GTTtCca	TGcCaacgGA	CAGcAGtTAT	ACCA	-	
	stx ₂	M21534	TAGGTATA	CGAGGGCTTG	ATGtTtAtca	gGaGCG...TACag	aTTTtCaGAT	TTTgCaCATa	TatCaTTG...ATTtCca	TGcCaacgGA	CAGcAGtTAT	ACCA	-	
	stx ₂	M36727	TAGGTATA	CGAGGGCTTG	ATGtTtAtca	gGaGCG...TACag	aTTTtCaGAT	TTTgCaCATa	TatCaTTG...ATTtCca	TGcCaacgGA	CAGcAGtTAT	ACCA	-	
20	stx ₂	X81415	TAGGTATA	CGAGGGCTTG	ATGtTtAtca	gGaGCG...TACag	aTTTtCaGAT	TTTgCaCATa	TatCaTTG...ATTtCca	TGcCaacgGA	CAGcAGtTAT	ACCA	-	
	stx ₂	X81416	TAGGTATA	CGAGGGCTTG	ATGtTtAtca	gGaGCG...TACag	aTTTtCaGAT	TTTgCaCATa	TatCaTTG...ATTtCca	TGcCaacgGA	CAGcAGtTAT	ACCA	-	
	stx ₂	X81417	TAGGTATA	CGAGGGCTTG	ATGtTtAtca	gGaGCG...TACag	aTTTtCaGAT	TTTgCaCATa	TatCaTTG...ATTtCca	TGcCaacgGA	CAGcAGtTAT	ACCA	-	
	stx ₂	X81418	TAGGTATA	CGAGGGCTTG	ATGtTtAtca	gGaGCG...TACag	aTTTtCaGAT	TTTgCaCATa	TatCaTTG...ATTtCca	TGcCaacgGA	CAGcAGtTAT	ACCA	-	
	stx ₂	E03962	TGGATATA	CGAGGGCTTG	ATGtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTtCaCATa	TatCaGtG...GTTtCca	TGcCaacgGA	CAGcAGtTAT	ACCA	-	
25	stx ₂	E03959	TGGATATA	CGAGGGCTTG	ATGtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTtCaCATa	TatCaGtG...GTTtCca	TGcCaacgGA	CAGcAGtTAT	ACCA	-	
	stx ₂	X07865	TGGATATA	CGAGGGCTTG	ATGtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTtCaCATa	TatCaGtG...GTTtCca	TGcCaacgGA	CAGcAGtTAT	ACCA	-	
25	stx ₂	Y10775	TGGATATA	CGAGGGCTTG	ATGtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTtCaCATa	TatCaGtG...GTTtCca	TGcCaacgGA	CAGcAGtTAT	ACCA	-	
	stx ₂	Z37725	TGGATATA	CGAGGGCTTG	ATGtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTtCaCATa	TatCaGtG...GTTtCca	TGcCaacgGA	CAGcAGtTAT	ACCA	1077	
	stx ₂	Z50754	TGGATATA	CGAGGGCTTG	ATGtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTtCaCATa	TatCaGtG...GTTtCca	TGcCaacgGA	CAGcAGtTAT	ACCA	-	
30	stx ₂	X67514	TGGATATA	CGAGGGCTTG	ATGtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTtCaCATa	TatCaGtG...GTTtCca	TGcCaacgGA	CAGcAGtTAT	ACCA	-	
	stx ₂	L11078	TGGATATA	CGAGGGCTTG	ATGtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTtCaCATa	TatCaGtG...GTTtCca	TGcCaacgGA	CAGcAGtTAT	ACCA	-	
	stx ₂	X65949	TGGATATA	CGAGGGCTTG	ATGtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTtCaCATa	TatCaGtG...GTTtCca	TGcCaacgGA	CAGcAGtTAT	ACCA	-	
	stx ₂	AF043627	TGGATATA	CGAGGGCTTG	ATGtctAtca	gGcGCG...TACag	aTTTtCaGAT	TTTgCaCATa	TatCaGtG...GTTtCca	TGcCaacgGA	CAGcAGtTAT	ACCA	-	
35	Selected sequence for amplification primer ATGTC AGAGGGATAG ATCCAGAGGA AGG													1081
40	Selected sequence for hybridization probe CG CTTTGTCTGAT TTTTCACATG TTACC													1084
40	Selected sequence for amplification primer ^a ACAT TGTCCTGGTGA CAGTAGCTAT A													1080

The sequence numbering refers to the *Escherichia coli stx*₁ gene fragment (SEQ ID NO. 1076). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^a This sequence is the reverse-complement of the selected primer.

Annex XXVII: Strategy for the selection of stx₂-specific amplification primers and hybridization probe.

	Accession #	543	570	614	641	684	708	SEQ ID NO.:
5	stx ₁	AGCGa	TgtTaCGgTT	TGTTACTGTC	ACA...CAAC	ACTGgATGAT	ctcAgTgBgC	gtTcTTA...A AGgtTgAGtA gCGTcCTgCC tGAC
	stx ₁	AGCGa	TgtTaCGgTT	TGTTACTGTC	ACA...CAAC	ACTGgATGAT	ctcAgTgBgC	gtTcTTA...A AGgtTgAGtA gCGTcCTgCC tGAC
	stx ₁	AGCGa	TgtTaCGgTT	TGTTACTGTC	ACA...CAAC	ACTGgATGAT	ctcAgTgBgC	gtTcTTA...A AGgtTgAGtA gCGTcCTgCC tGAC
	stx ₁	AGCGa	TgtTaCGgTT	TGTTACTGTC	ACA...CAAC	ACTGgATGAT	ctcAgTgBgC	gtTcTTA...A AGgtTgAGtA gCGTcCTgCC tGAT
	stx ₁	AGCGa	TgtTaCGgTT	TGTTACTGTC	ACA...CAAC	ACTGgATGAT	ctcAgTgBgC	gtTcTTA...A AGgtTgAGtA gCGTcCTgCC tGAT
10	stx ₁	AGCGa	TgtTaCGgTT	TGTTACTGTC	ACA...CAAC	ACTGgATGAT	ctcAgTgBgC	gtTcTTA...A AGgtTgAGtA gCGTcCTgCC tGAC
	stx ₁	AGCGa	TgtTaCGgTT	TGTTACTGTC	ACA...CAAC	ACTGgATGAT	ctcAgTgBgC	gtTcTTA...A AGgtTgAGtA gCGTcCTgCC tGAC
	stx ₁	AGCGa	TgtTaCGgTT	TGTTACTGTC	ACA...CAAC	ACTGgATGAT	ctcAgTgBgC	gtTcTTA...A AGgtTgAGtA gCGTcCTgCC tGAC
	stx ₁	AGCGa	TgtTaCGgTT	TGTTACTGTC	ACA...CAAC	ACTGgATGAT	ctcAgTgBgC	gtTcTTA...A AGgtTgAGtA gCGTcCTgCC tGAC
	stx ₁	AGCGa	TgtTaCGgTT	TGTTACTGTC	ACA...CAAC	ACTGgATGAT	ctcAgTgBgC	gtTcTTA...A AGgtTgAGtA gCGTcCTgCC tGAC
15	stx ₁	AGCGa	TgtTaCGgTT	TGTTACTGTC	ACA...CAAC	ACTGgATGAT	ctcAgTgBgC	gtTcTTA...A AGgtTgAGtA gCGTcCTgCC tGAC
	stx ₂	AGCAG	TTCTgCGgTT	TGTCACtGTC	ACA...AGGC	ACTGtCTGA.	..AACTGCTC	CTGTGTA...G CGAATCAGCA ATGTGCTTCC GGAG
	stx ₂	AGCAG	TTCTgCGgTT	TGTCACtGTC	ACA...AGGC	ACTGtCTGA.	..AACTGCTC	CTGTGTA...G CGAATCAGCA ATGTGCTTCC GGAG
	stx ₂	AGCAG	TTCTgCGgTT	TGTCACtGTC	ACA...AGGC	ACTGtCTGA.	..AACTGCTC	CTGTGTA...G CGAATCAGCA ATGTGCTTCC GGAG
	stx ₂	AGCAG	TTCTgCGgTT	TGTCACtGTC	ACA...AGGC	ACTGtCTGA.	..AACTGCTC	CTGTGTA...G CGAATCAGCA ATGTGCTTCC GGAG
	stx ₂	AGCAG	TTCTgCGgTT	TGTCACtGTC	ACA...AGGC	ACTGtCTGA.	..AACTGCTC	CTGTGTA...G CGAATCAGCA ATGTGCTTCC GGAG
20	stx ₂	AGCAG	TTCTgCGgTT	TGTCACtGTC	ACA...AGGC	ACTGtCTGA.	..AACTGCTC	CTGTGTA...G CGAATCAGCA ATGTGCTTCC GGAG
	stx ₂	AGCAG	TTCTgCGgTT	TGTCACtGTC	ACA...AGGC	ACTGtCTGA.	..AACTGCTC	CTGTGTA...G CGAATCAGCA ATGTGCTTCC GGAG
	stx ₂	AGCAG	TTCTgCGgTT	TGTCACtGTC	ACA...AGGC	ACTGtCTGA.	..AACTGCTC	CTGTGTA...G CGAATCAGCA ATGTGCTTCC GGAG
	stx ₂	AGCAG	TTCTgCGgTT	TGTCACtGTC	ACA...AGGC	ACTGtCTGA.	..AACTGCTC	CTGTGTA...G CGAATCAGCA ATGTGCTTCC GGAG
	stx ₂	AGCAG	TTCTgCGgTT	TGTCACtGTC	ACA...AGGC	ACTGtCTGA.	..AACTGCTC	CTGTGTA...G CGAATCAGCA ATGTGCTTCC GGAG
25	stx ₂	AGCAG	TTCTgCGgTT	TGTCACtGTC	ACA...AGGC	ACTGtCTGA.	..AACTGCTC	CTGTGTA...G CGAATCAGCA ATGTGCTTCC GGAG
30	stx ₂	AGCAG	TTCTgCGgTT	TGTCACtGTC	ACA...AGGC	ACTGtCTGA.	..AACTGCTC	CTGTGTA...G CGAATCAGCA ATGTGCTTCC GGAG
	stx ₂	AGCAG	TTCTgCGgTT	TGTCACtGTC	ACA...AGGC	ACTGtCTGA.	..AACTGCTC	CTGTGTA...G CGAATCAGCA ATGTGCTTCC GGAG
	stx ₂	AGCAG	TTCTgCGgTT	TGTCACtGTC	ACA...AGGC	ACTGtCTGA.	..AACTGCTC	CTGTGTA...G CGAATCAGCA ATGTGCTTCC GGAG
	stx ₂	AGCAG	TTCTgCGgTT	TGTCACtGTC	ACA...AGGC	ACTGtCTGA.	..AACTGCTC	CTGTGTA...G CGAATCAGCA ATGTGCTTCC GGAG
35	Selected sequence for amplification primer	AG	TTCTgCGgTT	TGTCACtGTC				1078
40	Selected sequence for hybridization probe				C	ACTGTCTGA.	..AACTGCTC	CTGT
	Selected sequence for amplification primer ^a							1085
								1079

The sequence numbering refers to the *Escherichia coli* stx₂ gene fragment (SEQ ID NO. 1077). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^a This sequence is the reverse-complement of the selected primer.

Annex XXVIII: Strategy for the selection of vanA-specific amplification primers from van sequences.

	Accession #	926	952	1230	1255	SEQ ID NO.:
5	vanA	X56895	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG		CCCGTGTGGA TATG	1139
	vanA	M97297	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG		CCCGTGTGGA TATG	1141
	vanA	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG		CCCGTGTGGA TATG	1051
	vanA	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG		CCCGTGTGGA TATG	1052
	vanA	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG		CCCGTGTGGA TATG	1053
10	vanA	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG		CCCGTGTGGA TATG	1054
	vanA	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG		CCCGTGTGGA TATG	1055
	vanA	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG		CCCGTGTGGA TATG	1056
	vanA	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG		CCCGTGTGGA TATG	1057
	vanA	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG		CCCGTGTGGA TATG	1049
15	vanA	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG		CCCGTGTGGA TATG	1050
	vanB	U94526	GTAAC gGtaCGGAaG AActTaACGC T...GC AGAGGgCTtG		CCCGTGTtGA TCtT	1117
	vanB	U94527	GTAAC AGtaCGGAaG AActTaaACGC T...GC AGAGGgCTtG		CtCGTGTtGA TCtT	-
	vanB	U94528	GTAAC gGtaCGGAaG AActTaACGC T...GC AGAGGgCTtG		CCCGTGTtGA TCtT	-
	vanB	U94529	GTAAC gGtaCGGAaG AActTaACGC T...GC AGAGGgCTtG		CCCGTGTtGA TCtT	-
20	vanB	U94530	GTAAC gGtaCGGAaG AActTaACGC T...GC AGAGGgCTtG		CCCGTGTtGA TCtT	-
26	vanB	Z83305	GTAAC gGtaCGGAaG AActTaACGC T...GC AGAGGgCTtG		CCCGTGTtGA TCtT	-
	vanB	U81452	GTAAC gGtaCGGAaG AActTaACGC T...GC AGAGGgCTtG		CCCGTGTtGA TCtT	-
	vanB	U35369	GTAAC AGtaCGGAaG AActTaaACGC T...GC AGAGGgCTtG		CtCGTGTtGA TCtT	-
	vanB	U72704	GTAAC gGtaCGGAaG AActTaACGC T...GC AGAGGgCTtG		CCCGTGTtGA TCtT	-
25	vanB	L06138	GTAAC AGtaCGGAaG AActTaaACGC T...GC AGAGGgCTtG		CtCGTGTtGA TCtT	-
	vanB	L15304	GTAAC gGtaCGGAaG AActTaACGC T...GC AGAGGgCTtG		CCCGTGTtGA TCtT	-
	vanB	U00456	GTAAC AGtaCGGAaG AActTaaACGC T...GC AGAGGgCTtG		CtCGTGTtGA TCtT	-
	vanD	AF130997	GTAatgc AagGCaGaaG AActGcAgGC A...GC AGAGGatTgG		CCCGcaTtGA cCTG	-
30	vanE	AF136925	GTAgaA caaaaaagtG AtTtatATAA A...GC AaAGGatTAG		CgaGaaTcGA cTtT	-
	Selected sequence for amplification primer AAT AGCGCGGACG AATTGGAC					1090
	Selected sequence for amplification primer ^a GAGGTCTAG CCCGTGTGGA T					1089

The sequence numbering refers to the *Enterococcus faecium* vanA gene fragment (SEQ ID NO. 1139). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^a This sequence is the reverse-complement of the above selected primer.

Annex XXIX: Strategy for the selection of vanB-specific amplification primers from van sequences.

	Accession #	470	495	608	633	SEQ ID NO.:
5	vanA	X56895	A CGCaATTGAA	tCgGCAAGAC AATAT...ACG	GaATCTTtCG tATtCATCAG GAA	1139
	vanA	M97297	A CGCaATTGAA	tCgGCAAGAC AATAT...ACG	GaATCTTtCG tATtCATCAG GAA	1141
	vanA	-	A CGCaATTGAA	tCgGCAAGAC AATAT...ACG	GaATCTTtCG tATtCATCAG GAA	1051
	vanA	-	A CGCaATTGAA	tCgGCAAGAC AATAT...ACG	GaATCTTtCG tATtCATCAG GAA	1052
	vanA	-	A CGCaATTGAA	tCgGCAAGAC AATAT...ACG	GaATCTTtCG tATtCATCAG GAA	1053
10	vanA	-	A CGCaATTGAA	tCgGCAAGAC AATAT...ACG	GaATCTTtCG tATtCATCAG GAA	1054
	vanA	-	A CGCaATTGAA	tCgGCAAGAC AATAT...ACG	GaATCTTtCG tATtCATCAG GAA	1055
	vanA	-	A CGCaATTGAA	tCgGCAAGAC AATAT...ACG	GaATCTTtCG tATtCATCAG GAA	1056
	vanA	-	A CGCaATTGAA	tCgGCAAGAC AATAT...ACG	GaATCTTtCG tATtCATCAG GAA	1057
	vanA	-	A CGCaATTGAA	tCgGCAAGAC AATAT...ACG	GaATCTTtCG tATtCATCAG GAA	1049
15	vanA	-	A CGCaATTGAA	tCgGCAAGAC AATAT...ACG	GaATCTTtCG tATtCATCAG GAA	1050
	vanB	U94526	C TCGGATAGAA	GCgGCAGGAC AATAT...ACG	GTATCTTtCCG CATCCATCAG GAA	1117
	vanB	U94527	C TCGGATAGAA	GCAGCAGGAC AATAT...ACG	GTATCTTtCCG CATCCATCAG GAA	-
	vanB	U94528	C TCGGATAGAA	GCgGCAGGAC AATAT...ACG	GTATCTTtCCG CATCCATCAG GAA	-
	vanB	U94529	C TCGGATAGAA	GCgGCAGGAC AATAT...ACG	GTATCTTtCCG CATCCATCAG GAA	-
	vanB	U94530	C TCGGATAGAA	GCgGCAGGAC AATAT...ACG	GTATCTTtCCG CATCCATCAG GAA	-
20	vanB	Z83305	C TCGGATAGAA	GCgGCAGGAC AATAT...ACG	GTATCTTtCCG CATCCATCAG GAA	-
	vanB	U81452	C TCGGATAGAA	GCgGCAGGAC AATAT...ACG	GTATCTTtCCG CATCCATCAG GAA	-
	vanB	U35369	C TCGGATAGAA	GCAGCAGGAC AATAT...ACG	GTATCTTtCCG CATCCATCAG GAA	-
	vanB	U72704	C TCGGATAGAA	GCgGCAGGAC AATAT...ATG	GTATCTTtCCG CATCCATCAG GAA	-
25	vanB	L06138	C TCGGATAGAA	GCAGCAGGAC AATAT...ACG	GTATCTTtCCG CATCCATCAG GAA	-
	vanB	L15304	C TCGGATAGAA	GCgGCAGGAC AATAT...ACG	GTATCTTtCCG CATCCATCAG GAA	-
	vanB	U00456	C TCGGATAGAA	GCAGCAGGAC AATAT...ACG	GTATCTTtCCG CATCCATCAG GAA	-
	vanD	AF130997	C AGCaATcGAA	GaAGCAAGaAa AATAT...ACG	GcTtTtTttaa gATtCATCAG GAA	-
30	vanE	AF136925	A AGCaATAGAC	GaAGCcttcaA AATAT...ATG	GcTtTtTtCga CtatgaagAG AAA	-
	Selected sequence for amplification primer		CGATAGAA	GCAGCAGGAC AA		1095
35	Selected sequence for amplification primer ^a				GTATCTTtCCG CATCCATCAG	1096

The sequence numbering refers to the *Enterococcus faecium* vanB gene fragment (SEQ ID NO. 1117). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^a This sequence is the reverse-complement of the above vanB sequence.

Annex XXX: Strategy for the selection of vanC-specific amplification primers from vanC sequences.

	Accession #	929	957	1064	1092	SEQ ID NO.	
5	vanC1	-	GT CGACGGGTTTT	TTTGATTTTG AAGAGAA...ACGGGTC	TGGCTCGAAT CGATTTTTTC	GT 1058	
	vanC1	-	GT CGACGGGTTTT	TTTGATTTTG AAGAGAA...ACGGGTC	TGGCTCGAAT CGATTTTTTC	GT 1059	
	vanC1	M75132	GT CGACGGGTTTT	TTTGATTTTG AAGAGAA...ACGGGTC	TGGCTCGAAT CGATTTTTTC	GT 1138	
	vanC2	-	GT AGACGGGCTTT	TTTCGATTTTG AAGAAAA...AAAGGTC	TTGCTCGCAT CGACTTTTTT	GT 1060	
10	vanC2	-	GT AGACGGGCTTT	TTTCGATTTTG AAGAAAA...AAAGGTC	TTGCTCGCAT CGACTTTTTT	GT 1061	
	vanC2	-	GT AGACGGGCTTT	TTTCGATTTTG AAGAAAA...AAAGGTC	TTGCTCGCAT CGACTTTTTT	GT 1062	
	vanC2	-	GT AGACGGGCTTT	TTTCGATTTTG AAGAAAA...AAAGGTC	TTGCTCGCAT CGACTTTTTT	GT 1063	
	vanC2	L29638	GT AGACGGGCTTT	TTTCGATTTTG AAGAAAA...AAAGGTC	TTGCTCGCAT CGACTTTTTT	GT -	
15	vanC2	L29638	GT AGACGGGCTTT	TTTCGATTTTG AAGAAAA...AAAGGTC	TTGCTCGCAT CGACTTTTTT	GT -	
	vanC3	-	GT AGACGGGCTTT	TTTCGATTTTG AAGAAAA...AAAGGTC	TTGCTCGCAT CGACTTTTTT	GT 1064	
	vanC3	-	GT AGACGGGCTTT	TTTCGATTTTG AAGAAAA...AAAGGTC	TTGCTCGCAT CGACTTTTTT	GT 1065	
	vanC3	-	GT AGACGGGCTTT	TTTCGATTTTG AAGAAAA...AAAGGTC	TTGCTCGCAT CGACTTTTTT	GT 1066	
20	vanC3	L29639	GT AGACGGGCTTT	TTTCGATTTTG AAGAAAA...AAAGGTC	TTGCTCGCAT CGACTTTTTT	GT -	
	Selected sequence for resistance primer		GACGGTTTT TTYGATTTTG AAGA				1101
	Selected sequence for resistance primer ^a		GGTC TKGCTCGMAT CGAYTTTTT				1102

25 The sequence numbering refers to the vanC1 gene fragment (SEQ ID NO. 1138). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequence displayed.

30 "R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a This sequence is the reverse-complement of the selected sequence.

Annex XXXI: Strategy for the selection of Streptococcus pneumoniae-specific amplification primers and hybridization probes from pbp1a sequences.

5		Accession #	453			505	678	706	SEQ ID NO.:			
	pbp1a	M90528	A	TTGACTAGCC	AAGCATACAC	TATGCTAAATG	CCATTTCGAG	TAATACAACC	GA...TATATG	ATGACCCGAAA	TGATGAAAAC	CGT...
	pbp1a	X67873	A	TCGACTAGCC	AAGCATACAC	TACTCAAATG	CCATTTCGAG	TAAGACAACC	GA...TATATG	ATGACCCGAAA	TGATGAAAAC	AGT...
	pbp1a	AB006868	A	TCGACTAGCC	AAGCATACAC	TACTCAAATG	CCATTTCGAG	TAAGACAACC	GA...TATATG	ATGACCCGACA	TGATGAAAAC	AGT...
	pbp1a	AF046234	A	TCGACTAGCC	AAGCATACAC	TACTCAAATG	CCATTTCGAG	TAAGACAACC	GA...TATATG	ATGACCCGAAA	TGATGAAAAC	TGT...
10	pbp1a		A	TCGACTAGCC	AAGCATACAC	TACTCAAATG	CCATTTCGAG	TAAGACAACC	GA...TATATG	ATGACCCGACA	TGATGAAAAC	TGT...
	pbp1a		A	TCGACTAGCC	AAGCATACAC	TACTCAAATG	CCATTTCGAG	TAAGACAACC	GA...TACATG	ATGACCCGAAA	TGATGAAAAC	TGT...
	pbp1a	AB006873	A	TCGACTAGCC	AAGCATACAC	TACTCAAATG	CCATTTCGAG	TAAGACAACC	GA...TATATG	ATGACCCGACA	TGATGAAAAC	AGT...
	pbp1a	AF139883	A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAATACAACC	GA...TATATG	ATGACCCGACA	TGATGAAAAC	AGT...
	pbp1a		A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAATACAACC	GA...TATATG	ATGACCCGACA	TGATGAAAAC	AGT...
	pbp1a		A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAATACAACC	GA...TATATG	ATGACCCGACA	TGATGAAAAC	AGT...
	pbp1a		A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAATACAACC	GA...TATATG	ATGACCCGACA	TGATGAAAAC	AGT...
	pbp1a		A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAATACAACC	GA...TATATG	ATGACCCGACA	TGATGAAAAC	AGT...
	pbp1a	AF159448	A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAATACAACC	GA...TATATG	ATGACCCGACA	TGATGAAAAC	AGT...
	pbp1a		A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAATACAACC	GA...TATATG	ATGACCCGACA	TGATGAAAAC	AGT...
	pbp1a		A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAATACAACC	GA...TACATG	ATGACCCGAAA	TGATGAAAAC	TGT...
	pbp1a		A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAATACAACC	GA...TACATG	ATGACCCGAAA	TGATGAAAAC	TGT...
	pbp1a		A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAATACAACC	GA...TACATG	ATGACCCGAAA	TGATGAAAAC	TGT...
	pbp1a	X67867	A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAATACAACC	GA...TACATG	ATGACCCGAAA	TGATGAAAAC	TGT...
	pbp1a		A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAATACAACC	GA...TATATG	ATGACCCGAAA	TGATGAAAAC	TGT...
	pbp1a	249094	A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAAGACAACC	GA...TATATG	ATGACCCGAAA	TGATGAAAAC	TGT...
	pbp1a		A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAAGACAACC	GA...TATATG	ATGACCCGAAA	TGATGAAAAC	TGT...
	pbp1a		A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAAGACAACC	GA...TATATG	ATGACCCGAAA	TGATGAAAAC	TGT...
	pbp1a		A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAAGACAACC	GA...TATATG	ATGACCCGAAA	TGATGAAAAC	TGT...
	pbp1a	X67870	A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAAGACAACC	GA...TATATG	ATGACCCGAAA	TGATGAAAAC	TGT...
	pbp1a		A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAATACAACC	GA...TATATG	ATGACCCGAAA	TGATGAAAAC	TGT...
	pbp1a		A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAATACAACC	GA...TACATG	ATGACCCGAAA	TGATGAAAAC	TGT...
	pbp1a	AJ002290	A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAATACAACC	GA...TATATG	ATGACCCGAAA	TGATGAAAAC	TGT...
	pbp1a	X67871	A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAATACAACC	GA...TACATG	ATGACCCGAAA	TGATGAAAAC	AGT...
	pbp1a		A	TCGACTATCC	AAGCATATCC	TATGCAAAACG	CCATTTCGAG	TAATACAACC	GA...TACATG	ATGACCCGAAA	TGATGAAAAC	AGT...

Selected sequences for amplification primers

GACTATCC AAGCATATCC TATG

ATG ATGACHGAMA TGATGAAAAC

1130
1129

Selected sequence for hybridization probe

CAAAAG CCAATTTCAAG TAATACAAC

1197

The sequence numbering refers to the Streptococcus pneumoniae pbp1a gene fragment (SEQ ID NO. 1004). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

"R", "Y", "M", "K", "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "H" stands for A, C or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

Annex XXXI: Strategy for the selection of *Streptococcus pneumoniae*-specific amplification primers and hybridization probes from *pbpla* sequences (continued).

Accession #	756	783	813	840	SEQ ID NO.
bbp1a	-
bbp1a	-
bbp1a	-
bbp1a	-
bbp1a	1014
bbp1a	1017
bbp1a	-
bbp1a	1169
bbp1a	1004
bbp1a	1007
bbp1a	1008
bbp1a	1009
bbp1a	1011
bbp1a	-
bbp1a	1005
bbp1a	1015
bbp1a	1006
bbp1a	1012
bbp1a	-
bbp1a	1010
bbp1a	-
bbp1a	1013
bbp1a	1016
bbp1a	-
bbp1a	1018
bbp1a	-
bbp1a	-
Selected sequence for hybridization probe	GGTAA	GACAGGTACT	TCTAACT		1193
Selected sequence for amplification primer ^a		ACTGGGTA	YGTAGCTCCA	GATG	1131

The sequence numbering refers to the *Streptococcus pneumoniae* pbpla gene fragment (SEQ ID NO. 1004). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed. "." indicates incomplete sequence data.

'R' 'Y' 'W' and 'S' designate nucleotide positions which are degenerated. 'R' stands for A or G; 'Y' stands for C or T; 'W' stands for A or T; 'S' stands for C or G. 'I' stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

. This sequence is the reverse-complement of the selected primer.

Annex XXXII: Specific and ubiquitous primers for nucleic acid amplification (toxin sequences).

5	Originating DNA fragment			
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Toxin gene: <i>cdtA</i>			
	2123	5'-TCT ACC ACT GAA GCA TTA C	2129 ^a	442-460
	2124 ^b	5'-TAG GTA CTG TAG GTT TAT TG	2129 ^a	580-599
15	Toxin gene: <i>cdtB</i>			
	2126	5'-ATA TCA GAG ACT GAT GAG	2130 ^a	2665-2682
	2127 ^b	5'-TAG CAT ATT CAG AGA ATA TTG T	2130 ^a	2746-2767
20	Toxin gene: <i>stx₁</i>			
	1081	5'-ATG TCA GAG GGA TAG ATC CA	1076 ^a	233-252
	1080 ^b	5'-TAT AGC TAC TGT CAC CAG ACA ATG T	1076 ^a	394-418
25	Toxin gene: <i>stx₂</i>			
	1078	5'-AGT TCT GCG TTT TGT CAC TGT C	1077 ^a	546-567
	1079 ^b	5'-CGG AAG CAC ATT GCT GAT T	1077 ^a	687-705
30	Toxin genes: <i>stx₁</i> and <i>stx₂</i>			
	1082	5'-TTG ARC RAA ATA ATT TAT ATG TG	1076 ^a	278-300
	1083 ^b	5'-TGA TGA TGR CAA TTC AGT AT	1076 ^a	781-800
35				

^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex XXXIII: Molecular beacon internal hybridization probes for specific detection of toxin sequences.

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
10	<u>Toxin gene:</u> <i>cdtA</i>			
	2125 ^b	5'- <u>CAC</u> GCG GAT TTT GAA TCT CTT CCT CTA GTA GCG <u>CGT</u> G	2129 ^c	462-488
15	<u>Toxin gene:</u> <i>cdtB</i>			
	2128	5'- <u>CAA</u> CGC TGG AGA ATC TAT ATT TGT AGA AAC TGC <u>GTT</u> G	2130 ^c	2714-2740
20	<u>Toxin gene:</u> <i>stx₁</i>			
	1084	5'- <u>CCA</u> CGC CGC TTT GCT GAT TTT TCA CAT GTT ACC <u>GCG</u> TGG	1076 ^c	337-363
25				
	2012 ^d	5'- <u>CCG</u> CGG ATT ATT AAA CCG CCC TTC CGC <u>GG-MR-HEG-ATG</u> TCA GAG GGA TAG ATC CA	1076 ^c	248-264
30	<u>Toxin gene:</u> <i>stx₂</i>			
	1085	5'- <u>CCA</u> CGC CAC TGT CTG AAA CTG CTC CTG TG <u>CGT</u> GG	1077 ^c	617-638

- 35
- ^a Underlined nucleotides indicate the molecular beacon's stem.
- ^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.
- ^c Sequences from databases.
- 40 ^d Scorpion primer.

Annex XXXIV: Specific and ubiquitous primers for nucleic acid amplification (van sequences).

5	SEQ ID NO. Nucleotide sequence		Originating DNA fragment	
			SEQ ID NO.	Nucleotide position
10	Resistance gene: vanA			
	1086	5'-CTA CTC CCG CCT TTT GGG TT	1049-1057 ^a	513-532 ^b
	1087 ^c	5'-CTC ACA GCC CGA AAC AGC CT	1049-1057 ^a	699-718 ^b
15	1086	5'-CTA CTC CCG CCT TTT GGG TT	1049-1057 ^a	513-532 ^b
	1088 ^c	5'-TGC CGT TTC CTG TAT CCG TC	1049-1057 ^a	885-904 ^b
	1086	5'-CTA CTC CCG CCT TTT GGG TT	1049-1057 ^a	513-532 ^b
	1089 ^c	5'-ATC CAC ACG GGC TAG ACC TC	1049-1057 ^a	933-952 ^b
20	1090	5'-AAT AGC GCG GAC GAA TTG GAC	1049-1057 ^a	629-649 ^b
	1091 ^c	5'-AAC GCG GCA CTG TTT CCC AA	1049-1057 ^a	734-753 ^b
	1090	5'-AAT AGC GCG GAC GAA TTG GAC	1049-1057 ^a	629-649 ^b
25	1089 ^c	5'-ATC CAC ACG GGC TAG ACC TC	1049-1057 ^a	933-952 ^b
	1092	5'-TCG GCA AGA CAA TAT GAC AGC	1049-1057 ^a	662-682 ^b
	1088 ^c	5'-TGC CGT TTC CTG TAT CCG TC	1049-1057 ^a	885-904 ^b
30	Resistance gene: vanB			
	1095	5'-CGA TAG AAG CAG CAG GAC AA	1117 ^d	473-492
	1096 ^c	5'-CTG ATG GAT GCG GAA GAT AC	1117 ^d	611-630
35	Resistance genes: vanA, vanB			
	1112	5'-GGC TGY GAT ATT CAA AGC TC	1049-1057,1117 ^a	437-456 ^b
	1113 ^c	5'-ACC GAC CTC ACA GCC CGA AA	1049-1057,1117 ^a	705-724 ^b
40	1112	5'-GGC TGY GAT ATT CAA AGC TC	1049-1057,1117 ^a	437-456 ^b
	1114 ^c	5'-TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-837 ^b
	1115	5'-TTT CGG GCT GTG AGG TCG GBT GHG CG	1049-1057,1117 ^a	705-730 ^b
5	1114 ^c	5'-TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-837 ^b
	1116	5'-TTT CGG GCT GTG AGG TCG GBT GHG CGG	1049-1057,1117 ^a	705-731 ^b
	1114 ^c	5'-TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-837 ^b
	1112	5'-GGC TGY GAT ATT CAA AGC TC	1049-1057,1117 ^a	437-456 ^b
10	1118 ^c	5'-TTT TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-840 ^b

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the vanA sequence fragment (SEQ ID NO. 1051).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d Sequences from databases.

Annex XXXIV: Specific and ubiquitous primers for nucleic acid amplification (van sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Resistance genes:</u> vanA, vanB (continued)			
	1115	5'-TTT CGG GCT GTG AGG TCG GBT GHG CG	1049-1057,1117 ^a	705-730 ^b
	1118 ^c	5'-TTT TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-840 ^b
15	1116	5'-TTT CGG GCT GTG AGG TCG GBT GHG CGG	1049-1057,1117 ^a	705-731 ^b
	1118 ^c	5'-TTT TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-840 ^b
	1119	5'-TTT CGG GCT GTG AGG TCG GBT GHG C	1049-1057,1117 ^a	705-729 ^b
	1118 ^c	5'-TTT TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-840 ^b
20	1120	5'-TTT CGG GCT GTG AGG TCG GBT GHG	1049-1057,1117 ^a	705-728 ^b
	1118 ^c	5'-TTT TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-840 ^b
	1121	5'-TGT TTG WAT TGT CYG GYA TCC C	1049-1057,1117 ^a	408-429 ^b
25	1111 ^c	5'-CTT TTT CCG GCT CGW YTT CCT GAT G	1049-1057,1117 ^a	806-830 ^b
	1112	5'-GGC TGY GAT ATT CAA AGC TC	1049-1057,1117 ^a	437-456 ^b
	1111 ^c	5'-CTT TTT CCG GCT CGW YTT CCT GAT G	1049-1057,1117 ^a	806-830 ^b
30	1123	5'-TTT CGG GCT GTG AGG TCG GBT G	1049-1057,1117 ^a	705-726 ^b
	1111 ^c	5'-CTT TTT CCG GCT CGW YTT CCT GAT G	1049-1057,1117 ^a	806-830 ^b
	1112	5'-GGC TGY GAT ATT CAA AGC TC	1049-1057,1117 ^a	437-456 ^b
	1124 ^c	5'-GAT TTG RTC CAC YTC GCC RAC A	1049-1057,1117 ^a	757-778 ^b
35	<u>Resistance gene:</u> vanC1			
	1103	5'-ATC CCG CTA TGA AAA CGA TC	1058-1059 ^a	519-538 ^d
40	1104 ^c	5'-GGA TCA ACA CAG TAG AAC CG	1058-1059 ^a	678-697 ^d
	<u>Resistance genes:</u> vanC1, vanC2, vanC3			
	1097	5'-TCY TCA AAA GGG ATC ACW AAA GTM AC	1058-1066 ^a	607-632 ^d
45	1098 ^c	5'-TCT TCA AAA TCG AAA AAG CCG TC	1058-1066 ^a	787-809 ^d
	1099	5'-TCA AAA GGG ATC ACW AAA GTM AC	1058-1066 ^a	610-632 ^d
	1100 ^c	5'-GTA AAK CCC GGC ATR GTR TTG ATT TC	1058-1066 ^a	976-1001 ^d
	1101	5'-GAC GGY TTT TTY GAT TTT GAA GA	1058-1066 ^a	787-809 ^d
50	1102 ^c	5'-AAA AAR TCG ATK CGA GCM AGA CC	1058-1066 ^a	922-944 ^d
	<u>Resistance genes:</u> vanC2, vanC3			
	1105	5'-CTC CTA CGA TTC TCT TGA YAA ATC A	1060-1066,1140 ^a	487-511 ^e
55	1106 ^c	5'-CAA CCG ATC TCA ACA CCG GCA AT	1060-1066,1140 ^a	690-712 ^e

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *vanA* sequence fragment (SEQ ID NO. 1051).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d The nucleotide positions refer to the *vanC1* sequence fragment (SEQ ID NO. 1058).

^e The nucleotide positions refer to the *vanC2* sequence fragment (SEQ ID NO. 1140).

Annex XXXIV: Specific and ubiquitous primers for nucleic acid amplification (van sequences) (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Resistance gene: <i>vanD</i>			
	1591	5'-ATG AGG TAA TAG AAC GGA TT	1594	797-837
	1592 ^b	5'-CAG TAT TTC AGT AAG CGT AAA	1594	979-999
15	Resistance gene: <i>vanE</i>			
	1595	5'-AAA TAA TGC TCC ATC AAT TTG CTG A	1599 ^a	74-98
	1596 ^b	5'-ATA GTC GAA AAA GCC ATC CAC AAG	1599 ^a	394-417
20	1597	5'-GAT GAA TTT GCG AAA ATA CAT GGA	1599 ^a	163-186
	1598 ^b	5'-CAG CCA ATT TCT ACC CCT TTC AC	1599 ^a	319-341
Sequencing primers (vanAB)				
25	1112	5'-GGC TGY GAT ATT CAA AGC TC	1139 ^a	737-756
	1111 ^b	5'-CTT TTT CCG GCT CGW YTT CCT GAT G	1139 ^a	1106-1130
Sequencing primers (vanA, vanX, vanY)				
30	1150	5'-TGA TAA TCA CAC CGC ATA CG	1141 ^a	860-879
	1151 ^b	5'-TGC TGT CAT ATT GTC TTG CC	1141 ^a	1549-1568
	1152	5'-ATA AAG ATG ATA GGC CGG TG	1141 ^a	1422-1441
	1153 ^b	5'-CTC GTA TGT CCC TAC AAT GC	1141 ^a	2114-2133
35	1154	5'-GTT TGA AGC ATA TAG CCT CG	1141 ^a	2520-2539
	1155 ^b	5'-CAG TGC TTC ATT AAC GTA GTC	1141 ^a	3089-3109

40

^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex XXXIV: Specific and ubiquitous primers for nucleic acid amplification (van sequences) (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID	Nucleotide NO. position
10	Sequencing primers (vanC1)			
	1110	5'-ACG AGA AAG ACA ACA GGA AGA CC	1138 ^a	122-144
	1109 ^b	5'-ACA TCG TGA TCG CTA AAA GGA GC	1138 ^a	1315-1337
15	Sequencing primers (vanC2, vanC3)			
	1108	5'-GTA AGA ATC GGA AAA GCG GAA GG	1140 ^a	1-23
	1107 ^b	5'-CTC ATT TGA CTT CCT CCT TTG CT	1140 ^a	1064-1086

20

^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex XXXV: Internal hybridization probes for specific detection of van sequences.

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Resistance gene:</u> vanA			
	1170	5'-ACG AAT TGG ACT ACG CAA TT	1049-1057 ^a	639-658 ^b
	2292	5'-GAA TCG GCA AGA CAA TAT G	2293 ^c	583-601
15	<u>Resistance gene:</u> vanB			
	1171	5'-ACG AGG ATG ATT TGA TTG TC	1117 ^c	560-579
	2294	5'-AAA CGA GGA TGA TTT GAT TG	2296 ^a	660-679
20	2295	5'-TTG AGC AAG CGA TTT CGG	2296 ^a	614-631
	<u>Resistance gene:</u> vanD			
25	2297	5'-TTC AGG AGG GGG ATC GC	1594 ^c	458-474

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the vanA sequence fragment (SEQ ID NO. 1051).

^c Sequences from databases.

Annex XXXVI: Specific and ubiquitous primers for nucleic acid amplification (pbp sequences).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Resistance gene: <i>pbp1a</i>			
	1129	5'-ATG ATG ACH GAM ATG ATG AAA AC	1004-1018 ^a	681-703 ^b
	1131 ^c	5'-CAT CTG GAG CTA CRT ARC CAG T	1004-1018 ^a	816-837 ^b
15	1130	5'-GAC TAT CCA AGC ATG CAT TAT G	1004-1018 ^a	456-477 ^b
	1131	5'-CAT CTG GAG CTA CRT ARC CAG T	1004-1018 ^a	816-837 ^b
	2015	5'-CCA AGA AGC TCA AAA ACA TCT G	2047 ^d	909-930
	2016 ^c	5'-TAD CCT GTC CAW ACA GCC AT	2047 ^d	1777-1796
20	Sequencing primers (<i>pbp1a</i>)			
	1125	5'-ACT CAC AAC TGG GAT GGA TG	1169 ^d	873-892
	1126 ^c	5'-TTA TGG TTG TGC TGG TTG AGG	1169 ^d	2140-2160
25	1125	5'-ACT CAC AAC TGG GAT GGA TG	1169 ^d	873-892
	1128 ^c	5'-GAC GAC YTT ATK GAT ATA CA	1169 ^d	1499-1518
	1127	5'-KCA AAY GCC ATT TCA AGT AA	1169 ^d	1384-1403
30	1126 ^c	5'-TTA TGG TTG TGC TGG TTG AGG	1169 ^d	2140-2160
	Sequencing primers (<i>pbp2b</i>)			
	1142	5'-GAT CCT CTA AAT GAT TCT CAG GTG G	1172 ^d	1-25
35	1143 ^c	5'-CAA TTA GCT TAG CAA TAG GTG TTG G	1172 ^d	1481-1505
	1142	5'-GAT CCT CTA AAT GAT TCT CAG GTG G	1172 ^d	1-25
	1145 ^c	5'-AAC ATA TTK GGT TGA TAG GT	1172 ^d	793-812
40	1144	5'-TGT YTT CCA AGG TTC AGC TC	1172 ^d	657-676
	1143 ^c	5'-CAA TTA GCT TAG CAA TAG GTG TTG G	1172 ^d	1481-1505
	Sequencing primers (<i>pbp2x</i>)			
45	1146	5'-GGG ATT ACC TAT GCC AAT ATG AT	1173 ^d	219-241
	1147 ^c	5'-AGC TGT GTT AGC VCG AAC ATC TTG	1173 ^d	1938-1961
	1146	5'-GGG ATT ACC TAT GCC AAT ATG AT	1173 ^d	219-241
50	1149 ^c	5'-TCC YAC WAT TTC TTT TTG WG	1173 ^d	1231-1250
	1148	5'-GAC TTT GTT TGG CGT GAT AT	1173 ^d	711-730
	1147 ^c	5'-AGC TGT GTT AGC VCG AAC ATC TTG	1173 ^d	1938-1961

55

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *pbp1a* sequence fragment (SEQ ID NO. 1004).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

60

^d Sequences from databases.

Annex XXXVII: Internal hybridization probes for specific detection of *pbp* sequences.

5	Originating DNA fragment			
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Resistance gene: <i>pbp1a</i>			
15	1132	5'-AGT GAA AAR ATG GCT GCT GC	1004-1018 ^a	531-550 ^b
	1133	5'-CAT CAA GAA CAC TGG CTA YGT AG	1004-1018 ^a	806-828 ^b
	1134	5'-CTA GAT AGA GCT AAA ACC TTC CT	1004-1018 ^a	417-439 ^b
	1135	5'-CAT TAT GCA AAC GCC ATT TCA AG	1004-1018 ^a	471-493 ^b
	1192	5'-GGT AAA ACA GGA ACC TCT AAC T	1004-1018 ^a	759-780 ^b
20	1193	5'-GGT AAG ACA GGT ACT TCT AAC T	1004-1018 ^a	759-780 ^b
	1194	5'-CAT TTC AAG TAA TAC AAC AGA ATC	1004-1018 ^a	485-508 ^b
	1195	5'-CAT TTC AAG TAA CAC AAC TGA ATC	1004-1018 ^a	485-508 ^b
	1196	5'-GCC ATT TCA AGT AAT ACA ACA GAA	1004-1018 ^a	483-506 ^b
	1197	5'-CAA ACG CCA TTT CAA GTA ATA CAA C	1004-1018 ^a	478-502 ^b
25	1094	5'-GGT AAA ACA GGT ACT TCT AAC TA	1004-1018 ^a	759-781 ^b
	1214	5'-GGT AAA ACA GGT ACC TCT AAC TA	1004-1018 ^a	759-781 ^b
	1216	5'-GGT AAG ACT GGT ACA TCA AAC TA	1004-1018 ^a	759-781 ^b
	1217	5'-CAA ATG CCA TTT CAA GTA ACA CAA C	1004-1018 ^a	478-502 ^b
	1218	5'-CAA ACG CCA TTT CAA GTA ACA CAA C	1004-1018 ^a	478-502 ^b
30	1219	5'-CAA ATG CTA TTT CAA GTA ATA CAA C	1004-1018 ^a	478-502 ^b
	1220	5'-CAA ACG CCA TTT CAA GTA ATA CGA C	1004-1018 ^a	478-502 ^b
	2017	5'-ACT TTG AAT AAG GTC GGT CTA G	2047 ^c	1306-1327
	2018	5'-ACA CTA AAC AAG GTT GGT TTA G	2063	354-375
	2019	5'-ACA CTA AAC AAG GTC GGT CTA G	2064	346-367
35	2020	5'-GTA GCT CCA GAT GAA ATG TTT G	2140 ^c	1732-1753
	2021	5'-GTA GCT CCA GAC GAA ATG TTT G	2057	831-852
	2022	5'-GTA GCT CCA GAT GAA ACG TTT G	2053 ^c	805-826
	2023	5'-GTA ACT CCA GAT GAA ATG TTT G	2056	819-840
	2024	5'-AGT GAA AAG ATG GCT GCT GC	2048 ^c	1438-1457
40	2025	5'-AGT GAG AAA ATG GCT GCT GC	2047 ^c	1438-1457
	2026	5'-TCC AAG CAT GCA TTA TGC AAA CG	2047 ^c	1368-1390
	2027	5'-TCG GTC TAG ATA GAG CTA AAA CG	2047 ^c	1319-1341
	2028	5'-TAT GCT CTT CAA CAA TCA CG	2047 ^c	1267-1286
	2029	5'-AGC CGT TGA GAC TTT GAA TAA G	2047 ^c	1296-1317
45	2030	5'-CTT AAT GGT CTT GGT ATC G	2047 ^c	1345-1366
	2031	5'-CGT GAC TGG GGT TCT GCT ATG A	2049 ^c	1096-1117
	2032	5'-CGT GAC TGG GGA TCA TCA ATG A	2047 ^c	1096-1117
	2033	5'-CGT GAC TGG GGT TCT GCC ATG A	2057	195-216
	2034	5'-ATC AAG AAC ACT GGC TAT GTA G	2050 ^c	787-808

50 ^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *pbp1a* sequence fragment (SEQ ID NO. 1004).

^c Sequence from databases.

Annex XXXVII: Internal hybridization probes for specific detection of *pbp* sequences (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Resistance gene:</u> <i>pbp1a</i> (continued)			
	2035	5'-ATC AAG AAC ACT GGC TAC GTA G	2051 ^C	787-808
	2036	5'-ATC AAG AAC ACT GGT TAC GTA G	2047	1714-1735
15	2037	5'-ATC AAA AAT ACT GGT TAT GTA G	2057	813-834
	2038	5'-ATC AAG AAT ACT GGC TAC GTA G	2052 ^C	757-778
	2039	5'-ATC AAA AAC ACT GGC TAT GTA G	2053 ^C	787-808
20				

[illegible][illegible]

amplification primer
GGCT GYGATATTT
TCA AAGCTC

35 Selected sequence for hybridization probe

ACGAATT GGACTACCA ATT (VADA)

The sequence numbering refers to the Entes to the selected sequences or match those s displayed.

Staphylococcus aureus (SEQ ID NO. 1139). Nucleotides in capitals are identical to the reference sequence. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences.

"R." "Y." "M." "K." "W." and "S." designate nucleotides which stand for A or C; "K" stands for G or T; analog that can bind to any of the four nucleotides.

nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide cleotides A, C, G or T.

[illegible]

40

The sequence numbering refers to the Enter to the selected sequences or match those sequences displayed. "R" and "W" designate nucleotide positions which are degenerated. "R" stands for A or G; "W" stands for A or T

• This sequence is the reverse-complement of the above selected primer.

Annex XXXIX: Internal hybridization probe for specific detection of *mecA*.

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Resistance gene:</u> <i>mecA</i>			
	1177	5'-GCT CAA CAA GTT CCA GAT TA	1178 ^a	1313-1332

15 ^a Sequence from databases.

Annex XL: Specific and ubiquitous primers for nucleic acid amplification (hexA sequences).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Bacterial species: <i>Streptococcus pneumoniae</i>			
	1179	5'-ATT TGG TGA CGG GTG ACT TT	1183 ^a	431-450
15	1181 ^b	5'-AGC AGC TTA CTA GAT GCC GT	1183-1191 ^c	652-671 ^d
	Sequencing primers			
	1179	5'-ATT TGG TGA CGG GTG ACT TT	1183 ^a	431-450
20	1182 ^b	5'-AAC TGC AAG AGA TCC TTT GG	1183 ^a	1045-1064

^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^c These sequences were aligned to derive the corresponding primer.

^d The nucleotide positions refer to the hexA sequence fragment (SEQ ID NO. 1183).

Annex XLI: Internal hybridization probe for specific detection of hexA sequences.

5	<hr/>			
			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
	<hr/>			
10	<u>Bacterial species:</u> <i>Streptococcus pneumoniae</i>			
	1180 ^a	5'-TCC ACC GTT GCC AAT CGC A	1183-1191 ^b	629-647 ^c
15	<hr/>			
	^a This sequences is from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.			
	^b These sequences were aligned to derive the corresponding primer.			
20	^c The nucleotide positions refer to the hexA sequence fragment (SEQ ID NO. 1183).			

Annex XLIII: Strategy for the selection of *Streptococcus pneumoniae* species-specific primers and hybridization probe from hexA sequences.

	428	453	626	674	1042	1067	SEQ ID NO.:
<i>S. pneumoniae</i>	TGG ATTGGGTGAC GGGTGAATTT	TAT...ATTG CGATTGGCAA	CGGTGGAGCA AACGGCATCT	AGTAAGCTGC	TCCA...AATCCAAAG	GATCTCTTGC	1183
<i>S. pneumoniae</i>	---	-----TGAC GGGTGAATTT	TAT...ATTG CGATTGGCAA	CGGTGGAGCA AACGGCATCT	AGTAAGCTGC	GATCTCTTGC	1184
<i>S. pneumoniae</i>	---	-----TGAC GGGTGAATTT	TAT...ATTG CGATTGGCAA	CGGTGGAGCA AACGGCATCT	AGTAAGCTGC	GATCTCTTGC	1185
<i>S. pneumoniae</i>	---	-----TGAC GGGTGAATTT	TAT...ATTG CGATTGGCAA	CGGTGGAGCA AACGGCATCT	AGTAAGCTGC	GATCTCTTGC	1186
<i>S. pneumoniae</i>	---	-----TGAC GGGTGAATTT	TAT...ATTG CGATTGGCAA	CGGTGGAGCA AACGGCATCT	AGTAAGCTGC	GATCTCTTGC	1187
<i>S. oralis</i>	---	-----TGAC GGGTGAATTT	TAT...ATTG CGATTGGCAA	CGGTGGAGCA AACGGCATCT	AGTAAGCTGC	GATCTCTTGC	1188
<i>S. mitis</i>	---	-----TGAC GGGTGAATTT	TAT...ATTG CGATTGGCAA	CGGTGGAGCA AACGGCATCT	AGTAAGCTGC	GATCTCTTGC	1189
<i>S. mitis</i>	---	-----TGAC GGGTGAATTT	TAT...ATTG CGATTGGCAA	CGGTGGAGCA AACGGCATCT	AGTAAGCTGC	GATCTCTTGC	1190
<i>S. mitis</i>	---	-----TGAC GGGTGAATTT	TAT...ATTG CGATTGGCAA	CGGTGGAGCA AACGGCATCT	AGTAAGCTGC	GATCTCTTGC	1191
Selected sequence for amplification primer	ATTGGGTGAC GGGTGAATTT						1179
Selected sequences for amplification primers*							
Selected sequence for hybridization probe*				ACGGCATCT AGTAAGCTGC T			1181
					CCAAAG GATCTCTTGC AGTT		1182
							1180

The sequence numbering refers to the *Streptococcus pneumoniae* hexA gene fragment (SEQ ID NO. 1183). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

* This sequence is the reverse-complement of the selected primer.

Annex XLIII: Specific and ubiquitous primers for nucleic acid amplification (pcp sequence).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<hr/>			
<u>Bacterial species:</u>		<i>Streptococcus pyogenes</i>	
1211	5'-ATT CTT GTA ACA GGC TTT GAT CCC	1215 ^a	291-314
1210 ^b	5'-ACC AGC TTG CCC AAT ACA AAG G	1215 ^a	473-494

^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex XLIV: Specific and ubiquitous primers for nucleic acid amplification of *S. saprophyticus* sequences of unknown coding potential.

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<hr/>			
<u>Bacterial species:</u>		<i>Staphylococcus saprophyticus</i>	
1208	5'-TCA AAA AGT TTT CTA AAA AAT TTA C	74,1093, 1198 ^b	169-193 ^c
1209 ^a	5'-ACG GGC GTC CAC AAA ATC AAT AGG A	74,1093, 1198 ^b	355-379 ^c

- ^a This sequence is from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.
- ^b These sequences were aligned to derive the corresponding primer.
- ^c The nucleotide positions refer to the *S. saprophyticus* unknown gene sequence fragment (SEQ ID NO. 1198).

Annex XLV: Molecular beacon internal hybridization probes for specific detection of antimicrobial agents resistance gene sequences.

SEQ ID NO. Nucleotide sequence ^a		Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Resistance gene: <i>gyrA</i>			
2250	5'- <u>CCG</u> <u>TCG</u> GAT GGT GTC GTA TAC CGC GGA GTC GCC <u>GAC</u> GG	1954 ^b	218-243
2251	5'- <u>CGG</u> <u>AGC</u> CGT TCT CGC TGC GTT ACA TGC TGG TGG <u>CTC</u> <u>CG</u>	1954 ^b	259-286
Resistance gene: <i>mecA</i>			
1231	5'- <u>GCG</u> <u>AGC</u> CCG AAG ATA AAA AAG AAC CTC TGC TGC <u>TCG</u> C	1178 ^b	1291-1315
Resistance gene: <i>parC</i>			
1938 ^b	5'- <u>CCG</u> <u>CGC</u> ACC ATT GCT TCG TAC ACT GAG GAG TCT CCG <u>CGC</u> GG	1321 ^c	232-260
1939	5'- <u>CGA</u> <u>CCC</u> <u>GGA</u> TGG TAG TAT CGA TAA TGA TCC GCC AGC GGC <u>CGG</u> <u>GTC</u> G	1321 ^c	317-346
1955 ^b	5'- <u>CGC</u> <u>GCA</u> ACC ATT GCT TCG TAC ACT GAG GAG TCT <u>GCG</u> <u>CG</u>	1321 ^c	235-260
Resistance gene: <i>vanA</i>			
1239	5'- <u>GCG</u> <u>AGC</u> GCA GAC CTT TCA GCA GAG GAG <u>GCT</u> <u>CGC</u>	1051	860-880
1240	5'- <u>GCG</u> <u>AGC</u> CGG CAA GAC AAT ATG ACA GCA AAA TCG <u>CTC</u> <u>GC</u>	1051	663-688
Resistance gene: <i>vanB</i>			
1241	5'- <u>GCG</u> <u>AGC</u> GGG GAA CGA GGA TGA TTT GAT TGG <u>CTC</u> <u>GC</u>	1117	555-577
Resistance gene: <i>vanD</i>			
1593	5'- <u>CCG</u> <u>AGC</u> <u>GAT</u> TTA CCG GAT ACT TGG CTG <u>ICG</u> <u>CTC</u> GG	1594	835-845

^a Underlined nucleotides indicate the molecular beacon's stem.

^b This sequence is from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^c Sequence from databases.

Annex XLVI: Molecular beacon internal hybridization probe for specific detection of *S. aureus* gene sequences of unknown coding potential.

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
<hr/>			
<u>Bacterial species:</u> <i>S. aureus</i>			
1232	5'- <u>GGA</u> <u>GCC</u> <u>GCG</u> CGA TTT TAT AAA TGA ATG TTG ATA ACC <u>GGC</u> <u>TCC</u>	1244	53-80

^a Underlined nucleotides indicate the molecular beacon's stem.

Annex XLVII: Molecular beacon internal hybridization probes for specific detection of tuf sequences.

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
Bacterial species: <i>Chlamydia pneumoniae</i>			
2091	5'- <u>CGC GAC</u> TTG AGA TGG AAC TTA GTG AGC TTC TTG <u>GTC GCG</u>	20	157-183
2092	5'- <u>CGC GAC</u> GAA AGA ACT TCC TGA AGG TCG TGC AGG <u>TCC AG</u>	20	491-516
Bacterial species: <i>Chlamydia trachomatis</i>			
2213	5'- <u>CGT GCC</u> ATT GAC ATG ATT TCC GAA GAA GAC GCT GAA <u>GGC ACG</u>	1739 ^b	412-441
Bacterial species: <i>Enterococcus faecalis</i>			
1236	5'- <u>GCG AGC</u> CGT GGT GAA GTT CGC GTT GGT <u>GGC TCG C</u>	883	370-391
Bacterial species: <i>Enterococcus faecium</i>			
1235	5'- <u>GCG AGC</u> CGA AGT TGA AGT TGT TGG TAT TGC TGG <u>CTC GC</u>	64	412-437
Bacterial species: <i>Legionella pneumophila</i>			
2084 ^c	5'- <u>CAC GCG</u> TCA ACA CCC GTA CAA GTC GTC TTT TGC <u>GCG TG</u>	112	461-486
Bacterial species: <i>Mycoplasma pneumoniae</i>			
2096 ^c	5'- <u>CGC GAC</u> CGG TAC CAC GGC CAG TAA TCG TGT <u>CGC G</u>	2097 ^b	658-679
Bacterial species: <i>Neisseria gonorrhoeae</i>			
2177	5'- <u>GGC ACG</u> GAC AAA CCA TTC CTG CTG CCT ATC GAA ACG TGT TCC <u>CGT GCC</u>	126	323-357
2178	5'- <u>GGC ACG</u> ACA AAC CAT TCC TGC TGC CTA TCG AAC <u>GTG CC</u>	126	323-348
2179	5'- <u>GGC AGC</u> TCT ACT TCC GTA CCA CTG ACG TAA CCG <u>GCT GCC</u>	126	692-718

^a Underlined nucleotides indicate the molecular beacon's stem.

^b Sequence from databases.

^c This sequence is from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex XLVII: Molecular beacon internal hybridization probes for specific detection of tuf sequences (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
Bacterial species: <i>Pseudomonas aeruginosa</i>			
2122	5'- <u>CCG</u> <u>AGC</u> GAA TGT AGG AGT CCA GGG TCT CTG <u>CTC</u> <u>GG</u>	153,880,2138 ^{b,c}	280-302 ^d
Bacterial species: <i>Staphylococcus aureus</i>			
2186	5'- <u>ACG</u> <u>CGC</u> TCA AAG CAG AAG TAT ACG TAT TAT CAA AAG ACG <u>CGC</u> <u>GT</u>	1728	615-646
Bacterial group: <i>Staphylococcus</i> sp. other than <i>S. aureus</i>			
1233	5'- <u>GCG</u> <u>AGC</u> GTT ACT GGT GTA GAA ATG TTC CGG <u>CTC</u> <u>GC</u>	878	372-394
Fungal species: <i>Candida albicans</i>			
2073	5'- <u>CCG</u> <u>AGC</u> AAC ATG ATT GAA CCA TCC ACC AAC TGG <u>CTC</u> <u>GG</u>	408	404-429
Fungal species: <i>Candida dubliniensis</i>			
2074	5'- <u>CCG</u> <u>AGC</u> AAC ATG ATT GAA GCT TCC ACC AAC TGG <u>CTC</u> <u>GG</u>	414	416-441
Fungal species: <i>Candida glabrata</i>			
2110 ^b	5'- <u>GCG</u> <u>GGC</u> CCT TAA CGA TTT CAG CGA ATC TGG ATT CAG <u>CCC</u> <u>GC</u>	417	307-335
2111	5'-GCG GGC ATG TTG AAG CCA CCA CCA ACG CTT CCT GGC CCG C	417	419-447
Fungal species: <i>Candida krusei</i>			
2112 ^b	5'- <u>GCG</u> <u>GGC</u> TTG ATG AAG TTT GGG TTT CCT TGA CAA TTG <u>CCC</u> <u>GC</u>	422	318-347
2113	5'- <u>GCG</u> <u>GGC</u> ACA AGG GTT GGA CTA AGG AAA CCA AGG CAG <u>CCC</u> <u>GC</u>	422	419-447
2114	5'- <u>GCG</u> <u>GGC</u> ATC GAT GCT ATT GAA CCA CCT GTC AGA CCG <u>CCC</u> <u>GC</u>	422	505-533

^a Underlined nucleotides indicate the molecular beacon's stem.

^b Sequence from databases.

^c These sequences were aligned to derive the corresponding primer.

^d The nucleotide positions refer to the *P. aeruginosa* tuf sequence fragment (SEQ ID NO. 153).

Annex XLVII: Molecular beacon internal hybridization probes for specific detection of tuf sequences (continued).

SEQ ID NO. Nucleotide sequence ^a		Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Fungal species: <i>Candida lusitanae</i>			
2115 ^b	5'- <u>GCG GGC</u> GGT AAG TCC ACC GGT AAG ACC TTG TTG <u>GCC CGC</u>	424	304-330
2116	5'- <u>GCG GGC</u> GTA AGT CAC CGG TAA GAC CTT GTT <u>GCC CCG</u> C	424	476-502
2117	5'- <u>GCG GGC</u> GAC GCC ATT GAG CCA CCT TCG AGA <u>GCC CGC</u>	424	512-535
Fungal species: <i>Candida parapsilosis</i>			
2118 ^b	5'- <u>GCG GGC</u> TCC TTG ACA ATT TCT TCG TAT CTG TTC TTG <u>GCC CGC</u>	426	301-330
Fungal species: <i>Candida tropicalis</i>			
2119	5'- <u>GCG GGC</u> TTA CAA CCC TAA GGC TGT TCC ATT CGT TGC <u>CCG C</u>	429	357-384
2120	5'- <u>GCG GGC</u> AGA AAC CAA GGC TGG TAA GGT TAC CGG AGC <u>CCG C</u>	429	459-487
Fungal species: <i>Cryptococcus neoformans</i>			
2106	5'- <u>GCG AGC</u> AGA GCA CGC CCT CCT CGC <u>CGC</u> TCG C	623,1985,1986 ^c	226-244 ^d
2107	5'- <u>GCG AGC</u> TCC CCA TCT CTG GTT GGC <u>ACG</u> CTC GC	623,1985,1986 ^c	390-408 ^d
Bacterial genus: <i>Legionella</i> sp.			
2083	5'- <u>CCG CCG</u> ATG TTC CGT AAA TTA CTT GAI GAA GGT CGA GCC <u>GCC GG</u>	111-112 ^a	488-519 ^e

^a Underlined nucleotides indicate the molecular beacon's stem.

^b This sequence is from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^c These sequences were aligned to derive the corresponding primer.

^d The nucleotide positions refer to the *C. neoformans* tuf (EF-1) sequence fragment (SEQ ID NO. 623).

^e The nucleotide positions refer to the *L. pneumophila* tuf (EF-1) sequence fragment (SEQ ID NO. 112).

Annex XLVII: Molecular beacon internal hybridization probes for specific detection of *tuf* sequences (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
<u>Fungal genus:</u> <i>Candida sp.</i>			
2108	5'- <u>GCG GGC</u> AAC TTC RTC AAG AAG GTT GGT TAC AAC CCG <u>CCC GC</u>	414,417, 422,424, 426,429,624 ^b	52-80 ^c
2109	5'- <u>GCG GGC</u> CCA ATC TCT GGT TGG AAY GGT GAC AAG <u>CCC GC</u>	Same as SEQ ID NO. 2108	100-125 ^c
<u>Bacterial group:</u> <i>Pseudomonads</i>			
2121	5'- <u>CGA CCG</u> CIA GCC GCA CAC CAA GTT <u>CCG</u> <u>GTC G</u>	153-155, 205,880,2137 ^d , 2138 ^{d,b}	598-616 ^e

^a Underlined nucleotides indicate the molecular beacon's stem.

^b These sequences were aligned to derive the corresponding primer.

^c The nucleotide positions refer to the *C. albicans tuf* (EF-1) sequence fragment (SEQ ID NO. 624).

^d Sequence from databases.

^e The nucleotide positions refer to the *P. aeruginosa tuf* sequence fragment (SEQ ID NO. 153).

Annex XLVIII: Molecular beacon internal hybridization probes for specific detection of *ddl* and *mtl* gene sequences.

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
<u>Bacterial species:</u> <i>E. faecium</i> (<i>ddl</i>)			
1237	5'- <u>GCG AGC</u> CGC GAA ATC GAA GTT GCT GTA TTA GGG <u>CTC GC</u>	1242 ^b	334-359
<u>Bacterial species:</u> <i>E. faecalis</i> (<i>mtl</i>)			
1238	5'- <u>GCG AGC</u> GGC GTT AAT TTT GGC ACC GAA GAA GAG <u>CTC GC</u>	1243 ^b	631-656

^a Underlined nucleotides indicate the molecular beacon's stem.

^b Sequence from databases.

**Annex XLIX: Internal hybridization probe for specific detection
of *S. aureus* sequences of unknown coding potential.**

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<u>Bacterial species:</u> <i>Staphylococcus aureus</i>			
1234	5'-ACT AAA TAA ACG CTC ATT CG	1244	35-54

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<hr/>			
<u>Resistance gene:</u> <i>aac(2')-Ia</i>			
1344	5'-AGC AGC AAC GAT GTT ACG CAG CAG	1348 ^a	163-186
1345 ^b	5'-CCC GCC GAG CAT TTC AAC TAT TG	1348 ^a	392-414
1346	5'-GAT GTT ACG CAG CAG GGC AGT C	1348 ^a	172-193
1347 ^b	5'-ACC AAG CAG GTT CGC AGT CAA GTA	1348 ^a	467-490
<u>Resistance gene:</u> <i>aac(3')-Ib</i>			
1349	5'-CAG CCG ACC AAT GAG TAT CTT GCC	1351 ^a	178-201
1350 ^b	5'-TAA TCA GGG CAG TTG CGA CTC CTA	1351 ^a	356-379
<u>Resistance gene:</u> <i>aac(3')-IIb</i>			
1352	5'-CCA CGC TGA CAG AGC CGC ACC G	1356 ^a	383-404
1353 ^b	5'-GGC CAG CTC CCA TCG GAC CCT G	1356 ^a	585-606
1354	5'-CAC GCT GAC AGA GCC GCA CCG	1356 ^a	384-404
1355 ^b	5'-ATG CCG TTG CTG TCG AAA TCC TCG	1356 ^a	606-629
<u>Resistance gene:</u> <i>aac(3')-IVa</i>			
1357	5'-GCC CAT CCA TTT GCC TTT GC	1361 ^a	295-314
1358 ^b	5'-GCG TAC CAA CTT GCC ATC CTG AAG	1361 ^a	517-540
1359	5'-TGC CCC TGC CAC CTC ACT C	1361 ^a	356-374
1360 ^b	5'-CGT ACC AAC TTG CCA TCC TGA AGA	1361 ^a	516-539
<u>Resistance gene:</u> <i>aac(3')-VIa</i>			
1362	5'-CGC CGC CAT CGC CCA AAG CTG G	1366 ^a	285-306
1363 ^b	5'-CGG CAT AAT GGA GCG CGG TGA CTG	1366 ^a	551-574
1364	5'-TTT CTC GCC CAC GCA GGA AAA ATC	1366 ^a	502-525
1365 ^b	5'-CAT CCT CGA CGA ATA TGC CGC G	1366 ^a	681-702
<u>Resistance gene:</u> <i>aac(6')-Ia</i>			
1367	5'-CAA ATA TAC TAA CAG AAG CGT TCA	1371 ^a	56-79
1368 ^b	5'-AGG ATC TTG CCA ATA CCT TTA T	1371 ^a	269-290
1379	5'-AAA CCT TTG TTT CGG TCT GCT AAT	1371 ^a	153-176
1380 ^b	5'-AAG CGA TTC CAA TAA TAC CTT GCT	1371 ^a	320-343

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
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<u>Resistance gene:</u> <i>aac(6')-Ic</i>			
1372	5'-GCT TTC GTT GCC TTT GCC GAG GTC	1376 ^a	157-180
1373 ^b	5'-CAC CCC TGT TGC TTC GCC CAC TC	1376 ^a	304-326
1374	5'-AGA TAT TGG CTT CGC CGC ACC ACA	1376 ^a	104-127
1375 ^b	5'-CCC TGT TGC TTC GCC CAC TCC TG	1376 ^a	301-323
 <u>Resistance gene:</u> <i>ant(3')-Ia</i>			
1377	5'-GCC GTG GGT CGA TGT TTG ATG TTA	1381 ^a	100-123
1378 ^b	5'-GCT CGA TGA CGC CAA CTA CCT CTG	1381 ^a	221-244
1379	5'-AGC AGC AAC GAT GTT ACG CAG CAG	1381 ^a	127-150
1380 ^b	5'-CGC TCG ATG ACG CCA ACT ACC TCT	1381 ^a	222-245
 <u>Resistance gene:</u> <i>ant(4')-Ia</i>			
1382	5'-TAG ATA TGA TAG GCG GTA AAA AGC	1386 ^a	149-172
1383 ^b	5'-CCC AAA TTC GAG TAA GAG GTA TT	1386 ^a	386-408
1384	5'-GAT ATG ATA GGC GGT AAA AAG C	1386 ^a	151-172
1385 ^b	5'-TCC CAA ATT CGA GTA AGA GGT A	1386 ^a	388-409
 <u>Resistance gene:</u> <i>aph(3')-Ia</i>			
1387	5'-TTA TGC CTC TTC CGA CCA TCA AGC	1391 ^a	233-256
1388 ^b	5'-TAC GCT CGT CAT CAA AAT CAC TCG	1391 ^a	488-511
1389	5'-GAA TAA CGG TTT GGT TGA TGC GAG	1391 ^a	468-491
1390 ^b	5'-ATG GCA AGA TCC TGG TAT CGG TCT	1391 ^a	669-692
 <u>Resistance gene:</u> <i>aph(3')-IIa</i>			
1392	5'-TGG GTG GAG AGG CTA TTC GGC TAT	1396 ^a	43-66
1393 ^b	5'-CAG TCC CTT CCC GCT TCA GTG AC	1396 ^a	250-272
1394	5'-GAC GTT GTC ACT GAA GCG GGA AGG	1396 ^a	244-267
1395 ^b	5'-CTT GGT GGT CGA ATG GGC AGG TAG	1396 ^a	386-409

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
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<u>Resistance gene:</u> <i>aph(3')-IIIa</i>			
1397	5'-GTG GGA GAA AAT GAA AAC CTA T	1401 ^a	103-124
1398 ^b	5'-ATG GAG TGA AAG AGC CTG AT	1401 ^a	355-374
1399	5'-ACC TAT GAT GTG GAA CGG GAA AAG	1401 ^a	160-183
1400 ^b	5'-CGA TGG AGT GAA AGA GCC TGA TG	1401 ^a	354-376
<u>Resistance gene:</u> <i>aph(3')-VIa</i>			
1402	5'-TAT TCA ACA ATT TAT CGG AAA CAG	1406 ^a	18-41
1403 ^b	5'-TCA GAG AGC CAA CTC AAC ATT TT	1406 ^a	175-197
1404	5'-AAA CAG CGT TTT AGA GCC AAA TAA	1406 ^a	36-59
1405 ^b	5'-TTC TCA GAG AGC CAA CTC AAC ATT	1406 ^a	177-200
<u>Resistance gene:</u> <i>blaCARB</i>			
1407	5'-CCC TGT AAT AGA AAA GCA AGT AGG	1411 ^a	351-374
1408 ^b	5'-TTG TCG TAT CCC TCA AAT CAC C	1411 ^a	556-577
1409	5'-TGG GAT TAC AAT GGC AAT CAG CG	1411 ^a	205-227
1410 ^b	5'-GGG GAA TAG GTC ACA AGA TCT GCT T	1411 ^a	329-353
<u>Resistance gene:</u> <i>blaCMY-2</i>			
1412	5'-GAG AAA ACG CTC CAG CAG GGC	1416 ^a	793-813
1413 ^b	5'-CAT GAG GCT TTC ACT GCG GGG	1416 ^a	975-995
1414	5'-TAT CGT TAA TCG CAC CAT CAC	1416 ^a	90-110
1415 ^b	5'-ATG CAG TAA TGC GGC TTT ATC	1416 ^a	439-459
<u>Resistance genes:</u> <i>blaCTX-M-1, blaCTX-M-2</i>			
1417	5'-TGG TTA ACT AYA ATC CSA TTG CGG A	1423 ^a	314-338
1418 ^b	5'-ATG CTT TAC CCA GCG TCA GAT T	1423 ^a	583-604
<u>Resistance gene:</u> <i>blaCTX-M-1</i>			
1419	5'-CGA TGA ATA AGC TGA TTT CTC ACG	1423 ^a	410-433
1420 ^b	5'-TGC TTT ACC CAG CGT CAG ATT ACG	1423 ^a	580-603
1421	5'-AAT TAG AGC GGC AGT CGG GAG GAA	1423 ^a	116-139
1422 ^b	5'-GAA ATC AGC TTA TTC ATC GCC ACG	1423 ^a	405-428

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
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<u>Resistance gene:</u> <i>blaCTX-M-2</i>			
1424	5'-GTT AAC GGT GAT GGC GAC GCT AC	1428 ^a	30-52
1425 ^b	5'-GAA TTA TCG GCG GTG TTA ATC AGC	1428 ^a	153-176
1426	5'-CAC GCT CAA TAC CGC CAT TCC A	1428 ^a	510-531
1427 ^b	5'-TTA TCG CCC ACT ACC CAT GAT TTC	1428 ^a	687-710
 <u>Resistance gene:</u> <i>blaIMP</i>			
1429	5'-TTT ACG GCT AAA GAT ACT GAA AAG T	1433 ^a	205-229
1430 ^b	5'-GTT TAA TAA AAC AAC CAC CGA ATA AT	1433 ^a	513-538
1431	5'-TAA TTG ACA CTC CAT TTA CGG CTA A	1433 ^a	191-215
1432 ^b	5'-ACC GAA TAA TAT TTT CCT TTC AGG CA	1433 ^a	497-522
 <u>Resistance gene:</u> <i>blaOXA2</i>			
1434	5'-CAC AAT CAA GAC CAA GAT TTG CGA T	1438 ^a	319-343
1435 ^b	5'-GAA AGG GCA GCT CGT TAC GAT AGA G	1438 ^a	532-556
 <u>Resistance gene:</u> <i>blaOXA10</i>			
1436	5'-CAG CAT CAA CAT TTA AGA TCC CCA	1439 ^a	194-217
1437 ^b	5'-CTC CAC TTG ATT AAC TGC GGA AAT TC	1439 ^a	479-504
 <u>Resistance gene:</u> <i>blaPER-1</i>			
1440	5'-AGA CCG TTA TCG TAA ACA GGG CTA AG	1442 ^a	281-306
1441 ^b	5'-TTT TTT GCT CAA ACT TTT TCA GGA TC	1442 ^a	579-604
 <u>Resistance gene:</u> <i>blaPER-2</i>			
1443	5'-CTT CTG CTC TGC TGA TGC TTG GC	1445 ^a	32-54
1444 ^b	5'-GGC GAC CAG GTA TTT TGT AAT ACT GC	1445 ^a	304-329
 <u>Resistance genes:</u> <i>blaPER-1, blaPER-2</i>			
1446	5'-GGC CTG YGA TTT GTT ATT TGA ACT GGT	1442 ^a	414-440
1447 ^b	5'-CGC TST GGT CCT GTG GTG GTT TC	1442 ^a	652-674
1448	5'-GAT CAG GTG CAR TAT CAA AAC TGG AC	1442 ^a	532-557
1449 ^b	5'-AGC WGG TAA CAA YCC TTT TAA CCG CT	1442 ^a	671-696

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
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<u>Resistance gene:</u> <i>blaSHV</i>			
1883	5'-AGC CGC TTG AGC AAA TTA AAC TA	1900 ^a	71-93
1884 ^b	5'-GTA TCC CGC AGA TAA ATC ACC AC	1900 ^a	763-785
1885	5'-AGC GAA AAA CAC CTT GCC GAC	1900 ^a	313-333
1884 ^b	5'-GTA TCC CGC AGA TAA ATC ACC AC	1900 ^a	763-785
<u>Resistance gene:</u> <i>blaTEM</i>			
1906	5'-CCT TAT TCC CTT TTT TGC GG	1927 ^a	27-46
1907 ^b	5'-CAC CTA TCT CAG CGA TCT GTC T	1927 ^a	817-838
1908	5'-AAC AGC GGT AAG ATC CTT GAG AG	1927 ^a	148-170
1907 ^b	5'-CAC CTA TCT CAG CGA TCT GTC T	1927 ^a	817-838
<u>Resistance gene:</u> <i>catI</i>			
2145	5'-GCA AGA TGT GGC GTG TTA CGG T	2147 ^a	363-384
2146 ^b	5'-GGG GCG AAG AAG TTG TCC ATA TT	2147 ^a	484-506
<u>Resistance gene:</u> <i>catII</i>			
2148	5'-CAG ATT AAA TGC GGA TTC AGC C	2150 ^a	67-88
2149 ^b	5'-ATC AGG TAA ATC ATC AGC GGA TA	2150 ^a	151-173
<u>Resistance gene:</u> <i>catIII</i>			
2151	5'-ATA TTT CAG CAT TAC CTT GGG TT	2153 ^a	419-441
2152 ^b	5'-TAC ACA ACT CTT GTA GCC GAT TA	2153 ^a	603-625
<u>Resistance gene:</u> <i>catP</i>			
2154	5'-CGC CAT TCA GAG TTT AGG AC	2156 ^a	178-197
2155 ^b	5'-TTC CAT ACC GTT GCG TAT CAC TT	2156 ^a	339-361
<u>Resistance gene:</u> <i>cat</i>			
2157	5'-CCA CAG AAA TTG ATA TTA GTG TTT TAT	2159 ^a	89-115
2158 ^b	5'-TCG CTA TTG TAA CCA GTT CTA	2159 ^a	201-221
2160	5'-TTT TGA ACA CTA TTT TAA CCA GC	2162 ^a	48-70
2161 ^b	5'-GAT TTA ACT TAT CCC AAT AAC CT	2162 ^a	231-253

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
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<u>Resistance gene:</u> <i>dfra</i>			
1450	5'-ACC ACT GGG AAT ACA CTT GTA ATG GC	1452 ^a	106-131
1451 ^b	5'-ATC TAC CTG GTC AAT CAT TGC TTC GT	1452 ^a	296-321
<u>Resistance gene:</u> <i>dhfrIa</i>			
1457	5'-CAA AGG TGA ACA GCT CCT GTT T	1461 ^a	75-96
1458 ^b	5'-TCC GTT ATT TTC TTT AGG TTG GTT AAA	1461 ^a	249-275
1459	5'-AAG GTG AAC AGC TCC TGT TT	1461 ^a	77-96
1560 ^b	5'-GAT CAC TAC GTT CTC ATT GTC A	1461 ^a	207-228
<u>Resistance genes:</u> <i>dhfrIa, dhfrXV</i>			
1453	5'-ATC GAA GAA TGG AGT TAT CGG RAA TG	1461 ^a	27-52
1454 ^b	5'-CCT AAA AYT RCT GGG GAT TTC WGG A	1461 ^a	384-408
1455	5'-CAG GTG GTG GGG AGA TAT ACA AAA	1461 ^a	290-313
1456 ^b	5'-TAT GTT AGA SRC GAA GTC TTG GKT AA	1461 ^a	416-441
<u>Resistance gene:</u> <i>dhfrIb</i>			
1466	5'-AAG CAT TGA CCT ACA ATC AGT GT	1470 ^a	98-120
1467 ^b	5'-AAT ACA ACT ACA TTG TCA TCA TTT GAT	1470 ^a	204-230
1468	5'-CGT TAC CCG CTC AGG TTG GAC ATC AA	1470 ^a	183-208
1469 ^b	5'-CAT CCC CCT CTG GCT CGA TGT CG	1470 ^a	354-376
<u>Resistance gene:</u> <i>dhfrV</i>			
1471	5'-GAT AAT GAC AAC GTA ATA GTA TTC CC	1475 ^a	208-233
1472 ^b	5'-GCT CAA TAT CAA TCG TCG ATA TA	1475 ^a	342-364
1473	5'-TTA AAG CCT TGA CGT ACA ACC AGT GG	1475 ^a	95-120
1474 ^b	5'-TGG GCA ATG TTT CTC TGT AAA TCT CC	1475 ^a	300-325
<u>Resistance genes:</u> <i>dhfrIb, dhfrV</i>			
1462	5'-GCA CTC CCY AAT AGG AAA TAC GC	1470 ^a	157-179
1463 ^b	5'-AGT GTT GCT CAA AAA CAA CTT CG	1470 ^a	405-427
1464	5'-ACG TTY GAA TCT ATG GGM GCA CT	1470 ^a	139-161
1465 ^b	5'-GTC GAT AAG TGG AGC GTA GAG GC	1470 ^a	328-350

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
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<u>Resistance gene:</u> <i>dhfrVI</i>			
1476	5'-GGC GAG CAG CTC CTA TTC AAA G	1480 ^a	79-100
1477 ^b	5'-TAG GTA AGC TAA TGC CGA TTC AAC A	1480 ^a	237-261
1478	5'-GAG AAT GGA GTA ATT GGC TCT GGA TT	1480 ^a	31-56
1479 ^b	5'-GCG AAA TAC ACA ACA TCA GGG TCA T	1480 ^a	209-233
<u>Resistance gene:</u> <i>dhfrVII</i>			
1485	5'-AAA ATG GCG TAA TCG GTA ATG GC	1489 ^a	32-54
1486 ^b	5'-CAT TTG AGC TTG AAA TTC CTT TCC TC	1489 ^a	189-214
1487	5'-AAT CGA AAA TAT GCA GTA GTG TCG AG	1489 ^a	166-191
1488 ^b	5'-AGA CTA TTG TAG ATT TGA CCG CCA	1489 ^a	294-317
<u>Resistance genes:</u> <i>dhfrVII</i> , <i>dhfrXVII</i>			
1481	5'-RTT ACA GAT CAT KTA TAT GTC TCT	1489 ^a	268-291
1482 ^b	5'-TAA TTT ATA TTA GAC AWA AAA AAC TG	1489 ^a	421-446
1483	5'-CAR YGT CAG AAA ATG GCG TAA TC	1489 ^a	23-45
1484 ^b	5'-TKC AAA GCR WTT TCT ATT GAA GGA AA	1489 ^a	229-254
<u>Resistance gene:</u> <i>dhfrVIII</i>			
1490	5'-GAC CTA TGA GAG CTT GCC CGT CAA A	1494 ^a	144-168
1491 ^b	5'-TCG CCT TCG TAC AGT CGC TTA ACA AA	1494 ^a	376-401
1492	5'-CAT TTT AGC TGC CAC CGC CAA TGG TT	1494 ^a	18-43
1493 ^b	5'-GCG TCG CTG ACG TTG TTC ACG AAG A	1494 ^a	245-269
<u>Resistance gene:</u> <i>dhfrIX</i>			
1495	5'-TCT CTA AAC ATG ATT GTC GCT GTC	1499 ^a	7-30
1496 ^b	5'-CAG TGA GGC AAA AGT TTT TCT ACC	1499 ^a	133-156
1497	5'-CGG ACG ACT TCA TGT GGT AGT CAG T	1499 ^a	171-195
1498 ^b	5'-TTT GTT TTC AGT AAT GGT CGG GAC CT	1499 ^a	446-471

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<u>Resistance gene:</u> <i>dhfrXII</i>			
1500	5'-ATC GGG TTA TTG GCA ATG GTC CTA	1504 ^a	50-73
1501 ^b	5'-GCG GTA GTT AGC TTG GCG TGA GAT T	1504 ^a	201-225
1502	5'-GCG GGC GGA GCT GAG ATA TAC A	1504 ^a	304-325
1503 ^b	5'-AAC GGA GTG GGT GTA CGG AAT TAC AG	1504 ^a	452-477
<u>Resistance gene:</u> <i>dhfrXIII</i>			
1505	5'-ATT TTT CGC AGG CTC ACC GAG AGC	1507 ^a	106-129
1506 ^b	5'-CGG ATG AGA CAA CCT CGA ATT CTG CTG	1507 ^a	413-439
<u>Resistance gene:</u> <i>dhfrXV</i>			
1508	5'-AGA ATG TAT TGG TAT TTC CAT CTA TCG	1512 ^a	215-241
1509 ^b	5'-CAA TGT CGA TTG TTG AAA TAT GTA AA	1512 ^a	336-361
1510	5'-TGG AGT GCC AAA GGG GAA CAA T	1512 ^a	67-88
1511 ^b	5'-CAG ACA CAA TCA CAT GAT CCG TTA TCG	1512 ^a	266-292
<u>Resistance gene:</u> <i>dhfrXVII</i>			
1513	5'-TTC AAG CTC AAA TGA AAA CGT CC	1517 ^a	201-223
1514 ^b	5'-GAA ATT CTC AGG CAT TAT AGG GAA T	1517 ^a	381-405
1515	5'-GTG GTC AGT AAA AGG TGA GCA AC	1517 ^a	66-88
1516 ^b	5'-TCT TTC AAA GCA TTT TCT ATT GAA GG	1517 ^a	232-257
<u>Resistance gene:</u> <i>emhR</i>			
2102	5'-CAC CTT CAC CCT GAC CGA CG	2105 ^a	822-841
2103 ^b	5'-CGA ACC AGC GGA AAT AGT TGG AC	2105 ^a	948-970
<u>Resistance genes:</u> <i>ereA, ereA2</i>			
1528	5'-AAC TTG AGC GAT TTT CGG ATA CCC TG	1530 ^a	80-105
1529 ^b	5'-TTG CCG ATG AAA TAA CCG CCG ACT	1530 ^a	317-340

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<u>Resistance gene:</u> ereB			
1531	5'-TCT TTT TGT TAC GAC ATA CGC TTT T	1535 ^a	152-176
1532 ^b	5'-AGT GCT TCT TTA TCC GCT GTT CTA	1535 ^a	456-479
1533	5'-CAG CGG ATA AAG AAG CAC TAC ACA TT	1535 ^a	461-486
1534 ^b	5'-CCT CCT GAA ATA AAG CCC GAC AT	1535 ^a	727-749
<u>Resistance gene:</u> gyrA			
1340	5'-GAA CAA GGT ATG ACA CCG GAT AAA T	1299 ^a	163-188
1341 ^b	5'-GAT AAC TGA AAT CCT GAG CCA TAC G	1299 ^a	274-299
1936	5'-TAC CAC CCG CAC GGC	1954 ^a	205-219
1937 ^b	5'-CGG AGT CGC CGT CGA TG	1954 ^a	309-325
1942	5'-GAC TGG AAC AAA GCC TAT AAA AAA TCA	1954 ^a	148-174
1937 ^b	5'-CGG AGT CGC CGT CGA TG	1954 ^a	309-325
2040	5'-TGT GAC CCC AGA CAA ACC C	2054 ^a	33-51
2041 ^b	5'-GTT GAG CGG CAG CAC TAT CT	2054 ^a	207-226
<u>Resistance gene:</u> inhA			
2098	5'-CTG AGT CAC ACC GAC AAA CGT C	2101 ^a	910-931
2099 ^b	5'-CCA GGA CTG AAC GGG ATA CGA A	2101 ^a	1074-1095
<u>Resistance genes:</u> linA, linA'			
1536 ^a	5'-AGA TGT ATT AAC TGG AAA ACA ACA A	1540 ^a	99-123
1537 ^b	5'-CTT TGT AAT TAG TTT CTG AAA ACC A	1540 ^a	352-376
1538	5'-TTA GAA GAT ATA GGA TAC AAA ATA GAA G	1540 ^a	187-214
1539 ^b	5'-GAA TGA AAA AGA AGT TGA GCT T	1540 ^a	404-425
<u>Resistance gene:</u> linB			
1541	5'-TGA TAA TCT TAT ACG TGG GGA ATT T	1545 ^a	246-270
1542 ^b	5'-ATA ATT TTC TAA TTG CCC TGT TTC AT	1545 ^a	359-384
1543	5'-GGG CAA TTA GAA AAT TAT TTA TCA GA	1545 ^a	367-392
1544 ^b	5'-TTT TAC TCA TGT TTA GCC AAT TAT CA	1545 ^a	579-604

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
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<u>Resistance gene:</u> <i>mefA</i>			
1546	5'-CAA GAA GGA ATG GCT GTA CTA C	1548 ^a	625-646
1547 ^b	5'-TAA TTC CCA AAT AAC CCT AAT AAT AGA	1548 ^a	816-842
<u>Resistance gene:</u> <i>mefE</i>			
1549	5'-GCT TAT TAT TAG GAA GAT TAG GGG GC	1551 ^a	815-840
1550 ^b	5'-TAG CAA GTG ACA TGA TAC TTC CGA	1551 ^a	1052-1075
<u>Resistance genes:</u> <i>mefA, mefE</i>			
1552	5'-GGC AAG CAG TAT CAT TAA TCA CTA	1548 ^a	50-73
1553 ^b	5'-CAA TGC TAC GGA TAA ACA ATA CTA TC	1548 ^a	318-343
1554	5'-AGA AAA TTA AGC CTG AAT ATT TAG GAC	1548 ^a	1010-1035
1555 ^b	5'-TAG TAA AAA CCA ATG ATT TAC ACC G	1548 ^a	1119-1143
<u>Resistance genes:</u> <i>mphA, mphK</i>			
1556	5'-ACT GTA CGC ACT TGC AGC CCG ACA T	1560 ^a	33-57
1557 ^b	5'-GAA CGG CAG GCG ATT CTT GAG CAT	1560 ^a	214-237
1558	5'-GTG GTG GTG CAT GGC GAT CTC T	1560 ^a	583-604
1559 ^b	5'-GCC GCA GCG AGG TAC TCT TCG TTA	1560 ^a	855-878
<u>Resistance gene:</u> <i>mupA</i>			
2142	5'-GCC TTA ATT TCG GAT AGT GC	2144 ^a	1831-1850
2143 ^b	5'-GAG AAA GAG CCC AAT TAT CTA ATG T	2144 ^a	2002-2026
<u>Resistance gene:</u> <i>parC</i>			
1342	5'-GAT GTT ATT GGT CAA TAT CAT CCA	1321 ^a	205-229
1343 ^b	5'-AAG AAA CTG TCT CTT TAT TAA TAT CAC GT	1321 ^a	396-425
1934	5'-GAA CGC CAG CGC GAA ATT CAA AAA G	1781	67-91
1935 ^b	5'-AGC TCG GCA TAC TTC GAC AGG	1781	277-297
2044	5'-ACC GTA AGT CGG CCA AGT CA	2055 ^a	176-195
2045 ^b	5'-GTT CTT TCT CCG TAT CGT C	2055 ^a	436-454

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
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<u>Resistance gene:</u> <i>ppflo-like</i>			
2163	5'-ACC TTC ATC CTA CCG ATG TGG GTT	2165 ^a	922-945
2164 ^b	5'-CAA CGA CAC CAG CAC TGC CAT TG	2165 ^a	1136-1158
<u>Resistance gene:</u> <i>rpoB</i>			
2065	5'-CCA GGA CGT GGA GGC GAT CAC A	2072 ^a	1218-1239
2066 ^b	5'-CAC CGA CAG CGA GCC GAT CAG A	2072 ^a	1485-1506
<u>Resistance gene:</u> <i>satG</i>			
1581	5'-AAT TGG GGA CTA CAC CTA TTA TGA TG	1585 ^a	93-118
1582 ^b	5'-GGC AAA TCA GTC AGT TCA GGA GT	1585 ^a	310-332
1583	5'-CGA TTG GCA ACA ATA CAC TCC TG	1585 ^a	294-316
1584 ^b	5'-TCA CCT ATT TTT ACG CCT GGT AGG AC	1585 ^a	388-413
<u>Resistance gene:</u> <i>sulII</i>			
1961	5'-GCT CAA GGC AGA TGG CAT TCC C	1965 ^a	222-243
1962 ^b	5'-GGA CAA GGC GGT TGC GTT TGA T	1965 ^a	496-517
1963	5'-CAT TCC CGT CTC GCT CGA CAG T	1965 ^a	237-258
1964 ^b	5'-ATC TGC CTG CCC GTC TTG C	1965 ^a	393-411
<u>Resistance gene:</u> <i>tetB</i>			
1966	5'-CAT GCC AGT CTT GCC AAC G	1970 ^a	66-84
1967 ^b	5'-CAG CAA TAA GTA ATC CAG CGA TG	1970 ^a	242-264
1968	5'-GGA GAG ATT TCA CCG CAT AG	1970 ^a	457-476
1969 ^b	5'-AGC CAA CCA TCA TGC TAT TCC A	1970 ^a	721-742
<u>Resistance gene:</u> <i>tetM</i>			
1586	5'-ATT CCC ACA ATC TTT TTT ATC AAT AA	1590 ^a	361-386
1587 ^b	5'-CAT TGT TCA GAT TCG GTA AAG TTC	1590 ^a	501-524
1588	5'-GTT TTT GAA GTT AAA TAG TGT TCT T	1590 ^a	957-981
1589 ^b	5'-CTT CCA TTT GTA CTT TCC CTA	1590 ^a	1172-1192

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
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<u>Resistance gene:</u> vatB			
1609	5'-GCC CTG ATC CAA ATA GCA TAT A	1613 ^a	11-32
1610 ^b	5'-CCT GGC ATA ACA GTA ACA TTC TG	1613 ^a	379-401
1611	5'-TGG GAA AAA GCA ACT CCA TCT C	1613 ^a	301-322
1612 ^b	5'-ACA ACT GAA TTC GCA GCA ACA AT	1613 ^a	424-446
 <u>Resistance gene:</u> vatC			
1614	5'-CCA ATC CAG AAG AAA TAT ACC C	1618 ^a	26-47
1615 ^b	5'-ATT AGT TTA TCC CCA ATC AAT TCA	1618 ^a	177-200
1616	5'-ATA ATG AAT GGG GCT AAT CAT CGT AT	1618 ^a	241-266
1617 ^b	5'-GCC AAC AAC TGA ATA AGG ATC AAC	1618 ^a	463-486
 <u>Resistance gene:</u> vga			
1619	5'-AAG GCA AAA TAA AAG GAG CAA AGC	1623 ^a	641-664
1620 ^b	5'-TGT ACC CGA GAC ATC TTC ACC AC	1623 ^a	821-843
1621	5'-AAT TGA AGG ACG GGT ATT GTG GAA AG	1623 ^a	843-868
1622 ^b	5'-CGA TTT TGA CAG ATG GCG ATA ATG AA	1623 ^a	975-1000
 <u>Resistance gene:</u> vgaB			
1624	5'-TTC TTT AAT GCT CGT AGA TGA ACC TA	1628 ^a	354-379
1625 ^b	5'-TTT TCG TAT TCT TCT TGT TGC TTT C	1628 ^a	578-602
1626	5'-AGG AAT GAT TAA GCC CCC TTC AAA AA	1628 ^a	663-688
1627 ^b	5'-TTA CAT TGC GAC CAT GAA ATT GCT CT	1628 ^a	849-874
 <u>Resistance genes:</u> vgb, vgh			
1629	5'-AAG GGG AAA GTT TGG ATT ACA CAA CA	1633 ^a	73-98
1630 ^b	5'-GAA CCA CAG GGC ATT ATC AGA ACC	1633 ^a	445-468
1631	5'-CGA CGA TGC TTT ATG GTT TGT	1633 ^a	576-596
1632 ^b	5'-GTT AAT TTG CCT ATC TTG TCA CAC TC	1633 ^a	850-875

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
Resistance gene: <i>vgbB</i>			
1634	5'-TTA ACT TGT CTA TTC CCG ATT CAG G	1882 ^a	23-47
1635 ^b	5'-GCT GTG GCA ATG GAT ATT CTG TA	1882 ^a	267-289
1636	5'-TTC CTA CCC CTG ATG CTA AAG TGA	1882 ^a	155-178
1637 ^b	5'-CAA AGT GCG TTA TCC GAA CCT AA	1882 ^a	442-464
Sequencing primers			
Resistance gene: <i>gyrA</i>			
1290	5'-GAY TAY GCI ATG ISI GTI ATH GT	1299 ^a	70-83
1292 ^b	5'-ARI SCY TCI ARI ATR TGI GC	1299 ^a	1132-1152
1291	5'-GCI YTI CCI GAY GTI MGI GAY GG	1299 ^a	100-123
1292 ^b	5'-ARI SCY TCI ARI ATR TGI GC	1299 ^a	1132-1152
1293	5'-ATG GCT GAA TTA CCT CAA TC	1299 ^a	1-21
1294 ^b	5'-ATG ATT GTT GTA TAT CTT CTT CAA C	1299 ^a	2626-2651
1295 ^b	5'-CAG AAA GTT TGA AGC GTT GT	1299 ^a	1255-1275
1296	5'-AAC GAT TCG TGA GTC AGA TA	1299 ^a	1188-1208
1297	5'-CGG TCA ACA TTG AGG AAG AGC T	1300 ^a	29-51
1298 ^b	5'-ACG AAA TCG ACC GTC TCT TTT TC	1300 ^a	415-437
Resistance gene: <i>gyrB</i>			
1301	5'-GTT MGT AWT MGT CCI GSI ATG TA	1307 ^a	82-105
1302 ^b	5'-TAI ADI GGI GGI KKI GCI ATR TA	1307 ^a	1600-1623
1303	5'-GGI GAI GAI DYI MGI GAR GG	1307 ^a	955-975
1304 ^b	5'-CIA RYT TIK YIT TIG TYT G	1307 ^a	1024-1043
1305	5'-ATG GTG ACT GCA TTG TCA GAT G	1307 ^a	1-23
1306 ^b	5'-GTC TAC GGT TTT CTA CAA CGT C	1307 ^a	1858-1888

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
Sequencing primers (continued)			
Resistance gene: <i>parC</i>			
1308	5'-ATG TAY GTI ATI ATG GAY MGI GC	1320 ^a	67-90
1309 ^b	5'-ATI ATY TTR TTI CCY TTI CCY TT	1320 ^a	1993-2016
1310	5'-ATI ATI TSI ATI ACY TCR TC	1320 ^a	1112-1132
1311 ^b	5'-GAR ATG AAR ATI MGI GGI GAR CA	1320 ^a	1288-1311
1312	5'-AAR TAY ATI ATI CAR GAR MGI GC	1321 ^a	67-90
1313 ^b	5'-AMI AYI CKR TGI GGI TTI TTY TT	1321 ^a	2212-2235
1314	5'-TAI GAI TTY ACI GAI SMI CAR GC	1321 ^a	1228-1251
1315 ^b	5'-ACI ATI GCI TCI GCY TGI KSY TC	1321 ^a	1240-1263
1316	5'-GTG AGT GAA ATA ATT CAA GAT T	1321 ^a	1-23
1317 ^b	5'-CAC CAA AAT CAT CTG TAT CTA C	1321 ^a	2356-2378
1318	5'-ACC TAY TCS ATG TAC GTR ATC ATG GA	1320 ^a	58-84
1319 ^b	5'-AGR TCG TCI ACC ATC GGY AGY TT	1320 ^a	832-855
Resistance gene: <i>parE</i>			
1322	5'-RTI GAI AAY ISI GTI GAY GAR G	1328 ^a	133-155
1325 ^b	5'-RTT CAT YTC ICC IAR ICC YTT	1328 ^a	1732-1752
1323	5'-ACI AWR SAI GGI GGI ACI CAY G	1328 ^a	829-850
1324 ^b	5'-CCI CCI GCI SWR TCI CCY TC	1328 ^a	1280-1302
1326	5'-TGA TTC AAT ACA GGT TTT AGA G	1328 ^a	27-49
1327 ^b	5'-CTA GAT TTC CTC CTC ATC AAA T	1328 ^a	1971-1993

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex LI: Internal hybridization probes for specific detection of antimicrobial agents resistance genes sequences.

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
Resistance gene: <i>aph3'VIa</i>			
2252	5'-CCA CAT ACA GTG TCT CTC	1406 ^a	149-166
Resistance gene: <i>blaSHV</i>			
1886	5'-GAC GCC CGC GCC ACC ACT	1900 ^a	484-501
1887	5'-GAC GCC CGC GAC ACC ACT A	1899 ^a	514-532
1888	5'-GAC GCC CGC AAC ACC ACT A	1901 ^a	514-532
1889	5'-GTT CGC AAC TGC AGC TGC TG	1899 ^a	593-612
1890	5'-TTC GCA ACG GCA GCT GCT G	1899 ^a	594-612
1891	5'-CCG GAG CTG CCG AIC GGG	1902 ^a	692-709
1892	5'-CGG AGC TGC CAA RCG GGG	1903 ^a	693-710
1893	5'-GGA GCT GGC GAR CGG GGT	1899 ^a	694-711
1894	5'-GAC CGG AGC TAG CGA RCG	1904 ^a	690-707
1895	5'-CGG AGC TAG CAA RCG GGG T	1905 ^a	693-711
1896	5'-GAA ACG GAA CTG AAT GAG GCG	1899 ^a	484-504
1897	5'-CAT TAC CAT GGG CGA TAA CAG	1899 ^a	366-386
1898	5'-CCA TTA CCA TGA GCG ATA ACAG	1899 ^a	365-386
Resistance gene: <i>blaTEM</i>			
1909	5'-ATG ACT TGG TTA AGT ACT CAC C	1928 ^a	293-314
1910	5'-ATG ACT TGG TTG AGT ACT CAC C	1927 ^a	293-314
1911	5'-CCA TAA CCA TGG GTG ATA ACA C	1928 ^a	371-392
1912	5'-CCA TAA CCA TGA GTG ATA ACA C	1927 ^a	371-392
1913	5'-CGC CTT GAT CAT TGG GAA CC	1928 ^a	475-494
1914	5'-CGC CTT GAT CGT TGG GAA CC	1927 ^a	475-494
1915	5'-CGC CTT GAT AGT TGG GAA CC	1929 ^a	475-494
1916	5'-CGT GGG TCT TGC GGT ATC AT	1927 ^a	712-731
1917	5'-CGT GGG TCT GGC GGT ATC AT	1930 ^a	712-731
1918	5'-GTG GGT CTC ACG GTA TCA TTG	1927 ^a	713-733
1919	5'-CGT GGG TCT CTC GGT ATC ATT	1931 ^a	712-732
1920	5'-CGT GGI TCT CGC GGT ATC AT	1927 ^a	712-731
1921	5'-CGT GGG TCT AGC GGT ATC ATT	1932 ^a	713-733
1922	5'-GTT TTC CAA TGA TTA GCA CTT TTA	1927 ^a	188-211
1923	5'-GTT TTC CAA TGA TAA GCA CTT TTA	1927 ^a	188-211
1924	5'-GTT TTC CAA TGC TGA GCA CTT TT	1932 ^a	188-210
1925	5'-CGT TTT CCA ATG ATG AGC ACT TT	1927 ^a	187-209
1926	5'-GTT TTC CAA TGG TGA GCA CTT TT	1933 ^a	188-210
2006	5'-TGG AGC CGG TGA GCG TGG	1927 ^a	699-716

^a Sequence from databases.

Annex LI: Internal hybridization probes for specific detection of antimicrobial agents resistance genes sequences (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
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<u>Resistance gene:</u> <i>blaTEM</i> (continued)			
2007	5'-TGG AGC CAG TGA GCG TGG	2010 ^a	699-716
2008	5'-TCT GGA GCC GAT GAG CGT G	1929 ^a	697-715
2009	5'-CTG GAG CCA GTA AGC GTG G	2011 ^a	698-716
2141	5'-CAC CAG TCA CAG AAA AGC	1927 ^a	311-328
<u>Resistance gene:</u> <i>dhfrIa</i>			
2253	5'-CAT TAC CCA ACC GAA AGT A	1461 ^a	158-176
<u>Resistance gene:</u> <i>embB</i>			
2104	5'-CTG GGC ATG GCI CGA GTC	2105 ^a	910-927
<u>Resistance gene:</u> <i>gyrA</i>			
1333	5'-TCA TGG TGA CTT ATC TAT TTA TG	1299 ^a	240-263
1334	5'-CAT CTA TTT ATA AAG CAA TGG TA	1299 ^a	251-274
1335	5'-CTA TTT ATG GAG CAA TGG T	1299 ^a	254-273
1940	5'-GTA TCG TTG GTG ACG TAA T	1299 ^a	206-224
1943	5'-GCT GGT GGA CGG CCA G	1954 ^a	279-294
1945	5'-CGG CGA CTA CGC GGT AT	1954 ^a	216-232
1946	5'-CGG CGA CTT CGC GGT AT	1954 ^a	216-232
1947	5'-CGG TAT ACG GCA CCA TCG T	1954 ^a	227-245
1948	5'-GCG GTA TAC AAC ACC ATC G	1954 ^a	226-244
1949	5'-CGG TAT ACG CCA CCA TCG T	1954 ^a	227-245
2042	5'-CAC GGG GAT TTC TCT ATT TA	2054 ^a	103-122
2043	5'-CAC GGG GAT TAC TCT ATT TA	2054 ^a	103-122
<u>Resistance gene:</u> <i>inhA</i>			
2100	5'-GCG AGA CGA TAG GTT GTC	2101 ^a	1017-1034
<u>Resistance gene:</u> <i>parC</i>			
1336	5'-TGG AGA CTA CTC AGT GT	1321 ^a	232-249
1337	5'-TGG AGA CTT CTC AGT GT	1321 ^a	232-249
1338	5'-GTG TAC GGA GCA ATG	1321 ^a	245-260
1339	5'-CCA GCG GAA ATG CGT	1321 ^a	342-357
1941	5'-GCA ATG GTC CGT TTA AGT	1321 ^a	253-270
1944	5'-TTT CGC CGC CAT GCG TTA C	1781	247-265
1950	5'-GGC GAC ATC GCC TGC	1781	137-151
1951	5'-GGC GAC AGA GCC TGC TA	1781	137-153

^a Sequence from databases.

Annex LI: Internal hybridization probes for specific detection of antimicrobial agents resistance genes sequences (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
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<u>Resistance gene:</u> <i>parC</i> (continued)			
1952	5'-CCT GCT ATG GAG CGA TGG T	1781	147-165
1953	5'-CGC CTG CTA TAA AGC GAT GGT	1781	145-165
2046	5'-ACG GGG ATT TTT CTA TCT AT	2055 ^a	227-246
<u>Resistance gene:</u> <i>rpoB</i>			
2067	5'-AGC TGA GCC AAT TCA TGG	2072 ^a	1304-1321
2068	5'-ATT CAT GGA CCA GAA CAA C	2072 ^a	1314-1332
2069	5'-CGC TGT CGG GGT TGA CCC	2072 ^a	1334-1351
2070	5'-GTT GAC CCA CAA GCG CCG	2072 ^a	1344-1361
2071	5'-CGA CTG TCG GCG CTG GGG	2072 ^a	1360-1377
<u>Resistance gene:</u> <i>tetM</i>			
2254	5'-ACC TGA ACA GAG AGA AAT G	1590 ^a	1062-1080

^a Sequence from databases.

Annex LII: Molecular beacon internal hybridization probes for specific detection of *atpD* sequences.

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
<u>Bacterial species:</u> <i>Bacteroides fragilis</i>			
2136	5'- <u>CCA</u> <u>ACG</u> <u>CGT</u> CCT CAA TCA TTT CTA ACT TCT ATG GCC <u>GCG</u> <u>GTT</u> <u>GG</u>	929	353-382
<u>Bacterial species:</u> <i>Bordetella pertussis</i>			
2182	5'- <u>GCG</u> <u>CGC</u> CAA CGA CTT CTA CCA CGA AAT GGA AGA GTC <u>GCG</u> <u>CGC</u>	1672	576-605
<u>Bacterial group:</u> <i>Campylobacter jejuni</i> and <i>C. coli</i>			
2133	5'- <u>CCA</u> <u>CGC</u> ACA WAA ACT TGT TTT AGA AGT AGC AGC WCA <u>GCG</u> <u>TGG</u>	1576, 1600,1849, 1863,2139 ^{b,c}	44-73 ^d
<u>Fungal species:</u> <i>Candida glabrata</i>			
2078	5'- <u>CCG</u> <u>AGC</u> CTT GGT CTT CGG CCA AAT GAA <u>CGC</u> <u>TCG</u> <u>G</u>	463	442-463
<u>Fungal species:</u> <i>Candida krusei</i>			
2075	5'- <u>CCG</u> <u>AGC</u> CAG GTT CTG AAG TCT CTG CAT TAT TAG GTG <u>CTC</u> <u>GG</u>	468	720-748
<u>Fungal species:</u> <i>Candida lusitanae</i>			
2080	5'- <u>CCG</u> <u>AGC</u> CGA AGA GGG CCA AGA TGT <u>CGC</u> <u>TCG</u> <u>G</u>	470	520-538
<u>Fungal species:</u> <i>Candida parapsilosis</i>			
2079	5'- <u>CCG</u> <u>AGC</u> GTT CAG TTA CTT CAG TCC AAG CCG <u>GCT</u> <u>CGG</u>	472	837-860
<u>Fungal species:</u> <i>Candida tropicalis</i>			
2077	5'- <u>CCG</u> <u>AGC</u> AAC CGA TCC AGC TCC AGC TAC <u>GCT</u> <u>CGG</u>	475	877-897
<u>Bacterial species:</u> <i>Klebsiella pneumoniae</i>			
2281	5'- <u>CCC</u> <u>CCA</u> GCT GGG CGG CGG TAT CGA TGG <u>GGG</u>	317	40-59

^a Underlined nucleotides indicate the molecular beacon's stem.

^b Sequence from databases.

^c These sequences were aligned to derive the corresponding primer.

^d The nucleotide positions refer to the *C. jejuni atpD* sequence fragment (SEQ ID NO. 1576).

Annex LII: Molecular beacon internal hybridization probes for specific detection of *atpD* sequences (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
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<u>Fungal genus:</u>		<i>Candida sp.</i>	
2076	5'- <u>CCG</u> <u>AGC</u> YGA YAA CAT TTT CAG ATT CAC CCA 460-478, RGC <u>GCT</u> <u>CGG</u>		697-723 ^c 663 ^b

^a Underlined nucleotides indicate the molecular beacon's stem.

^b These sequences were aligned to derive the corresponding primer.

^c The nucleotide positions refer to the *C. albicans atpD* sequence fragment (SEQ ID NO. 460).

Annex LIII: Internal hybridization probes for specific detection of *atpD* sequences.

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<hr/>			
<u>Bacterial species:</u> <i>Acinetobacter baumannii</i>			
2169	5'-CCC GTT TGC GAA AGG TGG	243	304-321
<u>Bacterial species:</u> <i>Klebsiella pneumoniae</i>			
2167	5'-CAG CAG CTG GGC GGC GGT	317	36-53

Annex LIV: Internal hybridization probes for specific detection of *ddl* and *mtl* sequences.

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
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<u>Bacterial species:</u>		<i>Enterococcus faecium (ddl)</i>	
2286	5'-AGT TGC TGT ATT AGG AAA TG	2288 ^a	784-803
2287	5'-TCG AAG TTG CTG TAT TAG GA	2288 ^a	780-799
<u>Bacterial species:</u>		<i>Enterococcus faecalis mtl)</i>	
2289	5'-CAC CGA AGA AGA TGA AAA AA	1243 ^a	264-283
2290	5'-TGG CAC CGA AGA AGA TGA	1243 ^a	261-278
2291	5'-ATT TTG GCA CCG AAG AAG A	1243 ^a	257-275

^a Sequence from databases.

What is claimed is:

1. A method for generating a repertory of nucleic acids of *tuf*, *fus*, *atpD* and/or *recA* genes from which are derived probes or primers, or both, useful for the detection of one, more than one related microorganisms, or substantially all microorganisms of a group selected from algae, archaea, bacteria, fungi and parasites, which comprises the step of:

- amplifying the nucleic acids of a plurality of determined algal, archaeal, bacterial, fungal and parasitical species with any combination of the primer pairs defined in SEQ ID NOs.: 543, 556-574, 636-655, 664, 681-683, 694, 696-697, 699-700, 708, 812-815, 911-917, 919-922, 935-938, 1203-1207, 1212-1213, 1221-1229, 1605-1606, 1974-1984, 1999-2003, 2282-2285.

2. A method for generating a repertory of nucleic acid sequences, which comprises the steps of:

- reproducing the method of claim 1, and
- adding the step of:
 - sequencing said nucleic acids.

3. A method for generating sequences of probes, or primers, or both, useful for the detection of one, more than one related microorganisms, or substantially all microorganisms of a group selected from algae, archaea, bacteria, fungi and parasites, which comprises the steps of:

- reproducing the method of claim 2, and
- adding the steps of:
 - aligning a subset of nucleic acid sequences of said repertory,
 - locating nucleic acid stretches that are present in the nucleic acids of strains or representatives of said one, more than one related microorganisms, or substantially all microorganisms of said group, and not present in the nucleic acid sequences of other microorganisms, and

- deriving consensus nucleic acid sequences useful as probes or primers from said stretches.

4. A bank of nucleic acids comprising the repertory of nucleic acids obtained from the method of claim 1.

5. A bank of nucleic acid sequences comprising the repertory of nucleic acid sequences obtained from the method of claim 2.

6. A method for generating sequences of probes, or primers, or both, useful for the detection of one, more than one related microorganisms, or substantially all microorganisms of a group selected from algae, archaea, bacteria, fungi and parasites, which comprises the steps of:

- aligning a subset of nucleic acid sequences of the bank as defined in claim 5,
- locating nucleic acid sequence stretches that are present in the nucleic acid sequences of strains or representatives of said one, more than one related microorganisms, or substantially all microorganisms of said group, and not present in the nucleic acid sequences of other microorganisms, and
- deriving consensus nucleic acid sequences useful as probes or primers from said stretches.

7. A method for generating probes, or primers or both, useful for the detection of one, more than one related microorganisms, or substantially all microorganisms of a group selected from algae, archaea, bacteria, fungi and parasites, which comprises the steps of:

- reproducing the method of claim 3 or 6, and
- adding the step of:
 - synthesising said probes or primers upon the nucleic acid sequences thereof.

8. A nucleic acid used for universal detection of any one of alga, archaeon, bacterium, fungus and parasite which is obtained from the method of claim 7.

9. A nucleic acid used for universal detection as set forth in claim 8, which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with said any one of alga, archaeon, bacterium, fungus and parasite and with any one of SEQ ID NOs.: 543, 556-574, 636-655, 658-661, 664, 681-683, 694, 696, 697, 699, 700, 708, 812-815, 911-917, 919-922, 935-938, 1203-1207, 1212-1213, 1221-1229, 1605-1606, 1974-1984, 1999-2003, 2282-2285.

10. A nucleic acid used for the specific and ubiquitous detection and for identification of any one of a algal, archaeal, bacterial, fungal and parasitital species, genus, family and group, which is obtained from the method of claim 7.

11. A nucleic acid as set forth in claim 10 having any one of the nucleotide sequences which are defined in SEQ ID NOs.:

539, 540	for the detection and/or identification of <i>Mycobacteriaceae</i> family
541, 542, 544, 2121	for the detection and/or identification of Pseudomonads group
545, 546	for the detection and/or identification of <i>Corynebacterium</i> sp.
547, 548, 1202	for the detection and/or identification of <i>Streptococcus</i> sp.
549, 550, 582, 583, 625, 626, 627, 628, 1199	for the detection and/or identification of <i>Streptococcus agalactiae</i>
551, 552, 2166, 2173, 2174, 2175, 2176, 2177, 2178, 2179	for the detection and/or identification of <i>Neisseria gonorrhoeae</i>
553, 575, 605, 606, 707, 1175, 1176	for the detection and/or identification of <i>Staphylococcus</i> sp.
554, 555, 2213	for the detection and/or identification of <i>Chlamydia trachomatis</i>

576, 631, 632, 633, 634, 635, 1163, 1164, 1167, 2076, 2108, 2109	for the detection and/or identification of <i>Candida</i> sp.
577, 1156, 1160 2073	for the detection and/or identification of <i>Candida albicans</i>
578, 1166, 1168, 2074	for the detection and/or identification of <i>Candida dubliniensis</i>
579, 2168	for the detection and/or identification of <i>Escherichia coli</i>
580, 603, 1174, 1236, 1238, 2289, 2290, 2291	for the detection and/or identification of <i>Enterococcus faecalis</i>
581	for the detection and/or identification of <i>Haemophilus influenzae</i>
584, 585, 586, 587, 588, 1232, 1234, 2186	for the detection and/or identification of <i>Staphylococcus aureus</i>
589, 590, 591, 592, 593	for the detection and/or identification of <i>Staphylococcus epidermidis</i>
594, 595	for the detection and/or identification of <i>Staphylococcus haemolyticus</i>
596, 597, 598	for the detection and/or identification of <i>Staphylococcus hominis</i>
599, 600, 601, 695, 1208, 1209	for the detection and/or identification of <i>Staphylococcus saprophyticus</i>
602, 1235, 1237, 1696, 1697, 1698, 1699, 1700, 1701, 2286, 2287	for the detection and/or identification of <i>Enterococcus faecium</i>
604	for the detection and/or identification of <i>Enterococcus gallinarum</i>
620, 1122	for the detection and/or identification of <i>Enterococcus casseliflavus</i> , <i>E. flavescens</i> and <i>E. gallinarum</i>
629, 630, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092	for the detection and/or identification of <i>Chlamydia pneumoniae</i>

- 636, 637, 638, 639, 640, 641, 642 for the detection and/or identification of at least the following:
Abiotrophia adiacens, *Abiotrophia defectiva*, *Acinetobacter baumannii*, *Acinetobacter lwoffii*, *Aerococcus viridans*, *Bacillus anthracis*, *Bacillus cereus*, *Bacillus subtilis*, *Brucella abortus*, *Burkholderia cepacia*, *Citrobacter diversus*, *Citrobacter freundii*, *Enterobacter aerogenes*, *Enterobacter agglomerans*, *Enterobacter cloacae*, *Enterococcus avium*, *Enterococcus casseliflavus*, *Enterococcus dispar*, *Enterococcus durans*, *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus flavescens*, *Enterococcus gallinarum*, *Enterococcus mundtii*, *Enterococcus raffinosus*, *Enterococcus solitarius*, *Escherichia coli*, *Gemella morbillorum*, *Haemophilus ducreyi*, *Haemophilus haemolyticus*, *Haemophilus influenzae*, *Haemophilus parahaemolyticus*, *Haemophilus parainfluenzae*, *Hafnia alvei*, *Kingella kingae*, *Klebsiella oxytoca*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Megamonas hypermegale*, *Moraxella atlantae*, *Moraxella catarrhalis*, *Morganella morganii*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella aerogenes*, *Pasteurella multocida*, *Peptostreptococcus magnus*, *Proteus mirabilis*, *Providencia alcalifaciens*, *Providencia rettgeri*, *Providencia rustigianii*, *Providencia stuartii*, *Pseudomonas aeruginosa*, *Pseudomonas fluorescens*, *Pseudomonas stutzeri*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enteritidis*, *Salmonella gallinarum*, *Salmonella typhimurium*, *Serratia liquefaciens*, *Serratia marcescens*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus capitis*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus lugdunensis*, *Staphylococcus saprophyticus*, *Staphylococcus simulans*, *Staphylococcus warneri*, *Stenotrophomonas maltophilia*, *Streptococcus acidominimus*, *Streptococcus agalactiae*, *Streptococcus anginosus*, *Streptococcus bovis*, *Streptococcus constellatus*, *Streptococcus cricetus*, *Streptococcus cristatus*, *Streptococcus dysgalactiae*, *Streptococcus equi*, *Streptococcus ferus*, *Streptococcus gordonii*, *Streptococcus intermedius*, *Streptococcus macacae*, *Streptococcus mitis*, *Streptococcus mutans*, *Streptococcus oralis*, *Streptococcus parasanguinis*, *Streptococcus parauberis*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Streptococcus ratti*, *Streptococcus salivarius*, *Streptococcus sanguinis*, *Streptococcus sobrinus*, *Streptococcus uberis*, *Streptococcus vestibularis*, *Vibrio cholerae*, *Yersinia enterocolitica*, *Yersinia pestis*, *Yersinia pseudotuberculosis*.
- 656, 657, 271, 1136, 1137 for the detection and/or identification of *Enterococcus* sp.
- 701, 702 for the detection and/or identification of *Leishmania* sp.

- 703, 704, 705, 706, for the detection and/or identification of *Entamoeba* sp.
793
- 794, 795 for the detection and/or identification of *Trypanosoma cruzi*
- 796, 797, 808, 809, for the detection and/or identification of *Clostridium* sp.
810, 811
- 798, 799, 800, 801, for the detection and/or identification of *Cryptosporidium*
802, 803, 804, 805, *parvum*
806, 807
- 816, 817, 818, 819 for the detection and/or identification of *Giardia* sp.
- 820, 821, 822 for the detection and/or identification of *Trypanosoma*
brucei
- 823, 824 for the detection and/or identification of *Trypanosoma* sp.
- 825, 826 for the detection and/or identification of *Bordetella* sp.
- 923, 924, 925, 926, for the detection and/or identification of *Trypanosomatidae*
927, 928 family
- 933, 934 for the detection and/or identification of *Enterobacteriaceae*
group
- 994, 995, 996, 997, for the detection and/or identification of *Streptococcus*
998, 999, 1000, *pyogenes*
1001, 1200, 1210,
1211
- 1157, 2079, 2118 for the detection and/or identification of *Candida*
parapsilosis
- 1158, 1159, 2078, for the detection and/or identification of *Candida glabrata*
2110, 2111
- 1160, 2077, 2119, for the detection and/or identification of *Candida tropicalis*
2120
- 1161, 2075, 2112, for the detection and/or identification of *Candida krusei*
2113, 2114
- 1162 for the detection and/or identification of *Candida*
guilliermondii
- 1162, 2080, 2115 for the detection and/or identification of *Candida lusitaniae*
2116, 2117
- 1165 for the detection and/or identification of *Candida*
zeylanoides
- 1201 for the detection and/or identification of *Streptococcus*
pneumoniae

1233	for the detection and/or identification of <i>Staphylococcus</i> sp. other than <i>S. aureus</i>
1329, 1330, 1331, 1332, 2167, 2281	for the detection and/or identification of <i>Klebsiella pneumoniae</i>
1661, 1665	for the detection and/or identification of <i>Escherichia coli</i> and <i>Shigella</i> sp.
1690, 1691, 1692, 1693, 2169	for the detection and/or identification of <i>Acinetobacter baumannii</i>
1694, 1695, 2122	for the detection and/or identification of <i>Pseudomonas aeruginosa</i>
1971, 1972, 1973	for the detection and/or identification of <i>Cryptococcus</i> sp.
2081, 2082, 2083	for the detection and/or identification of <i>Legionella</i> sp.
2084	for the detection and/or identification of <i>Legionella pneumophila</i>
2093, 2094, 2095, 2096	for the detection and/or identification of <i>Mycoplasma pneumoniae</i>
2106, 2107	for the detection and/or identification of <i>Cryptococcus neoformans</i>
2131, 2132, 2133	for the detection and/or identification of <i>Campylobacter jejuni</i> and <i>C. coli</i>
2134, 2135, 2136	for the detection and/or identification of <i>Bacteroides fragilis</i>
2170	for the detection and/or identification of <i>Abiotrophia adiacens</i>
2171	for the detection and/or identification of <i>Gemella</i> sp.
2172	for the detection and/or identification of <i>Enterococcus</i> sp., <i>Gemella</i> sp., <i>A. adiacens</i>
2180, 2181, 2182	for the detection and/or identification of <i>Bordetella pertussis</i> .

12. A method for detecting the presence in a test sample of a microorganism that is an alga, archaeum, bacterium, fungus or parasite, which comprises:

- a) putting in contact any test sample *tuf* or *atpD* or *recA* nucleic acids and nucleic acid primers and/or probes, said primers and/or probes having

been selected to be sufficiently complementary to hybridize to one or more *tuf* or *atpD* or *recA* nucleic acids that are specific to said group of microorganisms;

b) allowing the primers and/or probes and any test sample *tuf* or *atpD* or *recA* nucleic acids to hybridize under specified conditions such as said primers and/or probes hybridize to the *tuf* or *atpD* or *recA* nucleic acids of said microorganism and does not detectably hybridize to *tuf* or *atpD* or *recA* sequences from other microorganisms; and,

c) testing for hybridization of said primers and/or probes to any test sample *tuf* or *atpD* or *recA* nucleic acids.

13. The method of claim 12 wherein c) is based on a nucleic acid target amplification method.

14. The method of claim 12 wherein c) is based on a signal amplification method.

15. The method of any one of claims 12 to 14 wherein said primers and/or probes that are sufficiently complementary are perfectly complementary.

16. The method of any one of claims 12 to 14 wherein said primers and/or probes that are sufficiently complementary are not perfectly complementary.

17. A method for the specific detection and/or identification of a microorganism that is an algal, archaeal, bacterial, fungal or parasitical species, genus, family or group in any sample, using a panel of probes or amplification primers or both, each individual probe or primer being derived from a nucleic acid which has a nucleotide sequence of at least 12 nucleotides in length capable of hybridizing with the nucleic acids of said microorganism and with a nucleic acid having any one of the nucleotide sequences defined in SEQ ID NOs.:

539, 540	for the detection and/or identification of <i>Mycobacteriaceae</i> family
541, 542, 544, 2121	for the detection and/or identification of <i>Pseudomonads</i> group

- 545, 546 for the detection and/or identification of *Corynebacterium* sp.
- 547, 548, 1202 for the detection and/or identification of *Streptococcus* sp.
- 549, 550, 582, 583, for the detection and/or identification of *Streptococcus*
625, 626, 627, 628, *agalactiae*
1199
- 551, 552, 2166, for the detection and/or identification of *Neisseria*
2173, 2174, 2175, *gonorrhoeae*
2176, 2177, 2178,
2179
- 553, 575, 605, 606, for the detection and/or identification of *Staphylococcus* sp.
707, 1175, 1176
- 554, 555, 2213 for the detection and/or identification of *Chlamydia*
trachomatis
- 576, 631, 632, 633, for the detection and/or identification of *Candida* sp.
634, 635, 1163,
1164, 1167, 2076,
2108, 2109
- 577, 1156, 1160 for the detection and/or identification of *Candida albicans*
2073
- 578, 1166, 1168, for the detection and/or identification of *Candida*
2074 *dubliniensis*
- 579, 2168 for the detection and/or identification of *Escherichia coli*
- 580, 603, 1174, for the detection and/or identification of *Enterococcus*
1236, 1238, 2289, *faecalis*
2290, 2291
- 581 for the detection and/or identification of *Haemophilus*
influenzae
- 584, 585, 586, 587, for the detection and/or identification of *Staphylococcus*
588, 1232, 1234, *aureus*
2186
- 589, 590, 591, 592, for the detection and/or identification of *Staphylococcus*
593 *epidermidis*
- 594, 595 for the detection and/or identification of *Staphylococcus*
haemolyticus
- 596, 597, 598 for the detection and/or identification of *Staphylococcus*
hominis

- 599, 600, 601, 695, 1208, 1209 for the detection and/or identification of *Staphylococcus saprophyticus*
- 602, 1235, 1237, 1696, 1697, 1698, 1699, 1700, 1701, 2286, 2287 for the detection and/or identification of *Enterococcus faecium*
- 604 for the detection and/or identification of *Enterococcus gallinarum*
- 620, 1122 for the detection and/or identification of *Enterococcus casseliflavus*, *E. flavescens* and *E. gallinarum*
- 629, 630, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092 for the detection and/or identification of *Chlamydia pneumoniae*
- 636, 637, 638, 639, 640, 641, 642 for the detection and/or identification of at least the following:
Abiotrophia adiacens, *Abiotrophia defectiva*, *Acinetobacter baumannii*, *Acinetobacter lwoffii*, *Aerococcus viridans*, *Bacillus anthracis*, *Bacillus cereus*, *Bacillus subtilis*, *Brucella abortus*, *Burkholderia cepacia*, *Citrobacter diversus*, *Citrobacter freundii*, *Enterobacter aerogenes*, *Enterobacter agglomerans*, *Enterobacter cloacae*, *Enterococcus avium*, *Enterococcus casseliflavus*, *Enterococcus dispar*, *Enterococcus durans*, *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus flavescens*, *Enterococcus gallinarum*, *Enterococcus mundtii*, *Enterococcus raffinosus*, *Enterococcus solitarius*, *Escherichia coli*, *Gemella morbillorum*, *Haemophilus ducreyi*, *Haemophilus haemolyticus*, *Haemophilus influenzae*, *Haemophilus parahaemolyticus*, *Haemophilus parainfluenzae*, *Hafnia alvei*, *Kingella kingae*, *Klebsiella oxytoca*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Megamonas hypermegale*, *Moraxella atlantae*, *Moraxella catarrhalis*, *Morganella morganii*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella aerogenes*, *Pasteurella multocida*, *Peptostreptococcus magnus*, *Proteus mirabilis*, *Providencia alcalifaciens*, *Providencia rettgeri*, *Providencia rustigianii*, *Providencia stuartii*, *Pseudomonas aeruginosa*, *Pseudomonas fluorescens*, *Pseudomonas stutzeri*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enteritidis*, *Salmonella gallinarum*, *Salmonella typhimurium*, *Serratia liquefaciens*, *Serratia marcescens*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus capitis*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus lugdunensis*, *Staphylococcus saprophyticus*, *Staphylococcus simulans*, *Staphylococcus warneri*, *Stenotrophomonas*

- maltophilia, Streptococcus acidominimus, Streptococcus agalactiae, Streptococcus anginosus, Streptococcus bovis, Streptococcus constellatus, Streptococcus cricetus, Streptococcus cristatus, Streptococcus dysgalactiae, Streptococcus equi, Streptococcus ferus, Streptococcus gordonii, Streptococcus intermedius, Streptococcus macacae, Streptococcus mitis, Streptococcus mutans, Streptococcus oralis, Streptococcus parasanguinis, Streptococcus parauberis, Streptococcus pneumoniae, Streptococcus pyogenes, Streptococcus rattii, Streptococcus salivarius, Streptococcus sanguinis, Streptococcus sobrinus, Streptococcus uberis, Streptococcus vestibularis, Vibrio cholerae, Yersinia enterocolitica, Yersinia pestis, Yersinia pseudotuberculosis.*
- 656, 657, 271, 1136, 1137 for the detection and/or identification of *Enterococcus* sp.
- 701, 702 for the detection and/or identification of *Leishmania* sp.
- 703, 704, 705, 706, 793 for the detection and/or identification of *Entamoeba* sp.
- 794, 795 for the detection and/or identification of *Trypanosoma cruzi*
- 796, 797, 808, 809, 810, 811 for the detection and/or identification of *Clostridium* sp.
- 798, 799, 800, 801, 802, 803, 804, 805, 806, 807 for the detection and/or identification of *Cryptosporidium parvum*
- 816, 817, 818, 819 for the detection and/or identification of *Giardia* sp.
- 820, 821, 822 for the detection and/or identification of *Trypanosoma brucei*
- 823, 824 for the detection and/or identification of *Trypanosoma* sp.
- 825, 826 for the detection and/or identification of *Bordetella* sp.
- 923, 924, 925, 926, 927, 928 for the detection and/or identification of *Trypanosomatidae* family
- 933, 934 for the detection and/or identification of *Enterobacteriaceae* group
- 994, 995, 996, 997, 998, 999, 1000, 1001, 1200, 1210, 1211 for the detection and/or identification of *Streptococcus pyogenes*
- 1157, 2079, 2118 for the detection and/or identification of *Candida parapsilosis*

1158, 1159, 2078, 2110, 2111	for the detection and/or identification of <i>Candida glabrata</i>
1160, 2077, 2119, 2120	for the detection and/or identification of <i>Candida tropicalis</i>
1161, 2075, 2112, 2113, 2114	for the detection and/or identification of <i>Candida krusei</i>
1162	for the detection and/or identification of <i>Candida guilliermondii</i>
1162, 2080, 2115 2116, 2117	for the detection and/or identification of <i>Candida lusitaniae</i>
1165	for the detection and/or identification of <i>Candida zeylanoides</i>
1201	for the detection and/or identification of <i>Streptococcus pneumoniae</i>
1233	for the detection and/or identification of <i>Staphylococcus</i> sp. other than <i>S. aureus</i>
1329, 1330, 1331, 1332, 2167, 2281	for the detection and/or identification of <i>Klebsiella pneumoniae</i>
1661, 1665	for the detection and/or identification of <i>Escherichia coli</i> and <i>Shigella</i> sp.
1690, 1691, 1692, 1693, 2169	for the detection and/or identification of <i>Acinetobacter baumannii</i>
1694, 1695, 2122	for the detection and/or identification of <i>Pseudomonas aeruginosa</i>
1971, 1972, 1973	for the detection and/or identification of <i>Cryptococcus</i> sp.
2081, 2082, 2083	for the detection and/or identification of <i>Legionella</i> sp.
2084	for the detection and/or identification of <i>Legionella pneumophila</i>
2093, 2094, 2095, 2096	for the detection and/or identification of <i>Mycoplasma pneumoniae</i>
2106, 2107	for the detection and/or identification of <i>Cryptococcus neoformans</i>
2131, 2132, 2133	for the detection and/or identification of <i>Campylobacter jejuni</i> and <i>C. coli</i>
2134, 2135, 2136	for the detection and/or identification of <i>Bacteroides fragilis</i>

- 2170 for the detection and/or identification of *Abiotrophia adiacens*
 2171 for the detection and/or identification of *Gemella* sp.
 2172 for the detection and/or identification of *Enterococcus* sp.,
Gemella sp., *A. adiacens*
 2180, 2181, 2182 for the detection and/or identification of *Bordetella pertussis*,

said method comprising the step of contacting the nucleic acids of the sample with said primers or probes under suitable conditions of hybridization or of amplification and detecting the presence of hybridized probes or amplified products as an indication of the presence of said specific algal, archaeal, bacterial, fungal or parasitical species, genus, family or group.

18. A method for the universal detection of any bacterium, fungus or parasite in a sample, using a panel of probes or amplification primers or both, each individual probe or primer being derived from a nucleic acid as defined in claims 8 or 9, the method comprising the step of contacting the nucleic acids of the sample with said primers or probes under suitable conditions of hybridization or of amplification and detecting the presence of any alga, archaeon, bacterium, fungus or parasite.

19. A method as set forth in claim 17 or 18, which further comprises probes or primers, or both, for the detection of at least one antimicrobial agent resistance gene.

20. A method as set forth in claim 17, 18 or 19, which further comprises probes or primers, or both, for the detection of at least one toxin gene.

21. A method as set forth in claim 19 or 20, wherein the probes or primers for the detection of said antimicrobial agent resistance gene or toxin gene have at least 12 nucleotides in length capable of hybridizing with an antimicrobial agent resistance gene and/or toxin gene selected from SEQ ID NOs.:

- 1078, 1079, 1085 for the detection and/or identification of the *E. coli* Shiga-like toxin 2 (*stx*₂) gene

1080, 1081, 1084, 2012	for the detection and/or identification of the <i>E. coli</i> Shiga-like toxin 1 (<i>stx</i> ₁) gene
1082, 1083	for the detection and/or identification of <i>E. coli</i> Shiga-like toxins 1 and 2 (<i>stx</i>) genes
1086, 1087, 1088, 1089, 1090, 1091, 1092, 1170, 1239, 1240, 2292	for the detection and/or identification of the <i>vanA</i> resistance gene
1095, 1096, 1171, 1241, 2294, 2295	for the detection and/or identification of the <i>vanB</i> resistance gene
1111, 1112, 1113, 1114, 1115, 1116, 1118, 1119, 1120, 1121, 1123, 1124	for the detection and/or identification of the <i>vanAB</i> resistance genes
1103, 1104, 1109, 1110	for the detection and/or identification of the <i>vanC1</i> resistance gene
1105, 1106, 1107, 1108	for the detection and/or identification of the <i>vanC2</i> and <i>vanC3</i> resistance genes
1097, 1098, 1099, 1100, 1101, 1102	for the detection and/or identification of the <i>vanC1</i> , <i>vanC2</i> and <i>vanC3</i> resistance genes
1150, 1153, 1154, 1155	for the detection and/or identification of the <i>vanAXY</i> resistance genes
1094, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1192, 1193, 1194, 1195, 1196, 1197, 1214, 1216, 1217, 1218, 1219, 1220, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039	for the detection and/or identification of the <i>S. pneumoniae</i> <i>pbpla</i> gene

1142, 1143, 1144, 1145	for the detection and/or identification of the <i>S. pneumoniae</i> <i>pbp2b</i> gene
1146, 1147, 1148, 1149	for the detection and/or identification of the <i>S. pneumoniae</i> <i>pbp2x</i> gene
1177, 1231	for the detection and/or identification of the <i>mecA</i> resistance gene
1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1333, 1334, 1335, 1340, 1341, 1936, 1937, 1940, 1942, 1943, 1945, 1946, 1947, 1948, 1949, 2040, 2041, 2042, 2043, 2250, 2251	for the detection and/or identification of the <i>gyrA</i> resistance gene
1301, 1302, 1303, 1304, 1305, 1306	for the detection and/or identification of the <i>gyrB</i> resistance gene
1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1336, 1337, 1338, 1339, 1342, 1343, 1934, 1935, 1938, 1939, 1941, 1944, 1950, 1951, 1952, 1953, 1955, 2044, 2045, 2046	for the detection and/or identification of the <i>parC</i> resistance gene
1322, 1323, 1324, 1325, 1326, 1327	for the detection and/or identification of the <i>parE</i> resistance gene
1344, 1345, 1346, 1347	for the detection and/or identification of the <i>aac(2')-Ia</i> resistance gene
1349, 1350	for the detection and/or identification of the <i>aac(3')-Ib</i> resistance gene
1352, 1353, 1354, 1355	for the detection and/or identification of the <i>aac(3')-IIb</i> resistance gene
1357, 1358, 1359, 1360	for the detection and/or identification of the <i>aac(3')-IVa</i> resistance gene
1362, 1363, 1364, 1365	for the detection and/or identification of the <i>aac(3')-VIa</i> resistance gene

1367, 1368, 1369, 1370	for the detection and/or identification of the <i>aac(6')-Ia</i> resistance gene
1372, 1373, 1374, 1375	for the detection and/or identification of the <i>aac(6')-Ic</i> resistance gene
1377, 1378, 1379, 1380	for the detection and/or identification of the <i>ant(3')-Ia</i> resistance gene
1382, 1383, 1384, 1385	for the detection and/or identification of the <i>ant(4')-Ia</i> resistance gene
1387, 1388, 1389, 1390	for the detection and/or identification of the <i>aph(3')-Ia</i> resistance gene
1392, 1393, 1394, 1395	for the detection and/or identification of the <i>aph(3')-IIa</i> resistance gene
1397, 1398, 1399, 1400	for the detection and/or identification of the <i>aph(3')-IIIa</i> resistance gene
1402, 1403, 1404, 1405, 2252	for the detection and/or identification of the <i>aph(3')-VIa</i> resistance gene
1407, 1408, 1409 1410	for the detection and/or identification of the <i>blaCARB</i> resistance gene
1412, 1413, 1414, 1415	for the detection and/or identification of the <i>blaCMY-2</i> resistance gene
1417, 1418	for the detection and/or identification of the <i>blaCTX-M-1</i> and <i>blaCTX-M-2</i> resistance genes
1419, 1420, 1421, 1422	for the detection and/or identification of the <i>blaCTX-M-1</i> resistance gene
1424, 1425, 1426, 1427	for the detection and/or identification of the <i>blaCTX-M-2</i> resistance gene
1429, 1430, 1431, 1432	for the detection and/or identification of the <i>blaIMP</i> resistance gene
1434, 1435	for the detection and/or identification of the <i>blaOXA2</i> resistance gene
1436, 1437	for the detection and/or identification of the <i>blaOXA10</i> resistance gene
1440, 1441	for the detection and/or identification of the <i>blaPER-1</i> resistance gene

1443, 1444	for the detection and/or identification of the <i>blaPER-2</i> resistance gene
1446, 1447, 1448, 1449	for the detection and/or identification of the <i>blaPER-1</i> and <i>blaPER-2</i> resistance genes
1450, 1451	for the detection and/or identification of the <i>dfrA</i> resistance gene
1453, 1454, 1455, 1456	for the detection and/or identification of the <i>dhfrIa</i> and <i>dhfrXV</i> resistance genes
1457, 1458, 1459, 1460, 2253	for the detection and/or identification of the <i>dhfrIa</i> resistance gene
1462, 1463, 1464, 1465	for the detection and/or identification of the <i>dhfrIb</i> and <i>dhfrV</i> resistance genes
1466, 1467, 1468, 1469	for the detection and/or identification of the <i>dhfrIb</i> resistance gene
1471, 1472, 1473, 1474	for the detection and/or identification of the <i>dhfrV</i> resistance gene
1476, 1477, 1478, 1479	for the detection and/or identification of the <i>dhfrVI</i> resistance gene
1481, 1482, 1483, 1484	for the detection and/or identification of the <i>dhfrVII</i> and <i>dhfrXVII</i> resistance genes
1485, 1486, 1487, 1488	for the detection and/or identification of the <i>dhfrVII</i> resistance gene
1490, 1491, 1492, 1493	for the detection and/or identification of the <i>dhfrVIII</i> resistance gene
1495, 1496, 1497, 1498	for the detection and/or identification of the <i>dhfrIX</i> resistance gene
1500, 1501, 1502, 1503	for the detection and/or identification of the <i>dhfrXII</i> resistance gene
1505, 1506	for the detection and/or identification of the <i>dhfrXIII</i> resistance gene
1508, 1509, 1510, 1511	for the detection and/or identification of the <i>dhfrXV</i> resistance gene
1513, 1514, 1515, 1516	for the detection and/or identification of the <i>dhfrXVII</i> resistance gene

1528, 1529	for the detection and/or identification of the <i>ereA</i> and <i>ereA2</i> resistance genes
1531, 1532, 1533, 1534	for the detection and/or identification of the <i>ereB</i> resistance gene
1536, 1537, 1538, 1539	for the detection and/or identification of the <i>linA</i> and <i>linA'</i> resistance genes
1541, 1542, 1543, 1544	for the detection and/or identification of the <i>linB</i> resistance gene
1546, 1547	for the detection and/or identification of the <i>mefA</i> resistance gene
1549, 1550	for the detection and/or identification of the <i>mefE</i> resistance gene
1552, 1553, 1554, 1555	for the detection and/or identification of the <i>mefA</i> and <i>mefE</i> resistance genes
1556, 1557, 1558, 1559	for the detection and/or identification of the <i>mphA</i> and <i>mphK</i> resistance genes
1581, 1582, 1583, 1584	for the detection and/or identification of the <i>satG</i> resistance gene
1586, 1587, 1588, 1589, 2254	for the detection and/or identification of the <i>tetM</i> resistance gene
1591, 1592, 1593, 2297	for the detection and/or identification of the <i>vanD</i> resistance gene
1595, 1596, 1597, 1598	for the detection and/or identification of the <i>vanE</i> resistance gene
1609, 1610, 1611, 1612	for the detection and/or identification of the <i>vatB</i> resistance gene
1614, 1615, 1616, 1617	for the detection and/or identification of the <i>vatC</i> resistance gene
1619, 1620, 1621, 1622	for the detection and/or identification of the <i>vga</i> resistance gene
1624, 1625, 1626, 1627	for the detection and/or identification of the <i>vgaB</i> resistance gene
1629, 1630, 1631, 1632	for the detection and/or identification of the <i>vgb</i> and <i>vgh</i> resistance genes

1634, 1635, 1636, 1637	for the detection and/or identification of the <i>vgbB</i> resistance gene
1883, 1884, 1885, 1886, 1887, 1888, 1889, 1890, 1891, 1892, 1893, 1894, 1895, 1896, 1897, 1898	for the detection and/or identification of the <i>blaSHV</i> resistance gene
1906, 1907, 1908, 1909, 1910, 1911, 1912, 1913, 1914, 1915, 1916, 1917, 1918, 1919, 1920, 1921, 1922, 1923, 1924, 1925, 1926, 2006, 2007, 2008, 2009, 2141	for the detection and/or identification of the <i>blaTEM</i> resistance gene
1961, 1962, 1963, 1964	for the detection and/or identification of the <i>sulIII</i> resistance gene
1966, 1967, 1968, 1969	for the detection and/or identification of the <i>tetB</i> resistance gene
2065, 2066, 2067, 2068, 2069, 2070, 2071	for the detection and/or identification of the <i>therpoB</i> resistance gene
2098, 2099, 2100	for the detection and/or identification of the <i>inhA</i> resistance gene
2102, 2103, 2104	for the detection and/or identification of the <i>embB</i> resistance gene
2123, 2124, 2125	for the detection and/or identification of the <i>C. difficile cdtA</i> toxin gene
2126, 2127, 2128	for the detection and/or identification of the <i>C. difficile cdtB</i> toxin gene
2142, 2143	for the detection and/or identification of the <i>mupA</i> resistance gene
2145, 2146	for the detection and/or identification of the <i>catI</i> resistance gene
2148, 2149	for the detection and/or identification of the <i>catII</i> resistance gene

- | | |
|------------------------|--|
| 2151, 2152 | for the detection and/or identification of the <i>catIII</i> resistance gene |
| 2154, 2155 | for the detection and/or identification of the <i>catP</i> resistance gene |
| 2157, 2158, 2160, 2161 | for the detection and/or identification of the <i>cat</i> resistance gene |
| 2163, 2164 | for the detection and/or identification of the <i>ppflo</i> -like resistance gene. |

22. A composition of matter comprising a specific nucleic acid as set forth in claim 10 or 11, which is specific for a bacterial, fungal or parasitical species, genus, family, or group, or a nucleic acid as set forth in claim 8 or 9 which is universal for a bacterium, fungus or parasite, or both specific and universal nucleic acids, in conjunction with a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with an antimicrobial agent resistance gene and/or toxin gene.

23. A composition as set forth in claim 22, wherein the nucleic acid capable of hybridizing with an antimicrobial agent resistance gene and/or toxin gene is any one of:

- | | |
|--|--|
| 1078, 1079, 1085 | for the detection and/or identification of the <i>E. coli</i> Shiga-like toxin 2 (<i>stx₂</i>) gene |
| 1080, 1081, 1084, 2012 | for the detection and/or identification of the <i>E. coli</i> Shiga-like toxin 1 (<i>stx₁</i>) gene |
| 1082, 1083 | for the detection and/or identification of <i>E. coli</i> Shiga-like toxins 1 and 2 (<i>stx</i>) genes |
| 1086, 1087, 1088, 1089, 1090, 1091, 1092, 1170, 1239, 1240, 2292 | for the detection and/or identification of the <i>vanA</i> resistance gene |
| 1095, 1096, 1171, 1241, 2294, 2295 | for the detection and/or identification of the <i>vanB</i> resistance gene |
| 1111, 1112, 1113, 1114, 1115, 1116, 1118, 1119, 1120, 1121, 1123, 1124 | for the detection and/or identification of the <i>vanAB</i> resistance genes |

1103, 1104, 1109, 1110	for the detection and/or identification of the <i>vanC1</i> resistance gene
1105, 1106, 1107, 1108	for the detection and/or identification of the <i>vanC2</i> and <i>vanC3</i> resistance genes
1097, 1098, 1099, 1100, 1101, 1102	for the detection and/or identification of the <i>vanC1</i> , <i>vanC2</i> and <i>vanC3</i> resistance genes
1150, 1153, 1154, 1155	for the detection and/or identification of the <i>vanAXY</i> resistance genes
1094, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1192, 1193, 1194, 1195, 1196, 1197, 1214, 1216, 1217, 1218, 1219, 1220, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039	for the detection and/or identification of the <i>S. pneumoniae pbp1a</i> gene
1142, 1143, 1144, 1145	for the detection and/or identification of the <i>S. pneumoniae pbp2b</i> gene
1146, 1147, 1148, 1149	for the detection and/or identification of the <i>S. pneumoniae pbp2x</i> gene
1177, 1231	for the detection and/or identification of the <i>mecA</i> resistance gene
1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1333, 1334, 1335, 1340, 1341, 1336, 1937, 1940, 1942, 1943, 1945, 1946, 1947, 1948, 1949, 2040, 2041, 2042, 2043, 2250, 2251	for the detection and/or identification of the <i>gyrA</i> resistance gene

1301, 1302, 1303, 1304, 1305, 1306	for the detection and/or identification of the <i>gyrB</i> resistance gene
1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1336, 1337, 1338, 1339, 1342, 1343, 1934, 1935, 1938, 1939, 1941, 1944, 1950, 1951, 1952, 1953, 1955, 2044, 2045, 2046	for the detection and/or identification of the <i>parC</i> resistance gene
1322, 1323, 1324, 1325, 1326, 1327	for the detection and/or identification of the <i>parE</i> resistance gene
1344, 1345, 1346, 1347	for the detection and/or identification of the <i>aac(2')-Ia</i> resistance gene
1349, 1350	for the detection and/or identification of the <i>aac(3')-Ib</i> resistance gene
1352, 1353, 1354, 1355	for the detection and/or identification of the <i>aac(3')-IIb</i> resistance gene
1357, 1358, 1359, 1360	for the detection and/or identification of the <i>aac(3')-IVa</i> resistance gene
1362, 1363, 1364, 1365	for the detection and/or identification of the <i>aac(3')-VIa</i> resistance gene
1367, 1368, 1369, 1370	for the detection and/or identification of the <i>aac(6')-Ia</i> resistance gene
1372, 1373, 1374, 1375	for the detection and/or identification of the <i>aac(6')-Ic</i> resistance gene
1377, 1378, 1379, 1380	for the detection and/or identification of the <i>ant(3')-Ia</i> resistance gene
1382, 1383, 1384, 1385	for the detection and/or identification of the <i>ant(4')-Ia</i> resistance gene
1387, 1388, 1389, 1390	for the detection and/or identification of the <i>aph(3')-Ia</i> resistance gene
1392, 1393, 1394, 1395	for the detection and/or identification of the <i>aph(3')-IIa</i> resistance gene
1397, 1398, 1399, 1400	for the detection and/or identification of the <i>aph(3')-IIIa</i> resistance gene

1402, 1403, 1404, 1405, 2252	for the detection and/or identification of the <i>aph(3')-VIa</i> resistance gene
1407, 1408, 1409 1410	for the detection and/or identification of the <i>blaCARB</i> resistance gene
1412, 1413, 1414, 1415	for the detection and/or identification of the <i>blaCMY-2</i> resistance gene
1417, 1418	for the detection and/or identification of the <i>blaCTX-M-1</i> and <i>blaCTX-M-2</i> resistance genes
1419, 1420, 1421, 1422	for the detection and/or identification of the <i>blaCTX-M-1</i> resistance gene
1424, 1425, 1426, 1427	for the detection and/or identification of the <i>blaCTX-M-2</i> resistance gene
1429, 1430, 1431, 1432	for the detection and/or identification of the <i>blaIMP</i> resistance gene
1434, 1435	for the detection and/or identification of the <i>blaOXA2</i> resistance gene
1436, 1437	for the detection and/or identification of the <i>blaOXA10</i> resistance gene
1440, 1441	for the detection and/or identification of the <i>blaPER-1</i> resistance gene
1443, 1444	for the detection and/or identification of the <i>blaPER-2</i> resistance gene
1446, 1447, 1448, 1449	for the detection and/or identification of the <i>blaPER-1</i> and <i>blaPER-2</i> resistance genes
1450, 1451	for the detection and/or identification of the <i>dfrA</i> resistance gene
1453, 1454, 1455, 1456	for the detection and/or identification of the <i>dhfrIa</i> and <i>dhfrXV</i> resistance genes
1457, 1458, 1459, 1460, 2253	for the detection and/or identification of the <i>dhfrIa</i> resistance gene
1462, 1463, 1464, 1465	for the detection and/or identification of the <i>dhfrIb</i> and <i>dhfrV</i> resistance genes
1466, 1467, 1468, 1469	for the detection and/or identification of the <i>dhfrIb</i> resistance gene

1471, 1472, 1473, 1474	for the detection and/or identification of the <i>dhfrV</i> resistance gene
1476, 1477, 1478, 1479	for the detection and/or identification of the <i>dhfrVI</i> resistance gene
1481, 1482, 1483, 1484	for the detection and/or identification of the <i>dhfrVII</i> and <i>dhfrXVII</i> resistance genes
1485, 1486, 1487, 1488	for the detection and/or identification of the <i>dhfrVII</i> resistance gene
1490, 1491, 1492, 1493	for the detection and/or identification of the <i>dhfrVIII</i> resistance gene
1495, 1496, 1497, 1498	for the detection and/or identification of the <i>dhfrIX</i> resistance gene
1500, 1501, 1502, 1503	for the detection and/or identification of the <i>dhfrXII</i> resistance gene
1505, 1506	for the detection and/or identification of the <i>dhfrXIII</i> resistance gene
1508, 1509, 1510, 1511	for the detection and/or identification of the <i>dhfrXV</i> resistance gene
1513, 1514, 1515, 1516	for the detection and/or identification of the <i>dhfrXVII</i> resistance gene
1528, 1529	for the detection and/or identification of the <i>ereA</i> and <i>ereA2</i> resistance genes
1531, 1532, 1533, 1534	for the detection and/or identification of the <i>ereB</i> resistance gene
1536, 1537, 1538, 1539	for the detection and/or identification of the <i>linA</i> and <i>linA'</i> resistance genes
1541, 1542, 1543, 1544	for the detection and/or identification of the <i>linB</i> resistance gene
1546, 1547	for the detection and/or identification of the <i>mefA</i> resistance gene
1549, 1550	for the detection and/or identification of the <i>mefE</i> resistance gene
1552, 1553, 1554, 1555	for the detection and/or identification of the <i>mefA</i> and <i>mefE</i> resistance genes

1556, 1557, 1558, 1559	for the detection and/or identification of the <i>mphA</i> and <i>mphK</i> resistance genes
1581, 1582, 1583, 1584	for the detection and/or identification of the <i>satG</i> resistance gene
1586, 1587, 1588, 1589, 2254	for the detection and/or identification of the <i>tetM</i> resistance gene
1591, 1592, 1593, 2297	for the detection and/or identification of the <i>vanD</i> resistance gene
1595, 1596, 1597, 1598	for the detection and/or identification of the <i>vanE</i> resistance gene
1609, 1610, 1611, 1612	for the detection and/or identification of the <i>vatB</i> resistance gene
1614, 1615, 1616, 1617	for the detection and/or identification of the <i>vatC</i> resistance gene
1619, 1620, 1621, 1622	for the detection and/or identification of the <i>vga</i> resistance gene
1624, 1625, 1626, 1627	for the detection and/or identification of the <i>vgaB</i> resistance gene
1629, 1630, 1631, 1632	for the detection and/or identification of the <i>vgb</i> and <i>vgh</i> resistance genes
1634, 1635, 1636, 1637	for the detection and/or identification of the <i>vgbB</i> resistance gene
1883, 1884, 1885, 1886, 1887, 1888, 1889, 1890, 1891, 1892, 1893, 1894, 1895, 1896, 1897, 1898	for the detection and/or identification of the <i>blaSHV</i> resistance gene
1906, 1907, 1908, 1909, 1910, 1911, 1912, 1913, 1914, 1915, 1916, 1917, 1918, 1919, 1920, 1921, 1922, 1923, 1924, 1925, 1926, 2006, 2007, 2008, 2009, 2141	for the detection and/or identification of the <i>blaTEM</i> resistance gene
1961, 1962, 1963, 1964	for the detection and/or identification of the <i>sulII</i> resistance gene

1966, 1967, 1968, 1969	for the detection and/or identification of the <i>tetB</i> resistance gene
2065, 2066, 2067, 2068, 2069, 2070, 2071	for the detection and/or identification of the <i>rpoB</i> resistance gene
2098, 2099, 2100	for the detection and/or identification of the <i>inhA</i> resistance gene
2102, 2103, 2104	for the detection and/or identification of the <i>embB</i> resistance gene
2123, 2124, 2125	for the detection and/or identification of the <i>C. difficile cdtA</i> toxin gene
2126, 2127, 2128	for the detection and/or identification of the <i>C. difficile cdtB</i> toxin gene
2142, 2143	for the detection and/or identification of the <i>mupA</i> resistance gene
2145, 2146	for the detection and/or identification of the <i>catI</i> resistance gene
2148, 2149	for the detection and/or identification of the <i>catII</i> resistance gene
2151, 2152	for the detection and/or identification of the <i>catIII</i> resistance gene
2154, 2155	for the detection and/or identification of the <i>catP</i> resistance gene
2157, 2158, 2160, 2161	for the detection and/or identification of the <i>cat</i> resistance gene
2163, 2164	for the detection and/or identification of the <i>ppflo</i> -like resistance gene.

24. A nucleic acid having at least 12 nucleotides in length, capable of hybridizing with the nucleotide sequence of any one of the *tuf* sequences defined in SEQ ID NOs.: 1-73, 75-241, 399-457, 498-529, 612-618, 621-624, 675, 677, 717-736, 779-792, 840-855, 865, 868-888, 897-910, 932, 967-989, 992, 1266-1287, 1518-1526, 1561-1575, 1578-1580, 1662-1664, 1666-1667, 1669-1670, 1673-1683, 1685-1689, 1786-1843, 1874-1881, 1956-1960, 2183-2185, 2187-2188, 2193-2201, 2214-2249, 2255-2272.

25. A nucleic acid having at least 12 nucleotides in length, capable of hybridizing with the nucleotide sequence of any one of the *atpD* sequences defined in SEQ ID NOs.: 242-270, 272-398, 458-497, 530-538, 663, 667, 673, 674, 676, 678-680, 737-778, 827-832, 834-839, 856-862, 866-867, 889-896, 929-931, 941-966, 1245-1254, 1256-1265, 1527, 1576-1577, 1600-1604, 1638-1647, 1649-1660, 1671, 1684, 1844-1848, 1849-1865, 2189-2192.

26. A nucleic acid having at least 12 nucleotides in length, capable of hybridizing with the nucleotide sequence of any one of the *recA* sequences defined in SEQ ID NOs.: 990-991, 1003, 1288-1289, 1714, 1756-1763, 1866-1873 and 2202-2212.

27. A nucleic acid having at least 12 nucleotides in length, capable of selectively hybridizing with the nucleotide sequence of any one of the antimicrobial agent resistance gene sequences defined in SEQ ID NOs.: 1004-1075, 1255, 1607-1608, 1648, 1764-1785, 2013-2014, 2056-2064, 2273-2280.

28. The nucleic acid sequences of the nucleic acids of any one of claims 24 to 27.

29. The use of a nucleic acid having at least 12 nucleotides in length capable of hybridizing with the nucleic acids of any one of the antimicrobial agent resistance genes sequences defined in SEQ ID NOs.: 1004-1075, 1255, 1607-1608, 1648, 1764-1785, 2013-2014, 2056-2064, 2273-2280 for the detection and identification of microbial species.

30. The use of a nucleic acid having at least 12 nucleotides in length capable of hybridizing with the nucleic acids of any one of the toxin genes defined in SEQ ID NOs.: 1078-1085, 2012 and 2123 to 2128 for the detection and identification of microbial species.

31. A repertory of *hexA* nucleic acids used for the detection and/or identification of *Streptococcus pneumoniae*, which repertory is created by amplifying

the nucleic acids of any streptococcal species with any combination of primers SEQ ID NOs.: 1179, 1181 and 1182.

32. A repertory as defined in claim 31, which comprises the nucleic acids having a nucleotide sequence defined in SEQ ID NOs.: 1184 to 1191.

33. A repertory of nucleic acid sequences derived from the repertory of claim 31 or 32.

34. A nucleic acid used for the specific and ubiquitous detection and for identification of *Streptococcus pneumoniae*, which is derived from the repertory of claim 31.

35. A nucleic acid as set forth in claim 34 which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with said any *Streptococcus pneumoniae* and with any one of SEQ ID NOs.: 1184 to 1187.

36. A nucleic acid as set forth in claim 34, which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with the nucleic acids of *Streptococcus pneumoniae* and with any one of the nucleic acids having SEQ ID NOs.: 1179, 1180, 1181, 1182.

37. A peptide derived from the translation of the nucleic acids from the repertory obtained from the method of claim 1, 31 or 32, or of the nucleic acids defined in any one of claims 24 to 27, 35 and 36.

38. A peptide sequence derived from the peptide of claim 37.

39. A recombinant vector comprising a nucleic acid obtained from the method of claim 1, 31 or 32, or from the nucleic acids defined in any one of claims 24 to 27, 35 and 36.

40. A recombinant vector as defined in claim 39 which is an expression vector.

41. A recombinant host cell comprising the recombinant vector defined in claim 39 or 40.

42. The use of the nucleic acid sequences defined in claim 28 or 33, or obtained from the method of claim 2 and of the protein sequences deduced from said nucleic acid sequences, for the design of a therapeutic agent effective against said microorganisms.

43. The use as defined in claim 42, wherein said therapeutic agent is an antimicrobial agent, a vaccine or a genic therapeutic agent.

44. A method for identification of a microorganism in a test sample, comprising the steps of:

- a) obtaining a nucleic acid sequence for a *tuf*, *atpD*, and/or *recA* genes of said microorganisms, and
- b) comparing said nucleic acid sequence with the nucleic acid sequences of a bank as defined in claim 5, said repertory comprising a nucleic acid sequence obtained from the nucleic acids of said microorganism, whereby said microorganism is identified when said comparison results in a match between said sequences.

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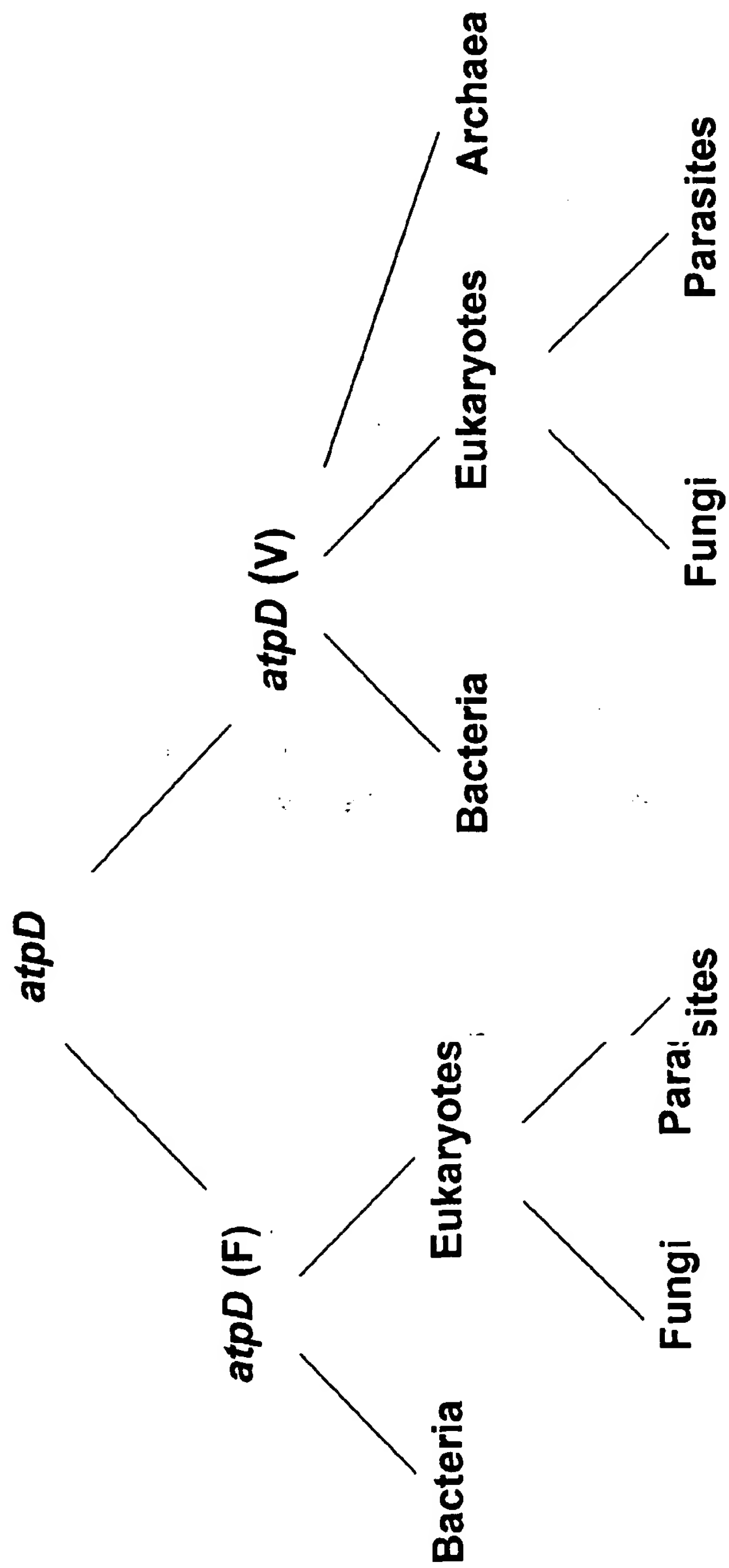
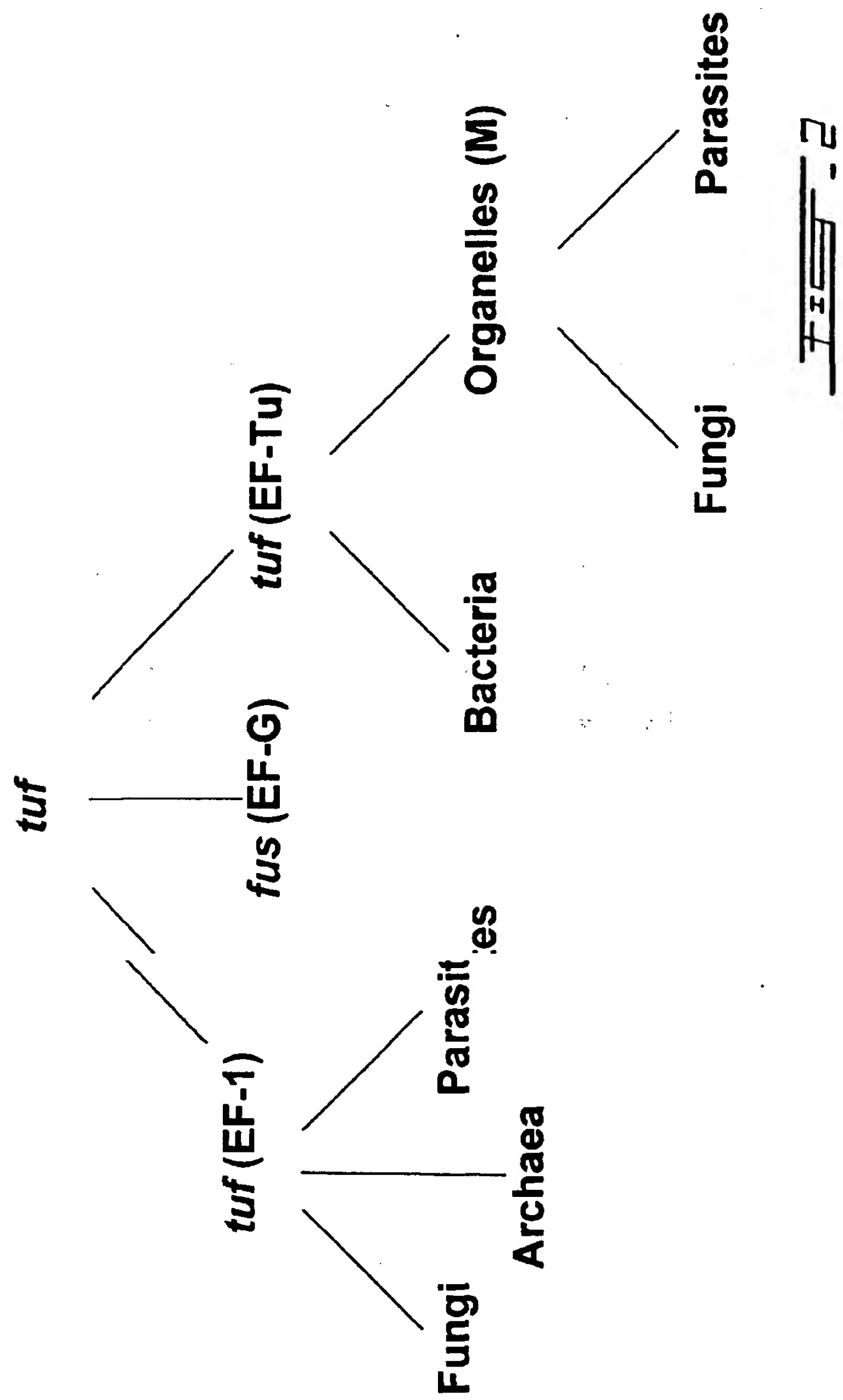
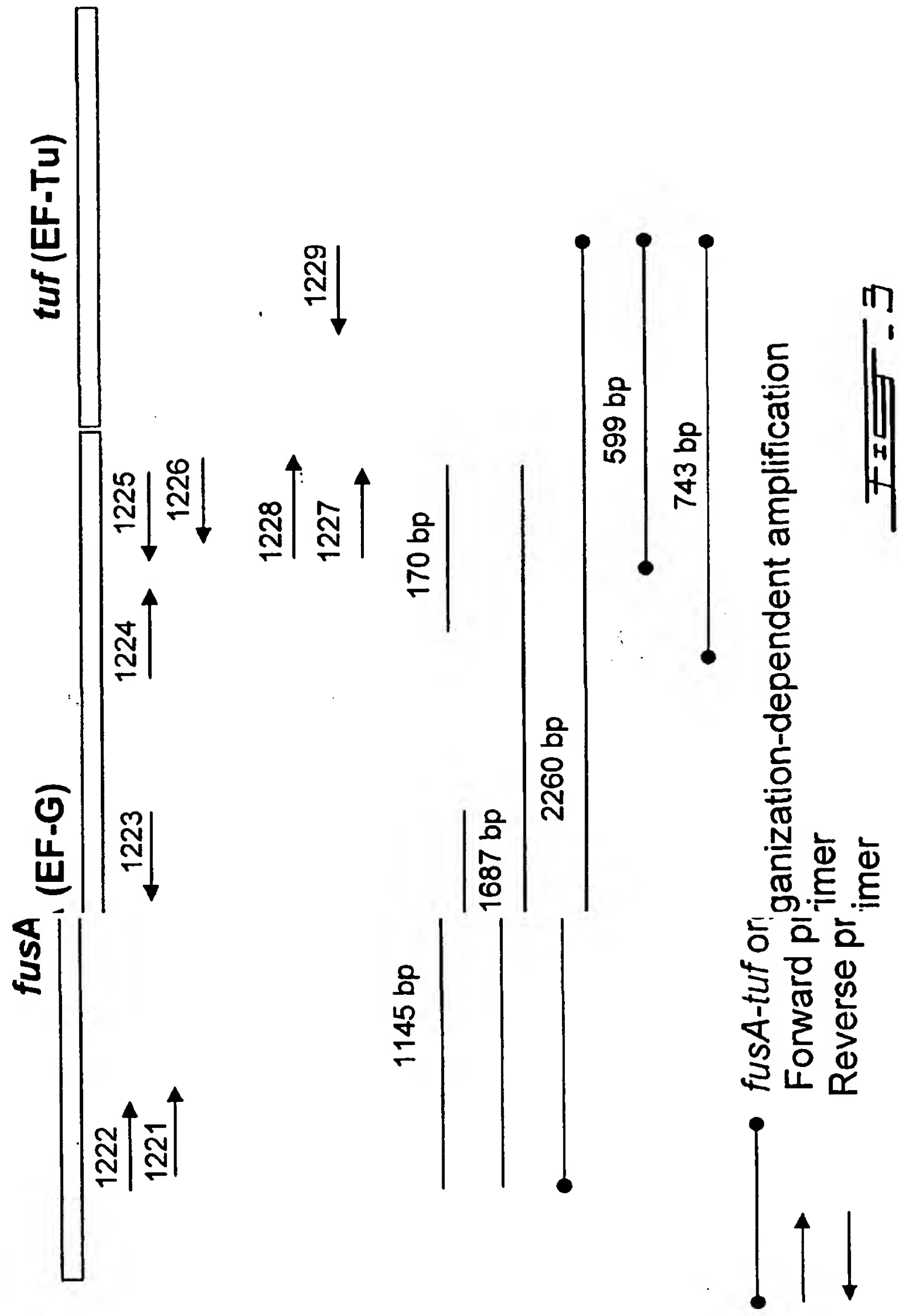


FIG. 1





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	210	220	230	240	250	260	270	280	290
<i>S. aureus</i>	TPERDSKPFMPVEDVI	SITGRGTMTGRVERGQIKVGEEVEIIGLH.DTSKTTVTGVE	EMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA						
<i>S. epidermidis</i>	TPERDSKPFMPVEDVI	SITGRGTMTGRVERGQIKVGEEVEIIGMH.ETSKTTVTGVE	EMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA						
<i>E. durans (A)</i>	TPERNDKPFMPVEDVI	SITGRGTMTGRVERGQIKVGEEVEIIGMH.ETSKTTVTGVE	EMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA						
<i>E. hirae (A)</i>	TPERNDKPFMPVEDVI	SITGRGTMTGRVERGQIKVGEEVEIIGMH.ETSKTTVTGVE	EMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA						
<i>E. mundtii (A)</i>	TPERNDKPFMPVEDVI	SITGRGTMTGRVERGQIKVGEEVEIIGMH.ETSKTTVTGVE	EMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA						
<i>E. faecium (A)</i>	TPERNDKPFMPVEDVI	SITGRGTMTGRVERGQIKVGEEVEIIGMH.ETSKTTVTGVE	EMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA						
<i>E. cecorum</i>	TPERNDKPFMPVEDVI	SITGRGTMTGRVERGQIKVGEEVEIIGMH.ETSKTTVTGVE	EMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA						
<i>E. columbae</i>	TPERNDKPFMPVEDVI	SITGRGTMTGRVERGQIKVGEEVEIIGMH.ETSKTTVTGVE	EMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA						
<i>E. cassel. flavus (A)</i>	TPERDTPKPFMPVEDVI	SITGRGTMTGRVERGQIKVGEEVEIIGMH.ETSKTTVTGVE	EMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA						
<i>E. gallinarum (A)</i>	TPERDTPKPFMPVEDVI	SITGRGTMTGRVERGQIKVGEEVEIIGMH.ETSKTTVTGVE	EMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA						
<i>E. faecalis</i>	TPERDTPKPFMPVEDVI	SITGRGTMTGRVERGQIKVGEEVEIIGMH.ETSKTTVTGVE	EMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA						
<i>E. avium (A)</i>	TPERDTPKPFMPVEDVI	SITGRGTMTGRVERGQIKVGEEVEIIGMH.ETSKTTVTGVE	EMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA						
<i>E. raffinosus (A)</i>	TPERDTPKPFMPVEDVI	SITGRGTMTGRVERGQIKVGEEVEIIGMH.ETSKTTVTGVE	EMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA						
<i>E. dispar (A)</i>	TPERDTPKPFMPVEDVI	SITGRGTMTGRVERGQIKVGEEVEIIGMH.ETSKTTVTGVE	EMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA						
<i>E. malodoratus (A)</i>	TPERDTPKPFMPVEDVI	SITGRGTMTGRVERGQIKVGEEVEIIGMH.ETSKTTVTGVE	EMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA						
<i>E. pseudoavium (A)</i>	TPERDTPKPFMPVEDVI	SITGRGTMTGRVERGQIKVGEEVEIIGMH.ETSKTTVTGVE	EMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA						
<i>E. sulfureus</i>	TPERDTEKPFMPVEDVI	SITGRGTMTGRVERGQIKVGEEVEIIGMH.ETSKTTVTGVE	EMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA						
<i>E. saccharolyticus</i>	TPERDTEKPFMPVEDVI	SITGRGTMTGRVERGQIKVGEEVEIIGMH.ETSKTTVTGVE	EMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA						
<i>E. solitarius</i>	TPERDHDKPFMPVEDVI	SITGRGTMTGRVERGQIKVGEEVEIIGMH.ETSKTTVTGVE	EMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA						

7-4b

<i>L. monocytogenes</i>	REHLLSRQVGVPYIVV	FMKKCMVDDDEELLEVEIRDLLTEYEFPGDDIPVIKGSALKALQ.....	GEADWEAKIDELMEAVDSYIP
<i>E. cassel. flavus (B)</i>	REHLLSRQVGVPYIVV	FINKTIDVDDDELIDLVEVEVRELLTEYDFPGDDIPVIKGSALKALE.....	GPDAAEAAILTMDTVDEYIP
<i>E. gallinarum (B)</i>	REHLLSRQVGVPYIVV	FINKTIDVDDDELIDLVEVEVRELLSEYNFPGDDIPVIKGSALKALE.....	GPDAAEAAILTMDTVDSYIP
<i>E. durans (B)</i>	REHLLSRQVGVPYIVV	FINKTIDVDDDELIDLVEVEVRELLSEYGFPGDDIPVIKGSALKALQ.....	GPDAAEAAILTMDTVDSYIP
<i>E. faecium (B)</i>	REHLLSRQVGVPYIVV	FINKTIDVDDDELIDLVEVEVRELLSEYGFPGDDIPVIKGSALKALQ.....	GPDAAEAAILTMDTVDSYIP
<i>E. hirae (B)</i>	REHLLSRQVGVPYIVV	FINKTIDVDDDELIDLVEVEVRELLSEYGFPGDDIPVIKGSALKALQ.....	GPDAAEAAILTMDTVDSYIP
<i>E. mundtii (B)</i>	REHLLSRQVGVPYIVV	FINKTIDVDDDELIDLVEVEVRELLSEYGFPGDDIPVIKGSALKALQ.....	GPDAAEAAILTMDTVDSYIP
<i>E. avium (B)</i>	REHLLSRQVGVPYIVV	FINKTIDVDDDELIDLVEVEVRELLSEYGFPGDDIPVIKGSALKALQ.....	GPDAAEAAILTMDTVDSYIP
<i>E. pseudoavium (B)</i>	REHLLSRQVGVPYIVV	FINKTIDVDDDELIDLVEVEVRELLSEYGFPGDDIPVIKGSALKALQ.....	GPDAAEAAILTMDTVDSYIP
<i>E. malodoratus (B)</i>	REHLLSRQVGVPYIVV	FINKTIDVDDDELIDLVEVEVRELLSEYGFPGDDIPVIKGSALKALQ.....	GPDAAEAAILTMDTVDSYIP
<i>E. raffinosus (B)</i>	REHLLSRQVGVPYIVV	FINKTIDVDDDELIDLVEVEVRELLSEYGFPGDDIPVIKGSALKALQ.....	GPDAAEAAILTMDTVDSYIP
<i>E. dispar (B)</i>	REHLLSRQVGVPYIVV	FINKTIDVDDDELIDLVEVEVRELLSEYGFPGDDIPVIKGSALKALQ.....	GPDAAEAAILTMDTVDSYIP
<i>S. pneumoniae</i>	REHLLSRQVGVPYIVV	FINKTIDVDDDELIDLVEVEVRELLSEYGFPGDDIPVIKGSALKALQ.....	GPDAAEAAILTMDTVDSYIP
<i>S. suis</i>	REHLLSRQVGVPYIVV	FINKTIDVDDDELIDLVEVEVRELLSEYGFPGDDIPVIKGSALKALQ.....	GPDAAEAAILTMDTVDSYIP
<i>S. pyogenes</i>	REHLLSRQVGVPYIVV	FINKTIDVDDDELIDLVEVEVRELLSEYGFPGDDIPVIKGSALKALQ.....	GPDAAEAAILTMDTVDSYIP
<i>S. mutans</i>	REHLLSRQVGVPYIVV	FINKTIDVDDDELIDLVEVEVRELLSEYGFPGDDIPVIKGSALKALQ.....	GPDAAEAAILTMDTVDSYIP
<i>L. lactis</i>	REHLLSRQVGVPYIVV	FINKTIDVDDDELIDLVEVEVRELLSEYGFPGDDIPVIKGSALKALQ.....	GPDAAEAAILTMDTVDSYIP
<i>T. aquaticus</i>	REHLLSRQVGVPYIVV	FINKTIDVDDDELIDLVEVEVRELLSEYGFPGDDIPVIKGSALKALQ.....	GPDAAEAAILTMDTVDSYIP
<i>E. coli</i>	REHLLSRQVGVPYIVV	FINKTIDVDDDELIDLVEVEVRELLSEYGFPGDDIPVIKGSALKALQ.....	GPDAAEAAILTMDTVDSYIP



<i>L. monocytogenes</i>	TPERTD	TKPFL	PVED	VFSIT	GRG	MA	GR	VER	CO	VK	VG	DE	VE	IG	IE	EE	SK	VV	TG	VE	MF	RK	LL	DY	AE	AG	DN	IG	AL	RG	VA	RE	DI	OR	GO	VLA
<i>E. cassel. flavus (B)</i>	TPERTD	TKPFL	LLPIED	VFSIT	GRG	MA	GR	VER	CO	VK	VG	DE	VE	IG	IE	EE	SK	VV	TG	VE	MF	RK	LL	DY	AE	AG	DN	IG	AL	RG	VA	RE	DI	OR	GO	VLA
<i>E. gallinarum (B)</i>	TPERTD	TKPFL	LLPVED	VFSIT	GRG	MA	GR	VER	CO	VK	VG	DE	VE	IG	IE	EE	SK	VV	TG	VE	MF	RK	TM	DF	GE	AG	DN	VG	VL	LR	GI	TR	DE	IE	RG	VLA
<i>E. durans (B)</i>	TPERTD	TKPFL	LLPVED	VFSIT	GRG	MA	GR	VER	CO	VK	VG	DE	VE	IG	IE	EE	SK	VV	TG	VE	MF	RK	TM	DF	GE	AG	DN	VG	VL	LR	GI	TR	DE	IE	RG	VLA
<i>E. faecium (B)</i>	TPERTD	TKPFL	LLPVED	VFSIT	GRG	MA	GR	VER	CO	VK	VG	DE	VE	IG	IE	EE	SK	VV	TG	VE	MF	RK	TM	DF	GE	AG	DN	VG	VL	LR	GI	TR	DE	IE	RG	VLA
<i>E. hira (B)</i>	TPERTD	TKPFL	LLPAED	VFSIT	GRG	MA	GR	VER	CO	VK	VG	DE	VE	IG	IE	EE	SK	VV	TG	VE	MF	RK	TL	DY	GE	AG	DN	VG	VL	LR	GI	OR	DE	IE	RG	VLA
<i>E. mundtii (B)</i>	TPERTD	TKPFL	LLPVED	VFSIT	GRG	MA	GR	VER	CO	VK	VG	DE	VE	IG	IE	EE	SK	VV	TG	VE	MF	RK	TL	DY	GE	AG	DN	VG	VL	LR	GI	OR	DE	IE	RG	VLA
<i>E. avium (B)</i>	TPERTD	TKPFL	LLPVED	VFSIT	GRG	MA	GR	VER	CO	VK	VG	DE	VE	IG	IE	EE	SK	VV	TG	VE	MF	RK	TL	DY	GE	AG	DN	VG	VL	LR	GI	OR	DE	IE	RG	VLA
<i>E. pseudoavium (B)</i>	TPERTD	TKPFL	LLPVED	VFSIT	GRG	MA	GR	VER	CO	VK	VG	DE	VE	IG	IE	EE	SK	VV	TG	VE	MF	RK	TL	DY	GE	AG	DN	VG	VL	LR	GI	TR	DE	IE	RG	VLA
<i>E. malodoratus (B)</i>	TPERTD	TKPFL	LLPVED	VFSIT	GRG	MA	GR	VER	CO	VK	VG	DE	VE	IG	IE	EE	SK	VV	TG	VE	MF	RK	TL	DY	GE	AG	DN	VG	VL	LR	GI	TR	DE	IE	RG	VLA
<i>E. raffinosus (B)</i>	TPERTD	TKPFL	LLPVED	VFSIT	GRG	MA	GR	VER	CO	VK	VG	DE	VE	IG	IE	EE	SK	VV	TG	VE	MF	RK	TL	DY	GE	AG	DN	VG	VL	LR	GI	TR	DE	IE	RG	VLA
<i>E. dispar (B)</i>	TPERTD	TKPFL	LLPVED	VFSIT	GRG	MA	GR	VER	CO	VK	VG	DE	VE	IG	IE	EE	SK	VV	TG	VE	MF	RK	TL	DY	GE	AG	DN	VG	VL	LR	GI	TR	DE	IE	RG	VLA
<i>S. pneumoniae</i>	TPERTD	TKPFL	LLPVED	VFSIT	GRG	MA	GR	VER	CO	VK	VG	DE	VE	IG	IE	EE	SK	VV	TG	VE	MF	RK	TL	DY	GE	AG	DN	VG	VL	LR	GI	TR	DE	IE	RG	VLA
<i>S. suis</i>	TPERTD	TKPFL	LLPVED	VFSIT	GRG	MA	GR	VER	CO	VK	VG	DE	VE	IG	IE	EE	SK	VV	TG	VE	MF	RK	TL	DY	GE	AG	DN	VG	VL	LR	GI	TR	DE	IE	RG	VLA
<i>S. pyogenes</i>	TPERTD	TKPFL	LLPVED	VFSIT	GRG	MA	GR	VER	CO	VK	VG	DE	VE	IG	IE	EE	SK	VV	TG	VE	MF	RK	TL	DY	GE	AG	DN	VG	VL	LR	GI	TR	DE	IE	RG	VLA
<i>S. mutans</i>	TPERTD	TKPFL	LLPVED	VFSIT	GRG	MA	GR	VER	CO	VK	VG	DE	VE	IG	IE	EE	SK	VV	TG	VE	MF	RK	TL	DY	GE	AG	DN	VG	VL	LR	GI	TR	DE	IE	RG	VLA
<i>L. lactis</i>	TPERTD	TKPFL	LLPVED	VFSIT	GRG	MA	GR	VER	CO	VK	VG	DE	VE	IG	IE	EE	SK	VV	TG	VE	MF	RK	TL	DY	GE	AG	DN	VG	VL	LR	GI	TR	DE	IE	RG	VLA
<i>T. aquaticus</i>	TPERTD	TKPFL	LLPVED	VFSIT	GRG	MA	GR	VER	CO	VK	VG	DE	VE	IG	IE	EE	SK	VV	TG	VE	MF	RK	TL	DY	GE	AG	DN	VG	VL	LR	GI	TR	DE	IE	RG	VLA
<i>E. coli</i>	TPERTD	TKPFL	LLPVED	VFSIT	GRG	MA	GR	VER	CO	VK	VG	DE	VE	IG	IE	EE	SK	VV	TG	VE	MF	RK	TL	DY	GE	AG	DN	VG	VL	LR	GI	TR	DE	IE	RG	VLA

⇒ a2 b2 ⇒ c2 ⇒ d2 ⇒ e2 ⇒ f2 g2 h2 i2 j2 ⇒ k2

7-4d

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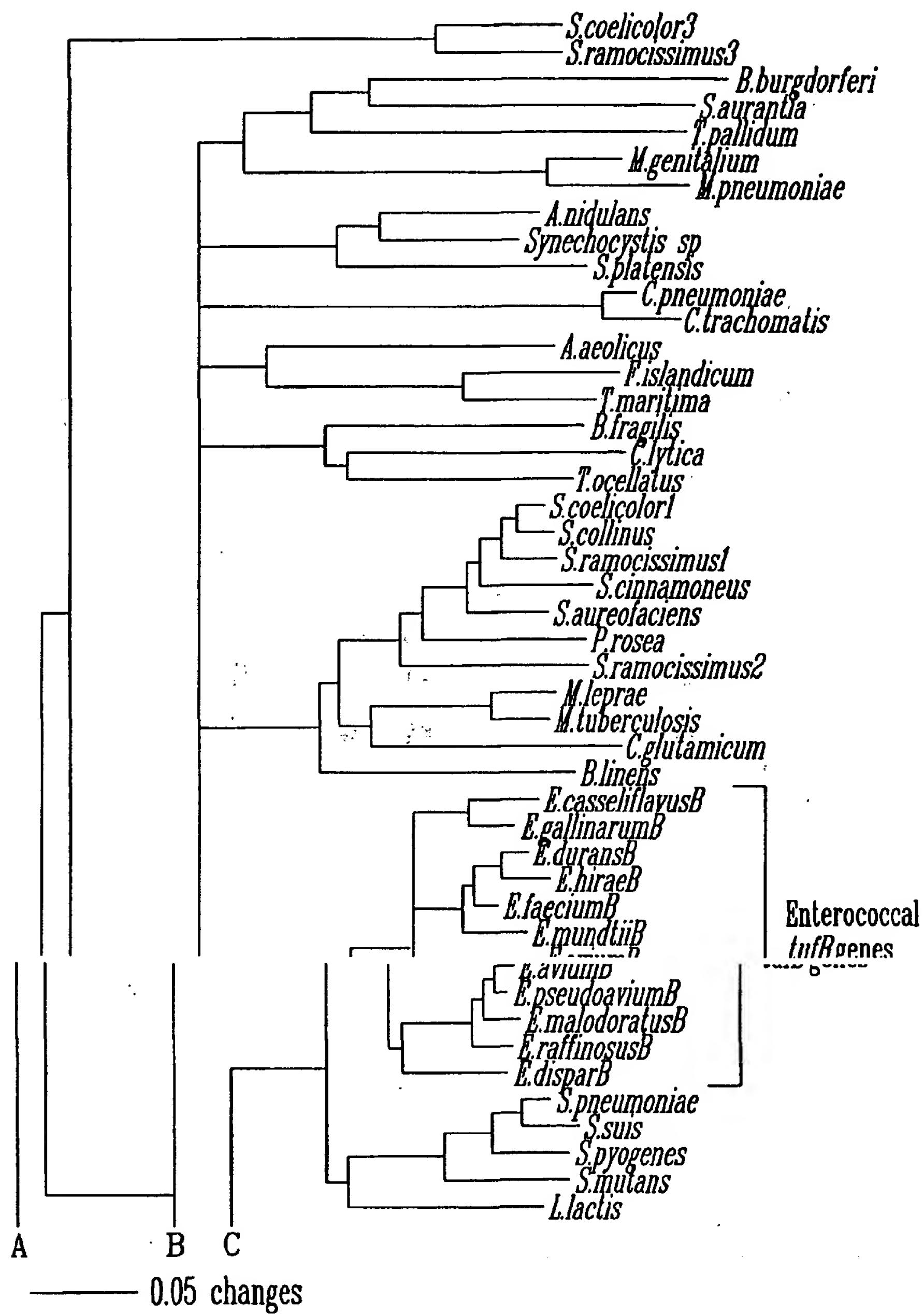


FIG. 5a

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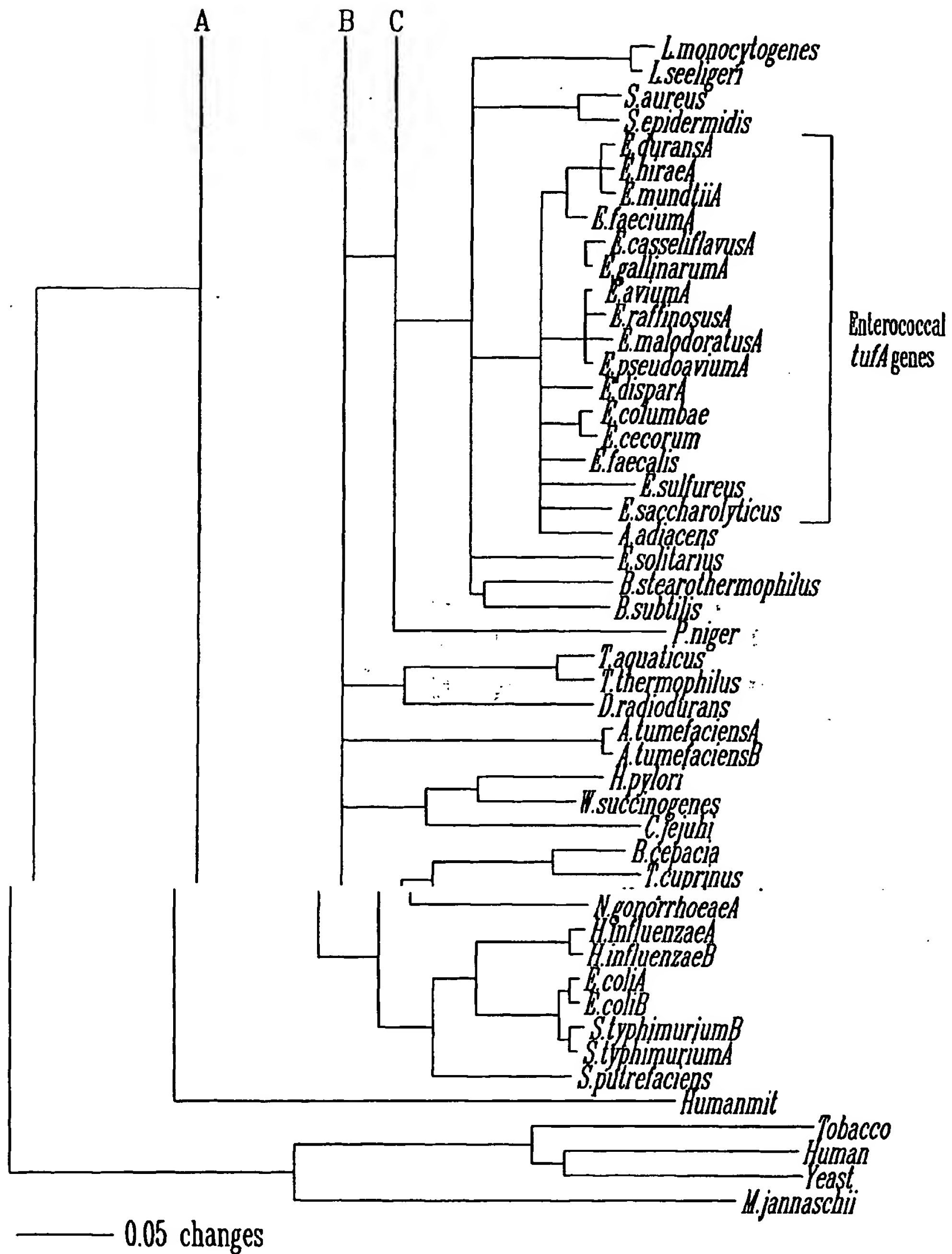


FIG - 56

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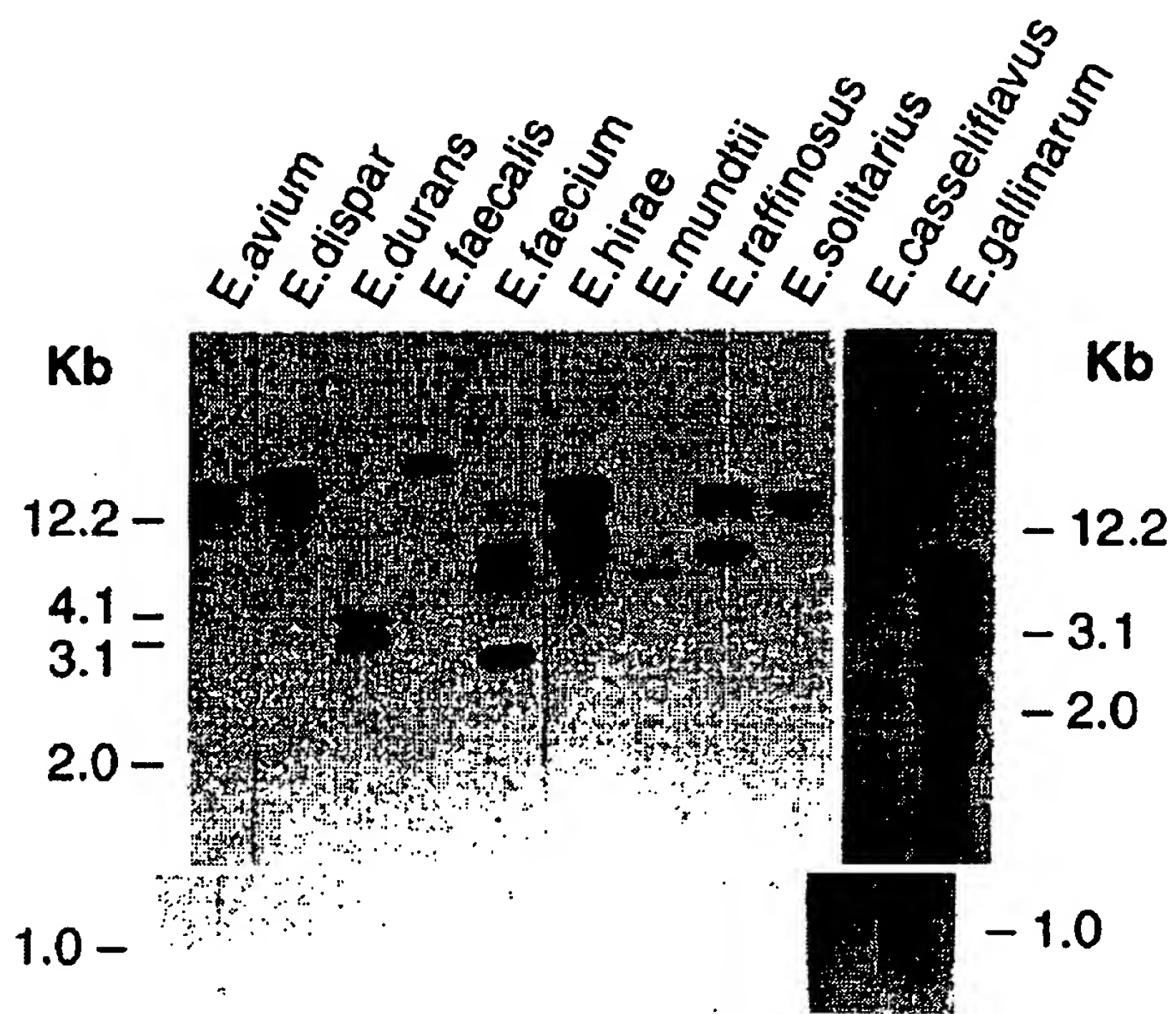
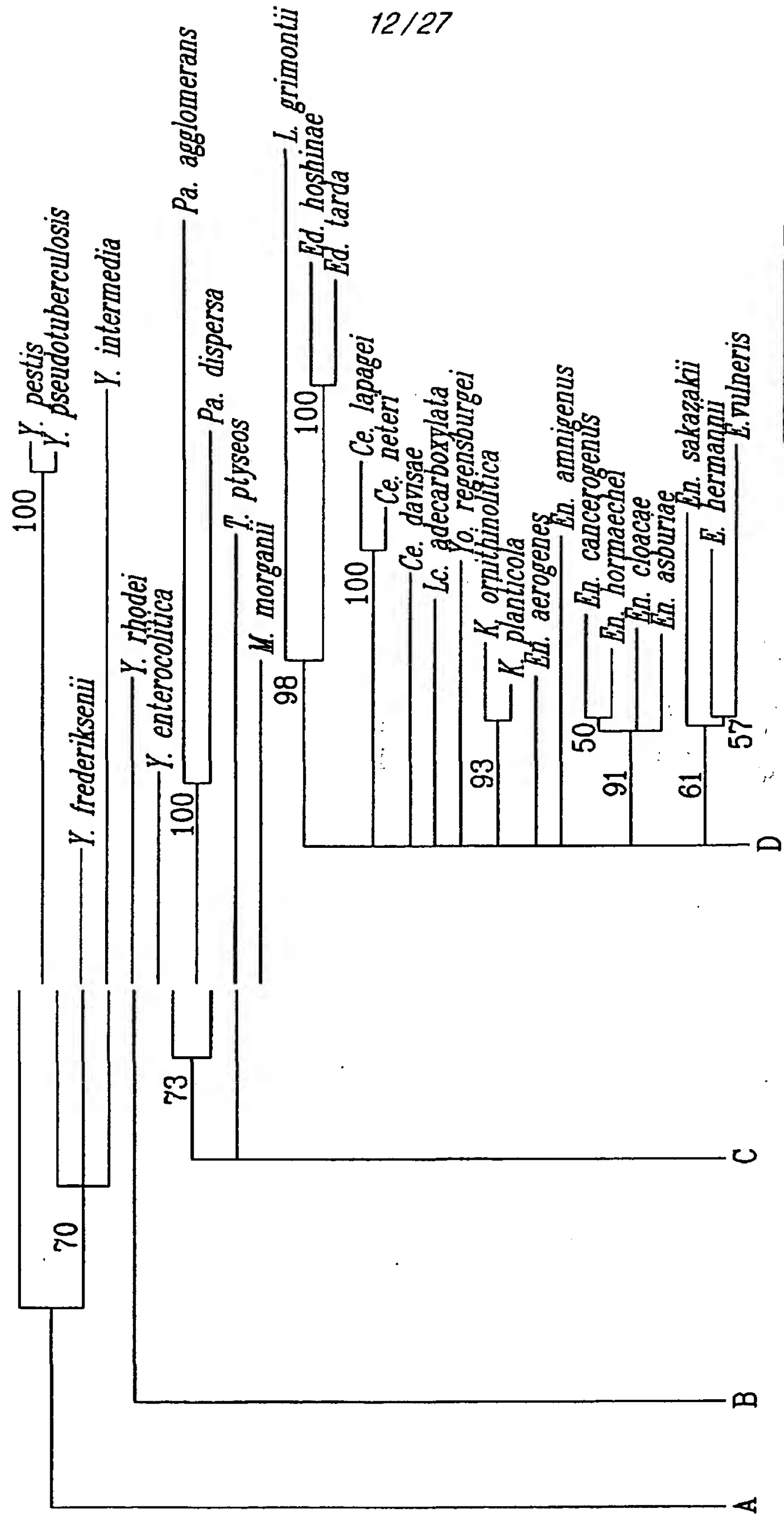


FIG. 6

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	301	311	321	331
E. coli	GAGATCGGT	AAGAAGACCG	TTGGG	CGATTCACCG
E. agglomerans	GACATCGGT	AAGAAGACCG	TTGGG	CGATTCACCG
P. agglomerans	GAGCTGAAA	AAGAAGATGG	CAGCGCAGTA	CTATTCACCG
P. dispersa	GACCTGAAA	AAGAAGACCG	CAGCGCTGTA	CTATTCATCG
T. ptyseos	GACCTGAAG	ACGAAGATGG	TAGCAATGTT	CTATTCACCG
E. coli	~I~G~E~	E~E~R~W~A~	I~H~R~
E. agglomerans	~I~G~E~	E~E~R~W~A~	I~H~R~
P. agglomerans	~L~K~E~	E~D~G~S~A~V~E~	~I~A~S~	I~H~R~
P. dispersa	~L~K~E~	E~D~G~S~A~V~E~	~V~S~	I~H~R~
T. ptyseos	~L~K~N~	E~D~G~S~N~V~E~	~V~N~S~	I~H~R~

FIG. 7



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FE - Ba

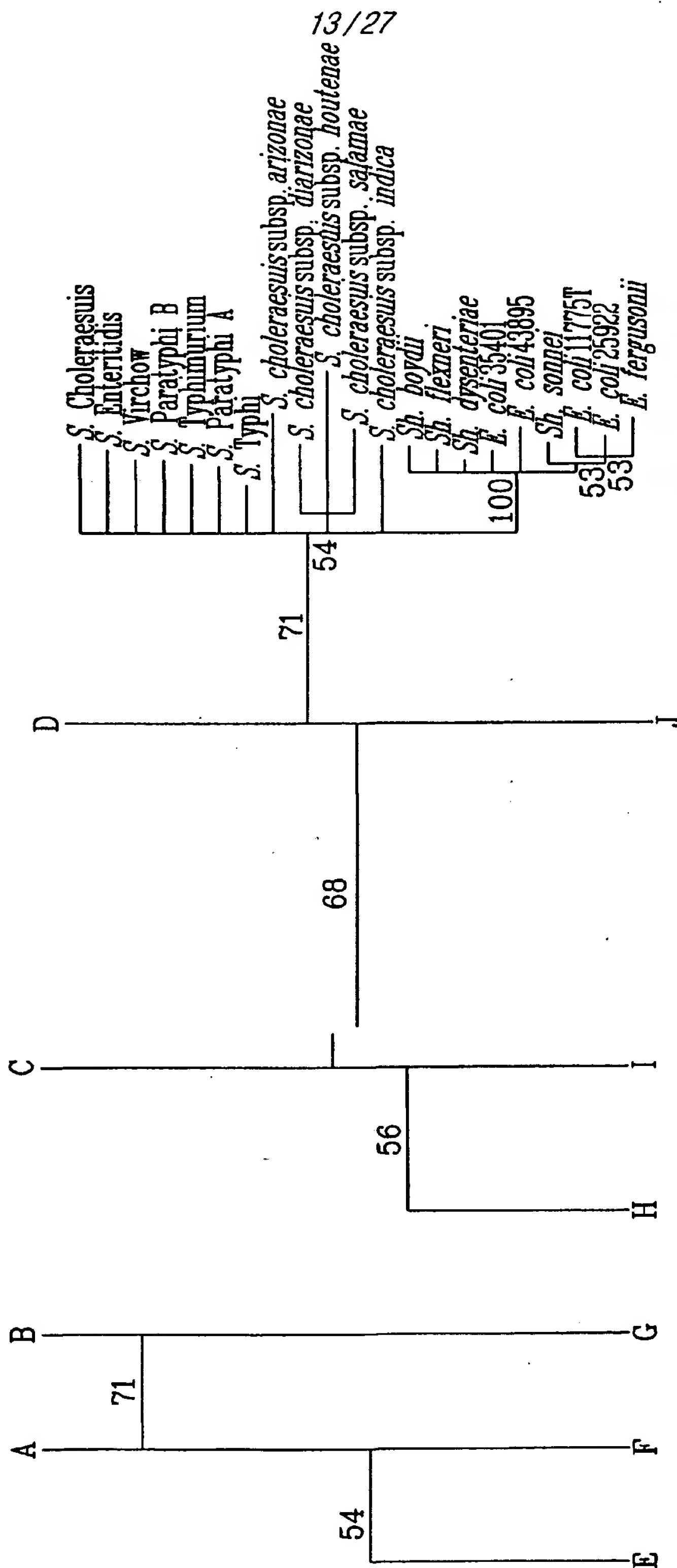
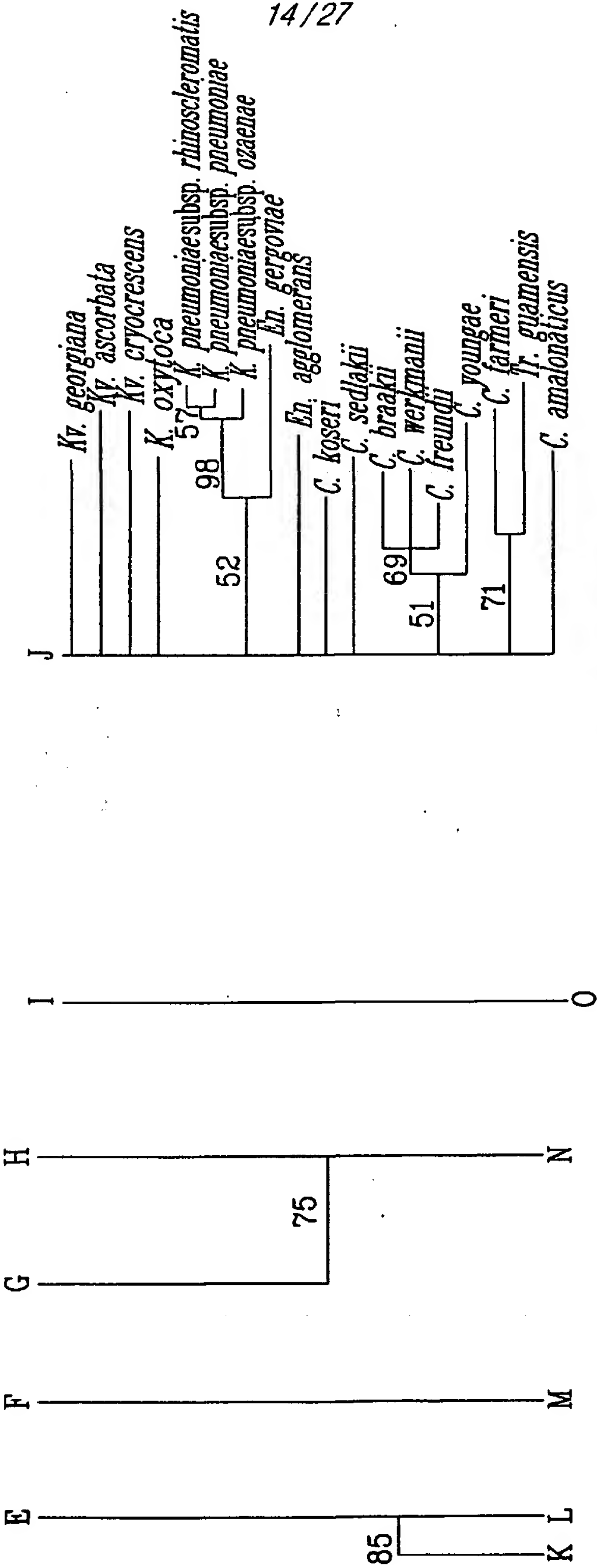


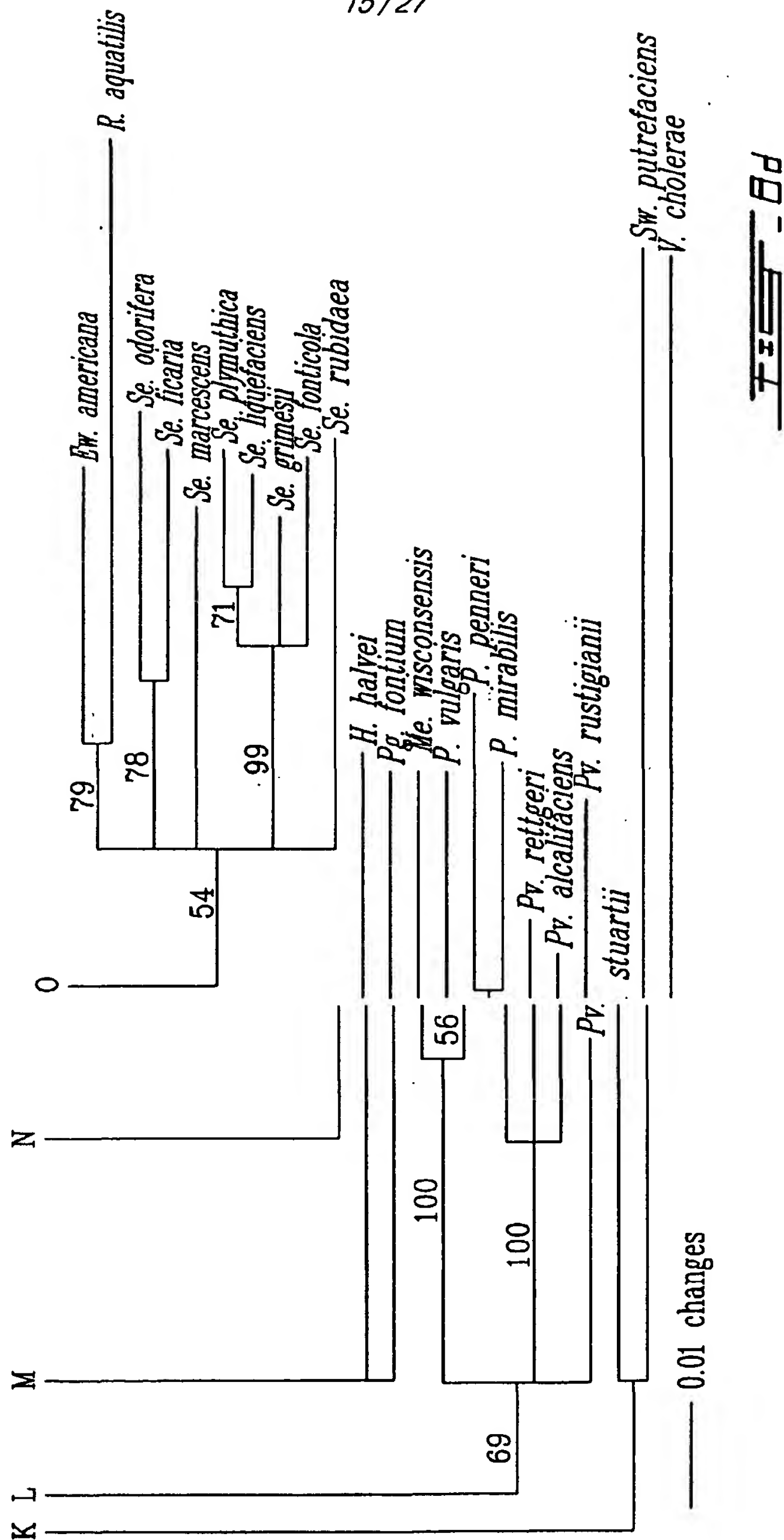
FIG. 1 - Bb

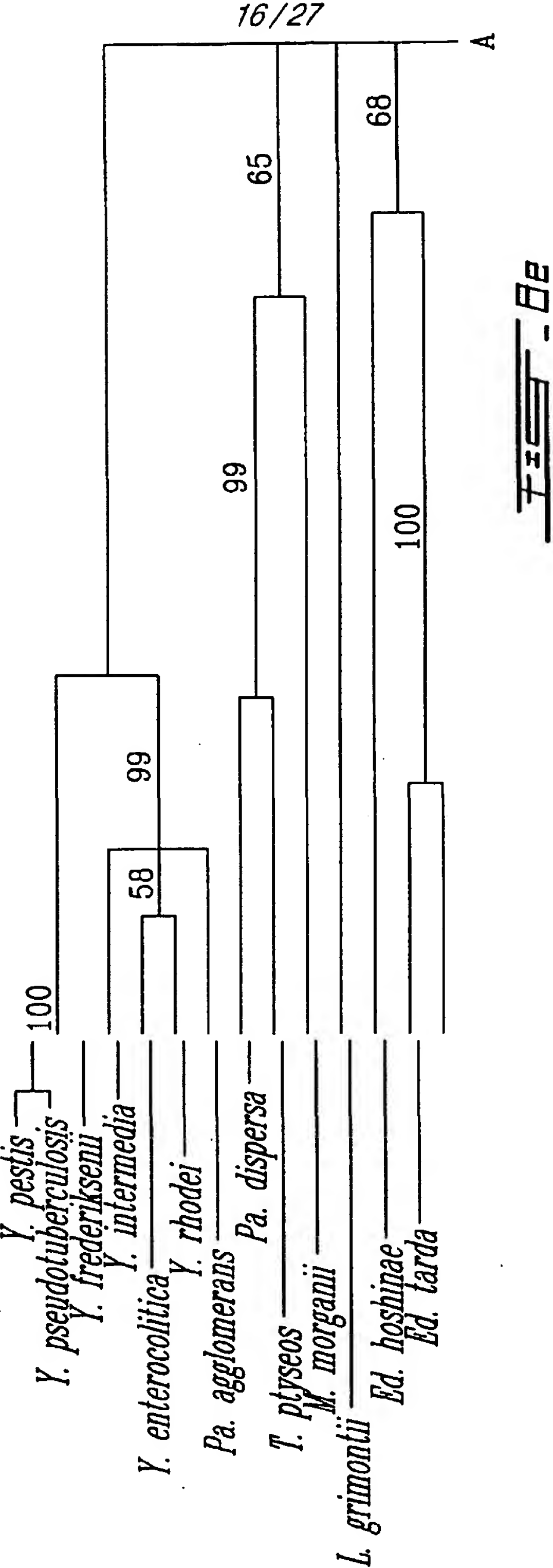
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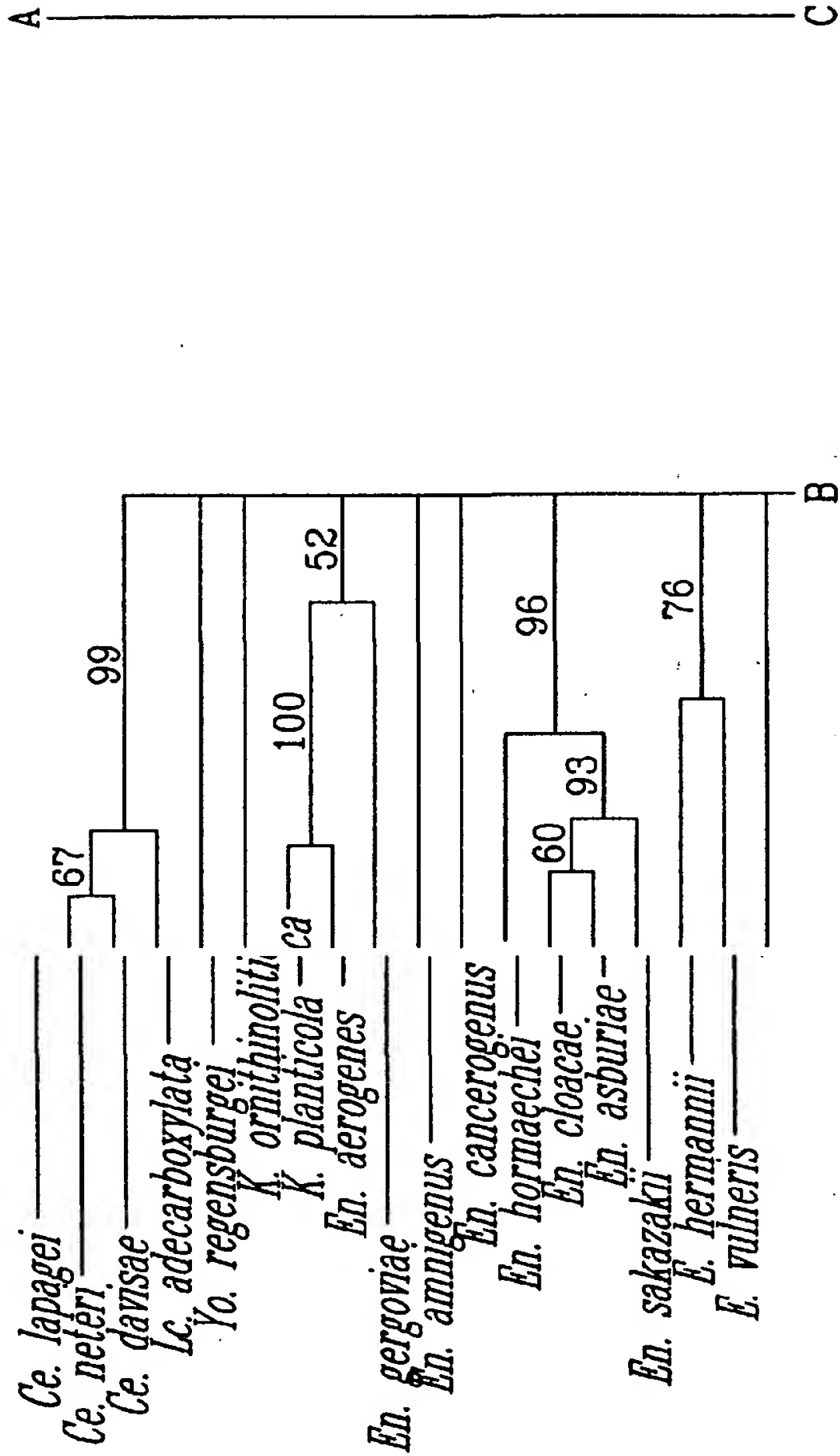


FEI - BC

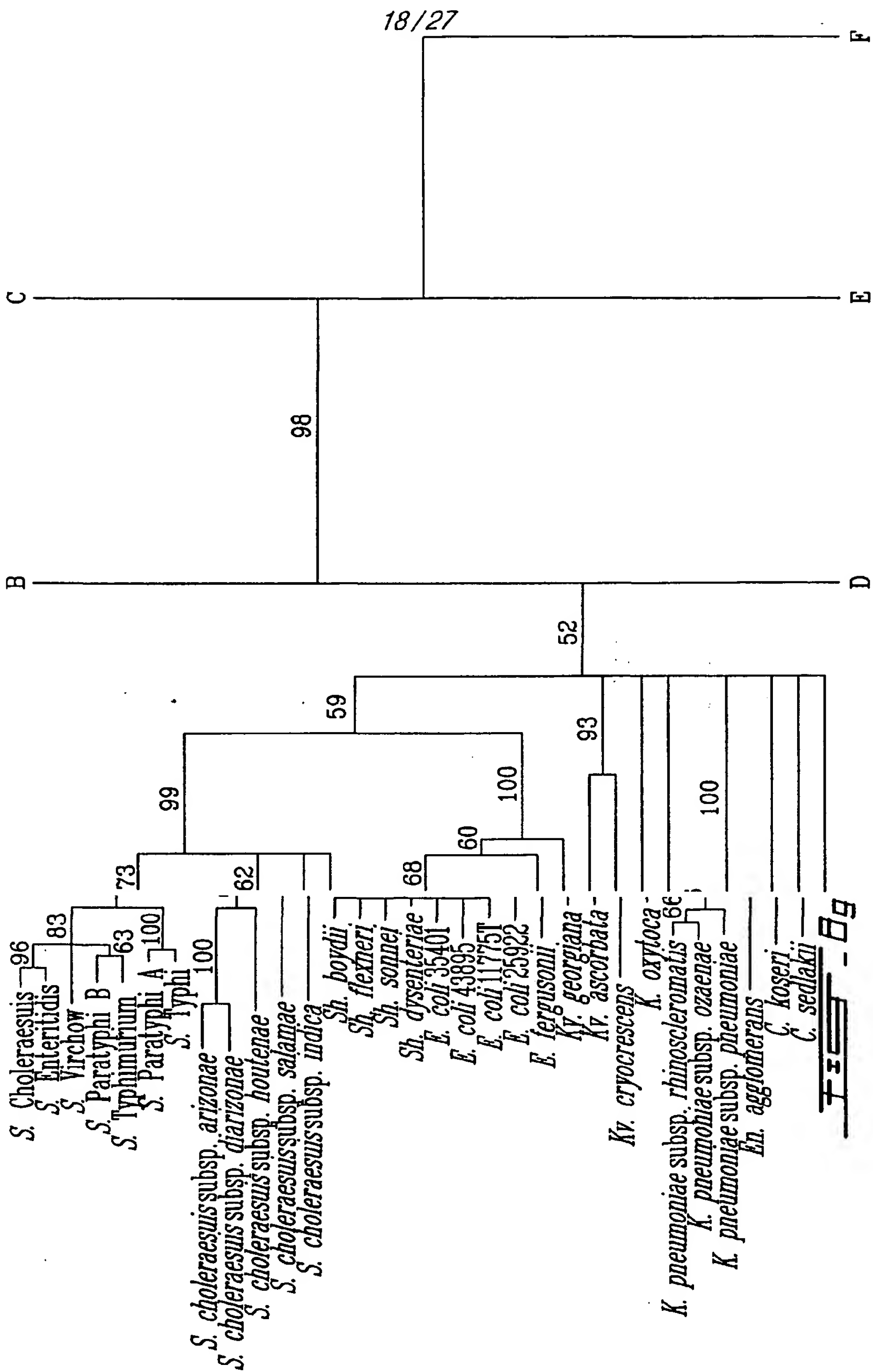
15/27

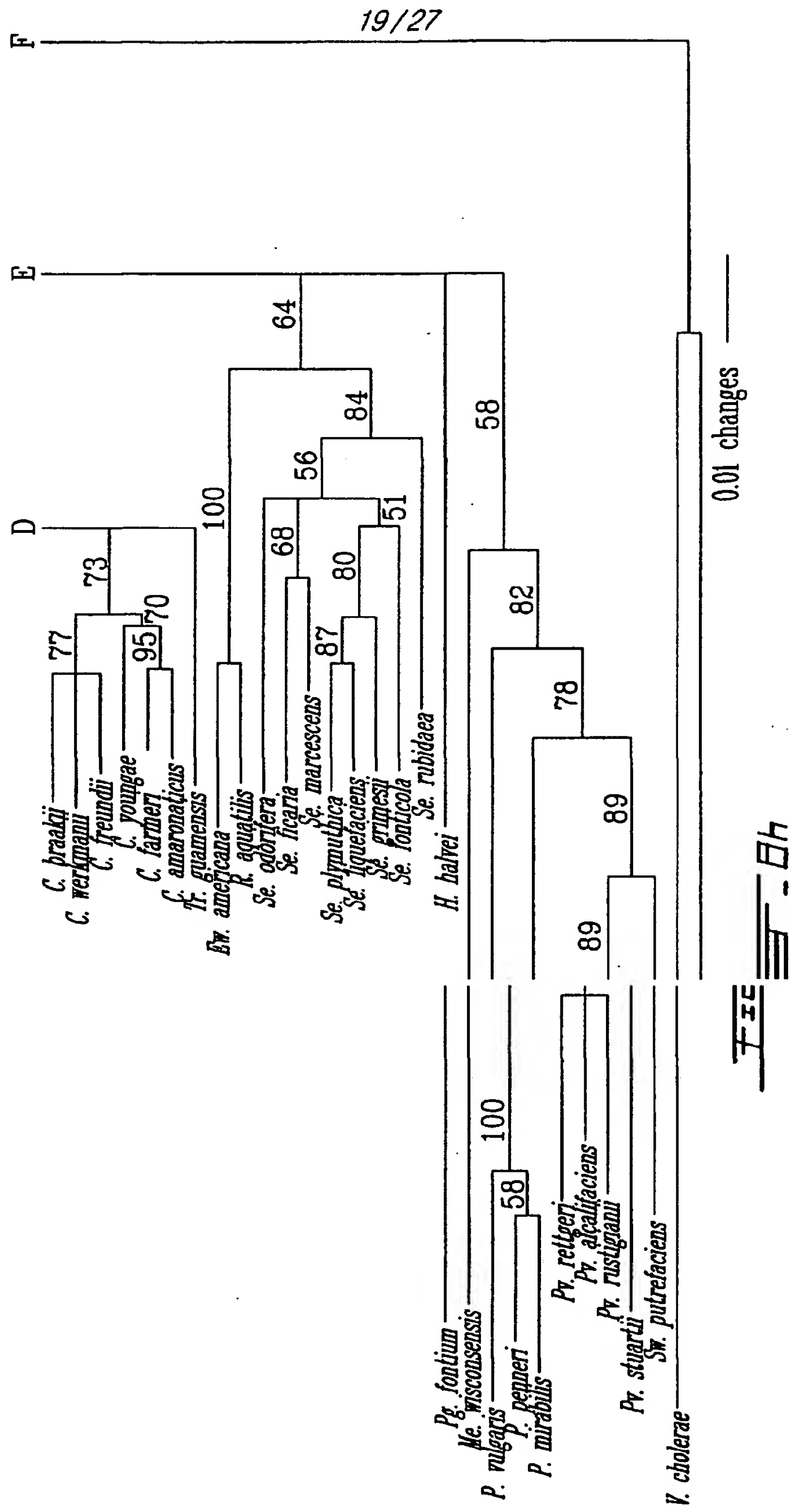




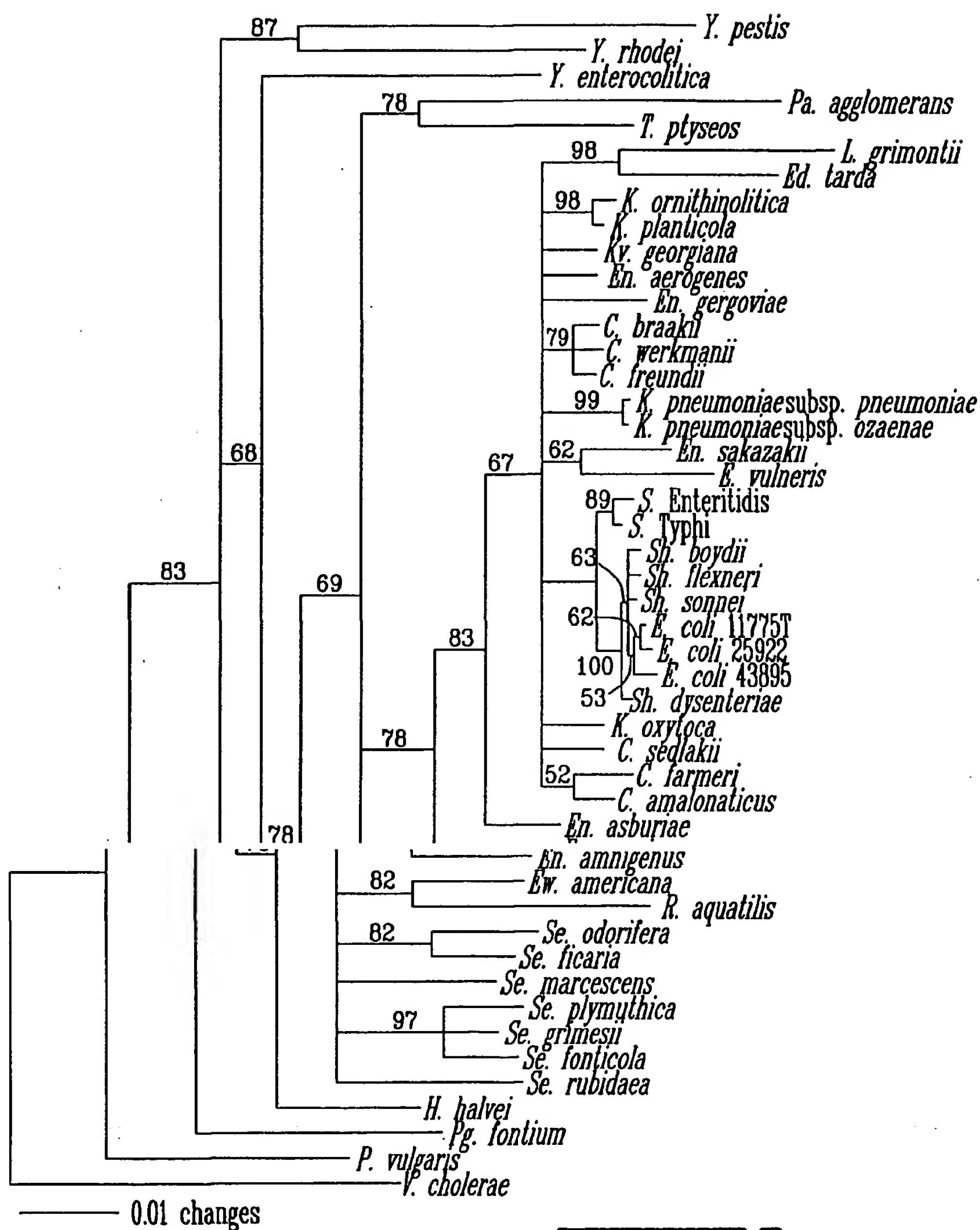


FEF-BF





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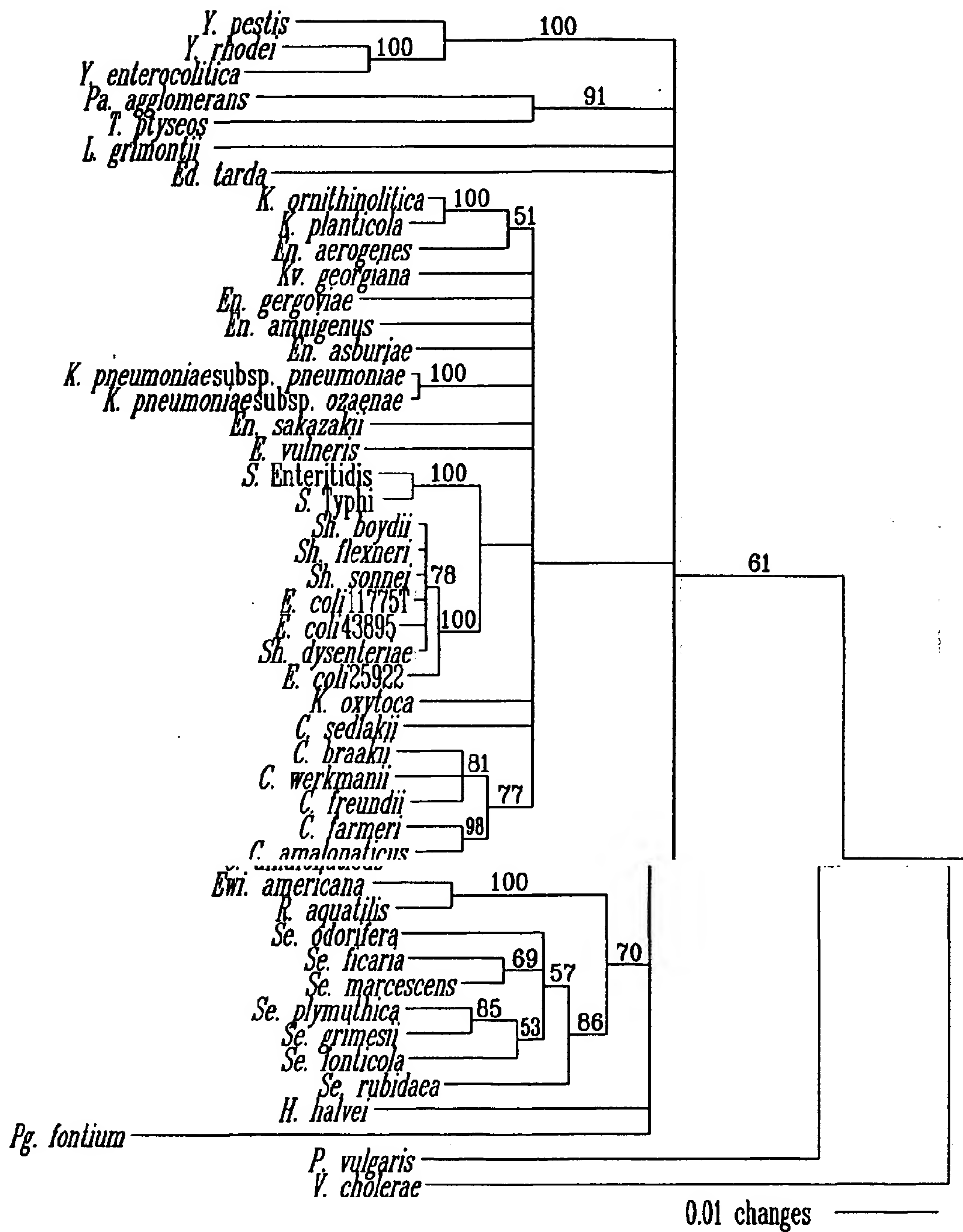
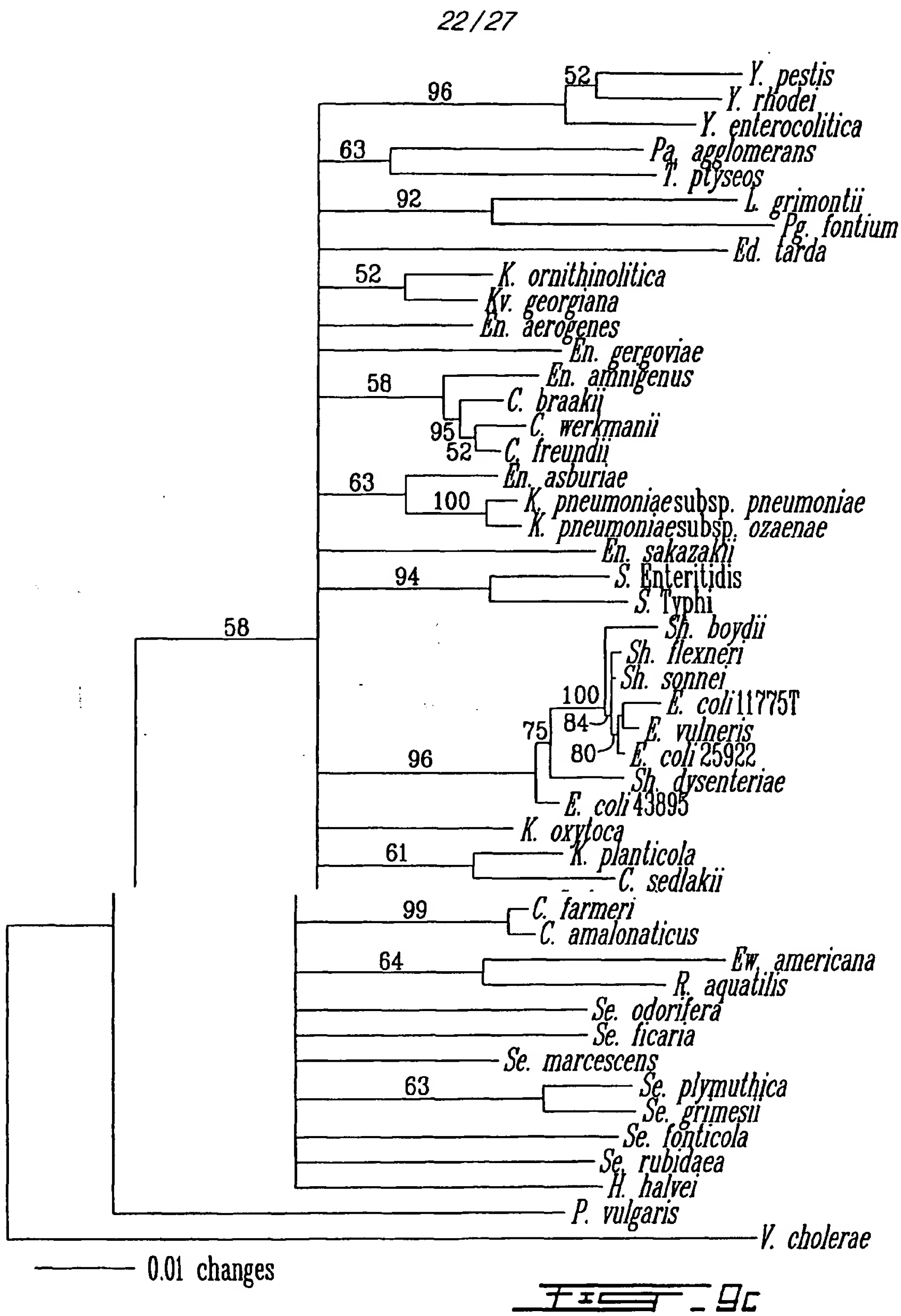
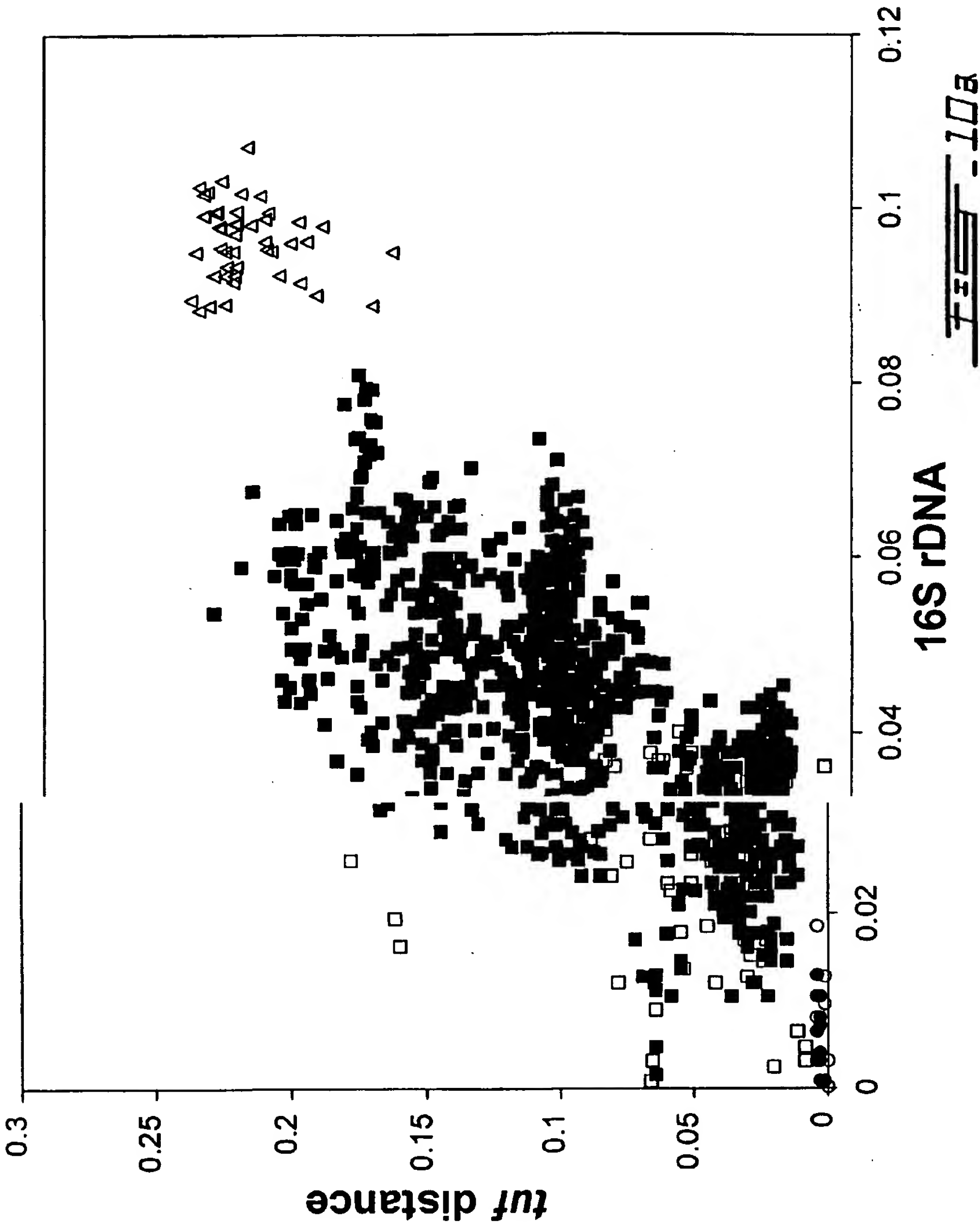
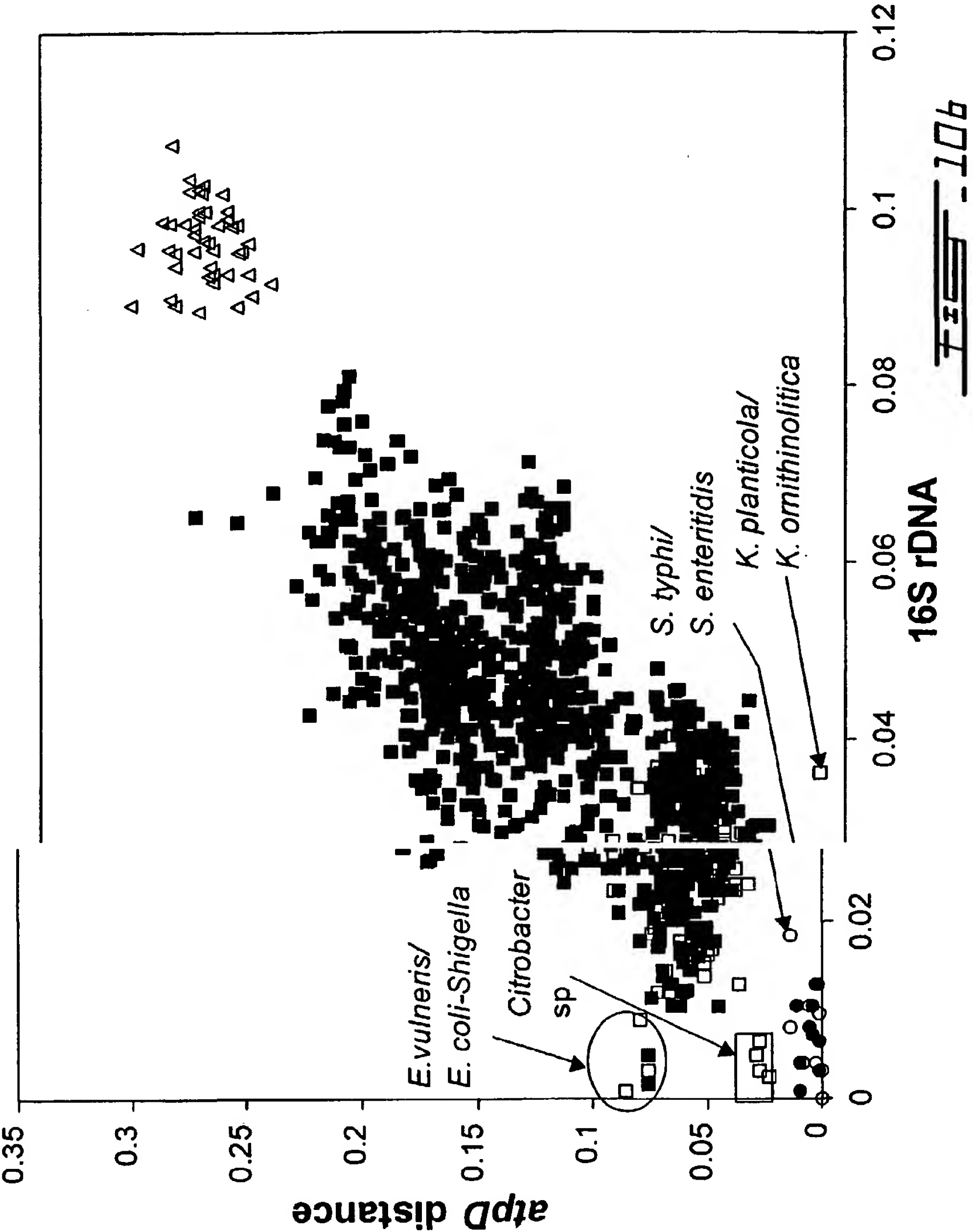


FIG. 9b

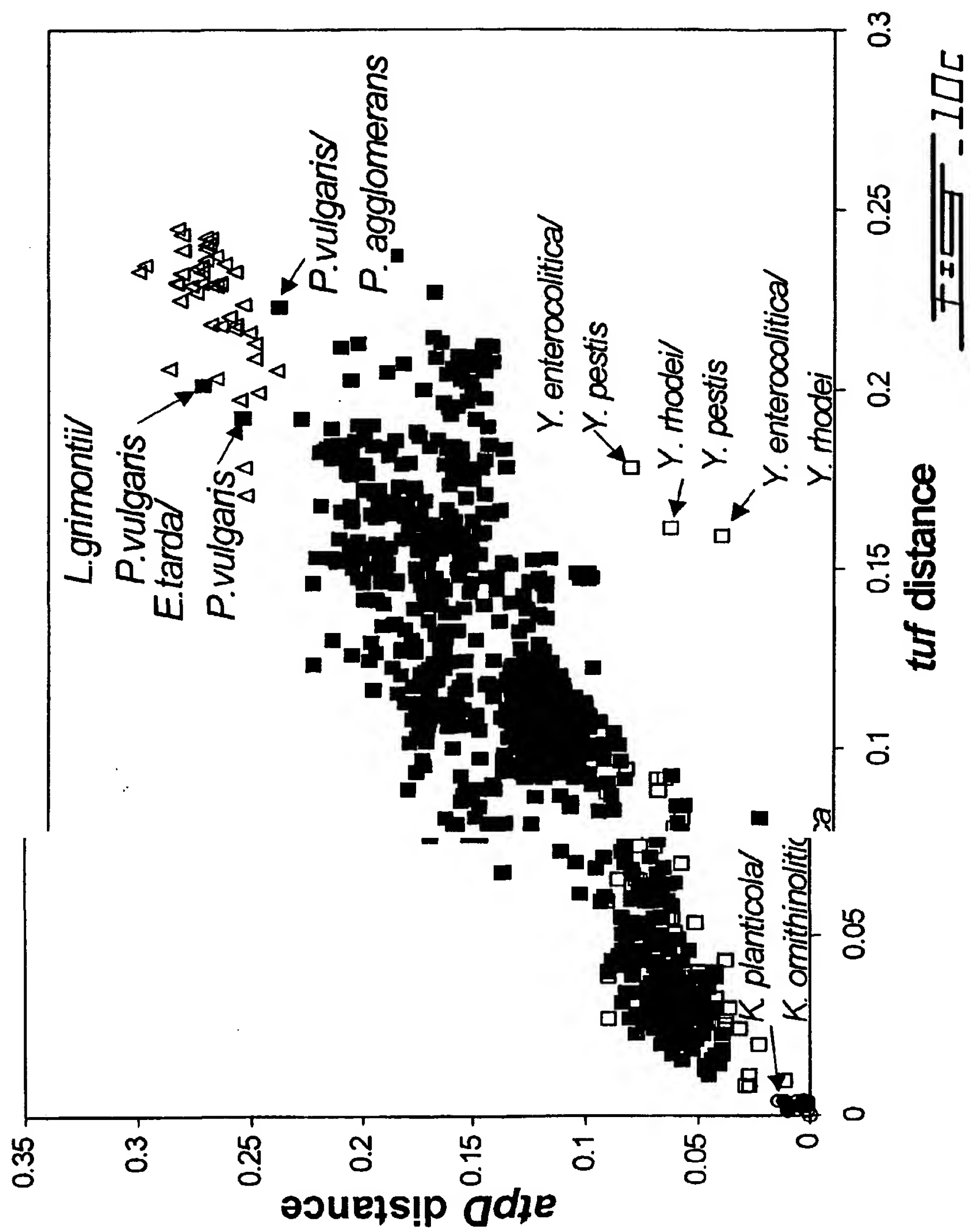


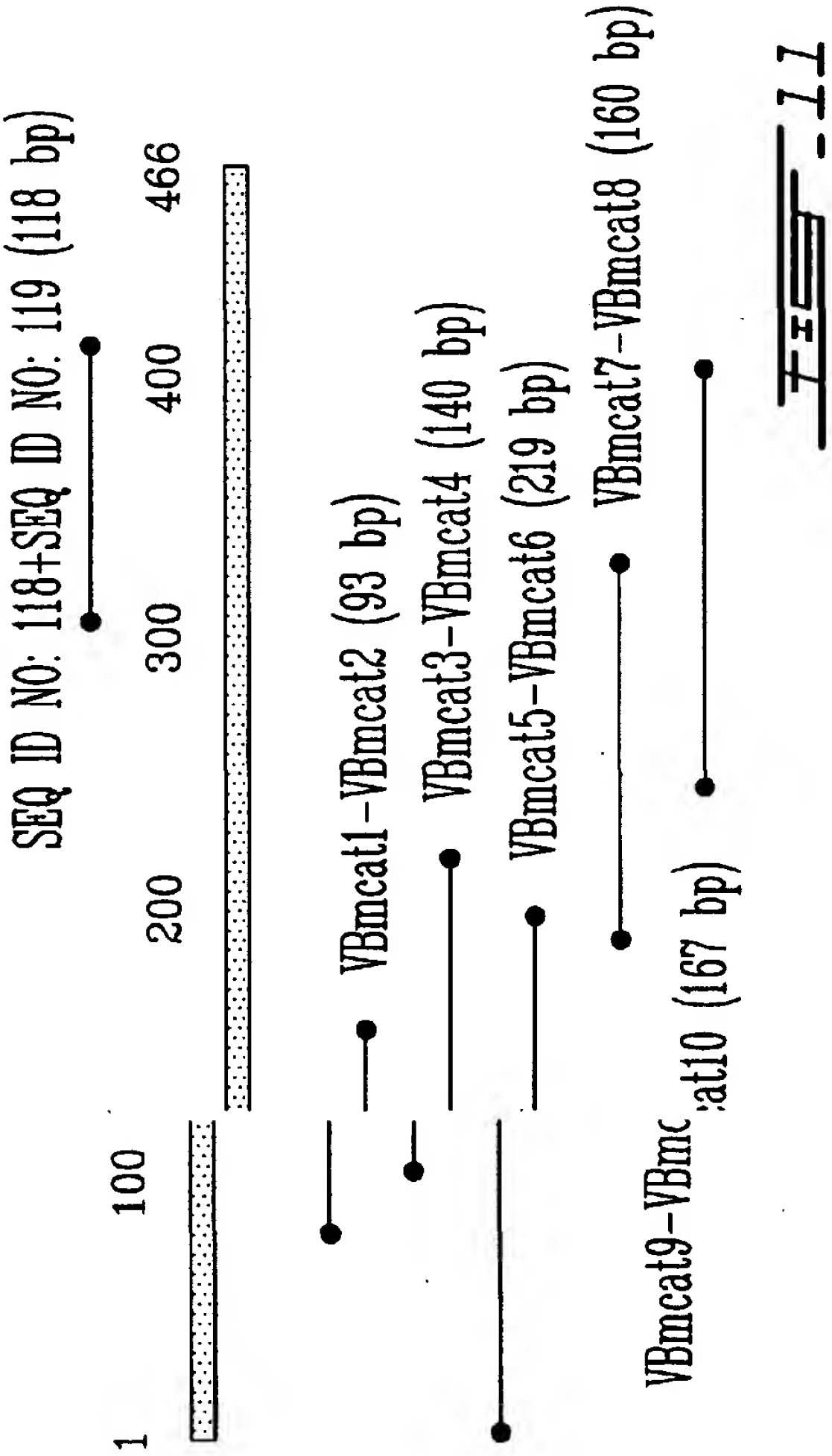
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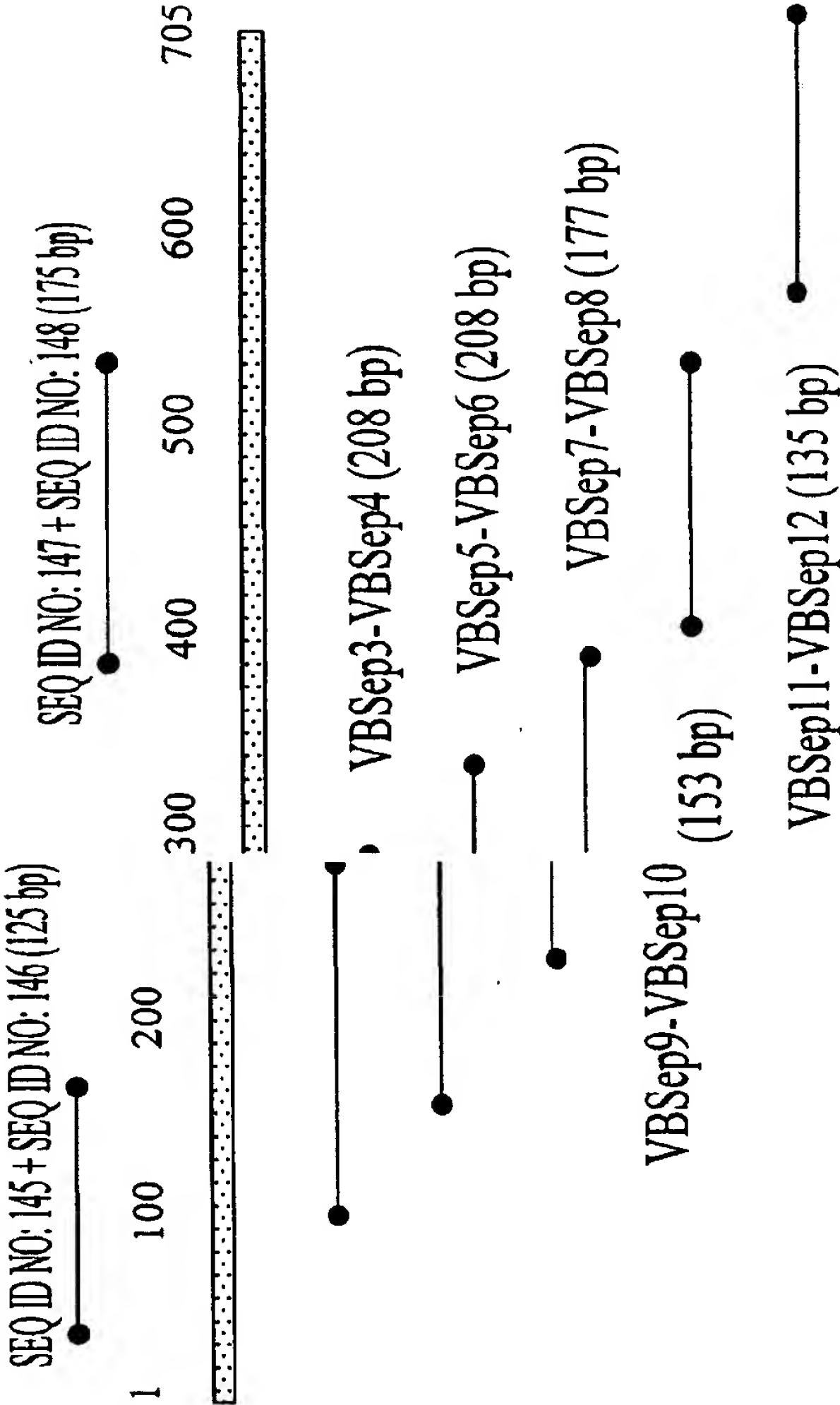


FIG. 12

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

5 BERGERON, Michel G. ¹, 1145 des Érables, Québec City,
 Québec, Canada, G2K 1T8
 BOISSINOT, Maurice ¹, 109 Jean-Bruchési, St-Augustin-
 de-Desmaures, Québec, Canada, G3A 2N2
 10 HULETSKY, Ann ¹, 1231 Av des Pins, Sillery, Québec,
 Canada, G1S 4J3
 MÉNARD, Christian ¹, 1174 Rue du Pont, St-Lambert-de-
 Lévis, Québec, Canada, G0S 2W0
 OUELLETTE, Marc ¹, 1035 de Ploërmel, Sillery, Québec,
 Canada, G1S 3S1
 15 PICARD, François J. ¹, 1245 de la Sapinière, Cap-
 Rouge, Québec, Canada, G1Y 1A1
 ROY, Paul H. ², 28 Charles Garnier, Loretteville,
 Québec, Canada, G2A 2X8

20 ¹:Canadian citizenship
²:American citizenship

(ii) TITLE OF THE INVENTION: HIGHLY CONSERVED GENES AN THEIR
 25 USE TO GENERATE SPECIES-SPECIFIC, GENUS-SPECIFIC AND
 UNIVERSAL NUCLEIC ACID PROBES AND AMPLIFICATION PRIMERS TO
 RAPIDLY DETECT AND IDENTIFY ALGAL, ARCHAEAL, BACTERIAL,
 FUNGAL AND PARASITICAL MICROORGANISMS FROM CLINICAL
 SPECIMENS FOR DIAGNOSIS

30 (iii) NUMBER OF SEQUENCES: 2297

(iv) CORRESPONDENCE ADDRESS:

35 (A) ADDRESSEE:
 (B) STREET:
 (C) CITY:
 (D) STATE:
 (E) COUNTRY:
 (F) ZIP:

40

(v) COMPUTER READABLE:

45 (A) MEDIUM TYPE:
 (B) COMPUTER:
 (C) OPERATING:
 (D) SOFTWARE:

(vi) CURRENT APPLICATION DATA:

50 (A) APPLICATION:
 (B) FILING DATE:
 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

55

(A) APPLICATION:
 (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME:
- (B) REGISTRATION NUMBER:

5

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE:
- (B) TELEFAX:

2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 750 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
 (B) STRAIN: ATCC 19606

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

CAAACCTCGTG AGCACATCCT TCTTTCTCGT CAGGTAGGTG TACCTTACAT 50
 CATCGTATTC TTAAACAAAT GCGACCTTGT TGATGACGAA GAATTACTTG 100
 20 AATTAGTAGA AATGGAAGTA CGTGAAGTTC TTTCTACTTA TGACTTCCCA 150
 GGTGATGACA CTCCAGTAAT CCGTGGTTCA GCTCTTGCAG CGCTTAACGG 200
 TGAAGCTGGT CCTTACGGTG AAGAATCAGT TCTTGCTCTT GTAGCAGCAC 250
 TTGACTCTTA CATCCCAGAG CCAGAGCGTG CAATCGACAA AGCATTCTTG 300
 ATGCCAATCG AAGACGTATT CTCAATTTCT GGTCGTGGTA CAGTAGTAAC 350
 25 AGGCCGTGTT GAAGCTGGTA TCATCAAAGT TGGTGAAGAA GTAGAGATCG 400
 TTGGTATTAA AGATACAGTT AAAACAAGT TAAGTGGCGT AGAAATGTTC 450
 CGTAAACTTC TTGACGAAGG CCGTGCAGGT GAGAACTGTG GTATCTTACT 500
 TCGTGGTACT AAGCGTGAAG AAGTACAACG TGGTCAAGTA CTTGCTAAAC 550
 CAGGTACAAT CAAGCCGCAC ACTAAATTCG ACGCAGAAGT ATACGTACTT 600
 30 TCTAAAGAAG AAGGTGGTCG TCACACTCCA TTCTTAAATG GTTACCGTCC 650
 ACAGTTCTAC TTCCGTACAA CTGACGTAAC TGGTGCRATC CAGTTGAAAG 700
 AAGGCGTTGA AATGGTAATG CCAGGTGACA ACGTTGAAAT GTCAGTAGAA 750

35

2) INFORMATION FOR SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
 (B) STRAIN: ATCC 35568

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

CGGTGCGATC CTCGTGGTCG CCGCGACCGA CGGCCCCATG GCCCAGACCC 50
 GCGAGCACGT CCTGCTCGCC CGTCAGGTCG GCGTTCCCAC CATCCTCATC 100
 GCCCTCAACA AGTCCGACAT GGTGACGAC GAGGAAATGA TGGAAGTGGT 150
 55 CGAGGAGGAG TGCCGCGACC TGCTGGAGTC CCAGGACTTC GATCGCGATG 200
 CCCCAGTCGT CCAGGTTTCC GCTCTGAAGG CCCTCGAGGG CGACGCGGAG 250
 TGGGTGCGCA AGATCGAGGA GCTCATGGAG GCTGTGGATT CCTACATCCC 300
 CACCCCGAG CGCGATATGG ACAAGCCCTT CCTCATGCCG ATCGAGGACG 350
 TCTTCACGAT CACAGGTCGT GGCACGGTCG TCACGGGGCG TGTTGAGCGT 400
 60 GGCAAGCTGC CGATCAACTC CGAGGTGCGA ATCCTCGGTA TCCGTGATCC 450

CCAGAAGACC ACGGTCACCG GCATCGAGAT GTTCCACAAG TCGATGGACG 500
 AGGCATGGGC CGGCGAGAAC TGTGGCCTGC TGCTGCGCGG TACCAAGCGC 550
 GATGAGGTTG AGCGCGGCCA GGTGTGGGCC ATTCCCGGCT CCATCACGCC 600
 TCACACCGAG TTCGAGGGCC AGGTTTACAT CCTCAAGAAG GAAGAGGGCG 650
 5 GCCGTCACAA CCCGTTCTTC TCGAACTACC GTCCGCAGTT CTACTTCCGT 700
 ACCACGGACG TGACCGGCGT CATCACCTC CCCGAGGGCA CCGACATGGT 750
 CATGCCTGGC GACACCACCG AGATCTCCGT TCAGCTGATC CAGCCCATCG 800
 CCATGGAGCC CGGCTGGGCT TCGCCA 826

10

2) INFORMATION FOR SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aerococcus viridans*
 (B) STRAIN: ATCC 11563

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

TGGTGCATC TTAGTAGTAT CTGCTGCTGA TGGTCCAATG CCACAAACTC 50
 GTGAGCACAT CCTTTTAGCT GGCCAAATCG GTGTTCTGCTG ATTCGTTAGTA 100
 30 TTCTTAAACA AAGTTGACCA AGTTGACGAT GAAGAATTAC TAGAATTAGT 150
 TGAAATGGAA GTTCGTGACT TATTATCTGA GTACAACTAC CCAGGTGACG 200
 ATCTACCTGT AATCGCTGGT TCTGCTTTAT TAGCATTACA AGGCGATGAA 250
 GCTCAAGAAG CTAAAATCAT GGAATTAATG GAAGCTGTAG ACTCTTACAT 300
 TCCAGAACCA GAACGTGACA ACGACAAACC ATTCATGATG CCAATTGAGG 350
 35 ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA 400
 CGTGGTGAAG TTCGTACAGG TGACGAAGTT GACATCGTTG GTATTGCTGA 450
 ACAAATCGGT AAATCAGTTG TAACTGGTGT TGAAATGTTC CGTAAAAACT 500
 TAGACTACGC TCAAGCTGGT GACAACATCG GTGCATTATT ACGTGGTGT 550
 CAACGTGAAG ACATCCAACG TGGTCAAGTA TTGGCTGCTC CTGTTCAAT 600
 40 CACTCCACAT ACTAAATTTA AAGCGCAAGT TTACGTTTAA TCTAAAGAAG 650
 AAGGTGGACG TCATACACCA TTCTTAACTA ACTACCGTCC ACAATTCTAC 700
 TTTCCGTACTA CTGACATTAAC TGGTGTATAT ACTTTTACCAG AAGACGTAGC 750
 TATGGTTATG CCTGGTGACA ACGTTGATAT GGACGTTGAA TTGATTCACC 800
 CAGTTGCGAT CGAAGATGGT ACTAAATTCT CTATC 835

45

2) INFORMATION FOR SEQ ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Achromobacter xylosoxidans* subsp.
denitrificans

(B) STRAIN: ATCC 15173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

5	CCTGGTGGTG	TCGGCCGCTG	ACGGCCCGAT	GCCGCAAACG	CGCGAACACA	50
	TCCTGCTGAG	CCGCCAGGTT	GGCGTGCCGT	ACATCATCGT	CTTCCTGAAC	100
	AAGGCCGACA	TGGTTGACGA	CGCCGAGCTG	CTTGAGCTGG	TGGAAATGGA	150
	AGTTCGCGAR	CTGCTGAGCA	AGTACGACTT	CCCGGGCGAC	GACACCCCGA	200
	TCGTGAAGGG	TTCGGCCAAG	CTGGCGCTGG	AAGGCGACAA	GGGCGAACTG	250
10	GGCGAACAGG	CCATCATGGC	GCTGGCCGCT	GCGCTGGACT	CGTACATCCC	300
	GACGCCTGAG	CGTGCCGTTG	ACGGCGCGTT	CCTGATGCCG	GTTGAAGACG	350
	TGTTCTCGAT	CTCGGGTCGC	GGCACC GTGG	TGACCGGCCG	TATCGAACGC	400
	GGCATCATCA	AGGTCGGCGA	GGAAATCGAA	ATCGTCGGTC	TGGTGCCGAC	450
	GGTGAAGACG	ACCTGCACGG	GCGTGGAAT	GTTCCGCAAG	CTGCTGGACC	500
15	AAGGTCAAGC	CGGCGACAAC	GTGGGCATCC	TRCTGCGCGG	CACCAAGCGT	550
	GAAGACGTCC	AGCGCGGCCA	GGTTCTGGCC	AAGCCGGGCT	CGATCACCCC	600
	GCACACGGAC	TTCACGTCCG	AGGTGTACAT	CCTGTCCAAG	GAAGAAGGCG	650
	GCCGTCACAC	TCCGTTCTTC	CAAGGCTATC	GTCCCCAGTT	CTACTTCCGC	700
	ACGACGGACG	TGACGGGCAC	GATCGAGCTG	CCGGCCGACA	AGGAAATGGT	750
20	CCTGCCGGGC	GACAACGTGG	CCATGACGGT	CAAGCTGCTG	GCTCCGATCG	800
	CCATGGAAGA	AGGCCTGCGT	TCGCCAC			827

25 2) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 823 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Anaerorhabdus furcosus</i>
	(B)	STRAIN: ATCC 25662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

40	TGGATCAATC	CTAGTAGTTG	CTGCAACTGA	TGGACCAATG	CCTCAAATC	50
	GTGAACATAT	CTTACTTGCT	CGTCAAGTAG	GTGTTCCAAG	AATGGTTGTA	100
	TTCTTGAACA	AATGCGACAT	GGTTGAAGAT	GAAGAATTAA	TCGACCTTGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTAAGTGC	TTACGGTTTC	GAAGGTGATG	200
45	ATACACCAGT	TATCCGTGGT	TCTGCATTAA	AATCTCTTGA	AGGAAATGCT	250
	GATTGGGAAG	CAAAAGTTGC	TGAATTAATG	GATGCAGTTG	ACTCTTGGAT	300
	TCCAACCTCA	ACTCATGAAA	CAGACAAACC	ATTCTTAATG	GCTGTTGAAG	350
	ATGTATTAC	AATTACAGGT	CGTGGTACAG	TTGCTACTGG	ACGTGTTGAA	400
	CGTGGACACT	TAAACCTTAA	CGAAGAAGTT	GAAATCGTTG	GTATTCATGA	450
50	TACTAAGAAA	TCAGTTGTTA	CTGGTATCGA	AATGTTCCGT	AAATTATTAG	500
	ACTATGCTGA	AGCAGGAGAC	AACATTGGTG	CATTATTACG	TGGTGTTTCT	550
	CGTGATGAAA	TCGAACGTGG	ACAATGTCTA	GCTAAACCTG	GATCAGTTAC	600
	TCCACATACA	GCTTTCAAAG	CTCAAGTATA	CGTATTAAC	AAAGAAGAAG	650
	GTGGACGTCA	TACACCATTG	GTAACCTAAT	ACCGTCCTCA	ATTCTATTTC	700
55	CGTACAAC	ACGTAAACAGG	AGTTGTTAAA	CTTCCTGAAG	GTACTGAAAT	750
	GGTTATGCCT	GGAGACAACA	TCGAAATGAT	CGTTGAATTA	ATCGCTCCAA	800
	TCGCTGTTGA	ACAAGGAACT	AAG			823

60

2) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: 4229

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

CGGCGGTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCTCAAACCTC 50
 GTGAGCACAT CCTTCTTTCT CGTCAAGTAG GTGTACCTTA CATCGTTGTA 100
 TTCTTAAACA AATGCGACAT GGTAGACGAC GAAGAATTAT TAGAATTAGT 150
 20 AGAAATGGAA GTTCGCGACC TATTATCTGA ATACGGATTC CCAGGCGACG 200
 ACATTCCTGT AATCAAAGGT TCTGCTCTTA AAGCTCTTCA AGGAGAAGCT 250
 GATTGGGAAG CAAAAATCAT TGAATTAATG GCTGAAGTTG ATGCTTACAT 300
 CCCAACTCCA GAACGTGAAA CTGACAAACC ATTCTTAATG CCTGTAGAGG 350
 ACGTATTCTC TATCACAGGT CGTGGTACAG TTGCTACTGG TCGTGTTGAG 400
 25 CGCGGTATCG TTAAAGTTGG TGACGTAGTA GAAATCATCG GTCTTGCTGA 450
 AGAAAATGCT TCTACAACTG TAACTGGTGT AGAGATGTTC CGTAAACTTC 500
 TTGACCAAGC TCAAGCTGGA GACAACATCG GTGCTTTACT TCGTGGGGTT 550
 GCTCGTGAAG ACATCCAACG TGGACAAGTA CTTGCAAAAA GCGGTTCTGT 600
 AAAAGCTCAC GCTAAATTCA AAGCTGAAGT TTTCGTATTA TCTAAAGAAG 650
 30 AAGGTGGACG TCACACTCCA TTCTTCGCTA ACTACCGTCC TCAGTTCTAC 700
 TTCCGTACAA CTGACGTAAC TGGTATCATC CAATTACCAG AAGGTACTGA 750
 AATGGTAATG CCTGGTGACA ACATCGAAAT GACTATCGAA CTTATCGCTC 800
 CAATCGCTAT CGAAGAGGGA ACTAA 825

35

2) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 14579

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

CGGCGGTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCTCAAACAC 50
 GTGAGCACAT CCTTCTTTCT CGTCAAGTAG GTGTTCTTA CATCGTTGTA 100
 55 TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAATTAT TAGAATTAGT 150
 AGAAATGGAA GTTCGCGACC TATTATCTGA ATACGGATTC CCAGGCGACG 200
 ACATTCCTGT AATCAAAGGT TCTGCTCTTA AAGCTCTTCA AGGAGAAGCT 250
 GATTGGGAAG CAAAAATCAT TGAATTAATG GCTGAAGTTG ATGCTTACAT 300
 CCCAACTCCA GAACGTGAAA CTGACAAACC ATTCTTAATG CCTGTAGAGG 350
 60 ACGTATTCTC TATCACAGGT CGTGGTACAG TTGCTACTGG TCGTGTTGAG 400

CGCGGTATCG TTAAAGTTGG TGACGTAGTA GAAATCATCG GTCTTGCTGA 450
 AGAAAATGCT TCTACAACTG TAACTGGTGT AGAGATGTTC CGTAAACTTC 500
 TTGACCAAGC TCAAGCTGGA GACAACATCG GTGCTTTACT TCGTGGGGTT 550
 GCTCGTGAAG ACATCCAACG TGGACAAGTA CTTGCAAAAA GCGGTTCTGT 600
 5 AAAAGCTCAC GCTAAATTCA AAGCTGAAGT TTTCGTATTA TCTAAAGAAG 650
 AAGGTGGACG TCACACTCCA TTCTTCGCTA ACTACCGTCC TCAGTTCTAC 700
 TTCCGTACAA CTGACGTAAC TGGTATCATC CAATTACCAG AAGGTACTGA 750
 AATGGTAATG CCTGGTGACA ACATTGAAAT GACTATCGAA CTTATCGCTC 800
 CAATCGCTAT CGAAGAGGGA ACTAAATTC 829
 10

2) INFORMATION FOR SEQ ID NO: 8

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: *Bacteroides distasonis*
 (B) STRAIN: ATCC 8503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

CGGTGCTATC ATCGTAGTTG CTGCTACTGA TGGTCCTATG CCTCAAACCTC 50
 30 GCGAGCACAT CCTTTTGGCT CGTCAGGTAA ACGTTCCGAG ATTGGTTGTA 100
 TTCATGAACA AGTGTGACAT GGTGACGAC GAGGAAATGT TGGAATTGGT 150
 TGAGATGGAG ATGAGAGAGT TGCTTTCATT CTATCAATTC GACGGTGACA 200
 ACACTCCGAT CATCCGTGGT TCTGCTCTTG GTGCATTGAA CCGTGATGCT 250
 CAATGGGAAG ATAAAGTAAT GGAGTTGATG GAAGCTTGATG ATACTTGGAT 300
 35 TCCTCTGCCT CCGCGCGAAA TCGACAAGCC GTTCTTGATG CCGGTTGAGG 350
 ACGTATTCTC AATCACGGGT CGTGGTACTG TTGCTACAGG TCGTATCGAG 400
 ACAGGTATTG TTAAGGTTGG TGAGGAAGTT CAGATCATCG GTCTTGGCGC 450
 TGCTGGTAAG AAATCTGTTG TTACAGGTGT TGAGATGTTC CGTAAGTTAT 500
 TGGATCAAGG TGAGGCTGGT GATAACGTTG GTTTGTTGCT TCGCGGTATC 550
 40 GATAAGAATG AGATCAAGCG TGGTATGGTA ATCTGCCACC CGGGTCAGGT 600
 TAAAGAGCAT TCTAAGTTCA AGGCTGAGGT TTATATCTTG AAGAAAGAGG 650
 AAGGTGGTCG TCACACTCCG TTCCACAACA AATATCGTCC TCAGTTCTAT 700
 ATCCGTACAT TGGATGTAAC TGGTGAGATC ACTTTGCCGG AAGGAACTGA 750
 AATGGTAATG CCGGGTGATA ACGTAACGAT CGAGGTTGAG TTGATCTATC 800
 45 CGGTAGCATG TAGCGTAG 818

2) INFORMATION FOR SEQ ID NO: 9

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 639 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: R763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9

5	GGTCCTATGC	CTCAAACACG	TGAACACATC	TTGTTATCAC	GTAACGTTGG	50
	TGTACCATAC	ATCGTTGTTT	TCTTAAACAA	AATGGATATG	GTTGATGACG	100
	AAGAATTACT	AGAATTAGTT	GAAATGGAAG	TTCGTGACTT	ATTGTCAGAA	150
	TATGACTTCC	CAGGCGACGA	TGTTCTGTGA	ATCGCTGGTT	CTGCTTTGAA	200
	AGCTCTTGAA	GGCGATGCTT	CATACGAAGA	AAAAATCATG	GAATTAATGG	250
10	CTGCAGTTGA	CGAATACGTT	CCAACTCCAG	AACGTGACAC	TGACAAACCA	300
	TTCATGATGC	CAGTCGAAGA	CGTATTCTCA	ATCACTGGAC	GTGGTACTGT	350
	TGCTACAGGC	CGTGTTGAAC	GTGGACAAGT	TCGCGTTGGT	GACGAAGTTG	400
	AAATCGTTGG	TATTGCTGAA	GAAACTGCTA	AAACAACGTG	AACTGGTGTT	450
	GAAATGTTCC	GTAAATTGTT	AGACTATGCT	GAAGCAGGGG	ATAACATTGG	500
15	TGCATTGCTA	CGTGGTGTTG	CTCGTGAAGA	CATCCAACGT	GGACAAGTAT	550
	TGGCTAAAGC	TGGTACAATC	ACACCTCATA	CAAAATTTAA	AGCTGAAGTT	600
	TACGTTTTAA	CAAAAGAAGA	AGGTGGACGT	CACACACCA		639

20

2) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 692 bases
25	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Staphylococcus saprophyticus</i>
	(B)	STRAIN: CSG 197

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10

	GAACACATTC	TTTTATCACG	TAACGTTGGT	GTTCCAGCAT	TAGTTGTATT	50
	CTTAAACAAA	GTTGACATGG	TTGACGATGA	AGAATTATTA	GAATTAGTAG	100
	AAATGGAAGT	TCGTGACTTA	TTAAGCGAAT	ATGACTTCCC	AGGTGACGAT	150
40	GTACCTGTAA	TCTCTGGTTC	TGCATTAAAA	GCTTTAGAAG	GCGACGCTGA	200
	CTATGAGCAA	AAAATCTTAG	ACTTAATGCA	AGCTGTTGAT	GACTTCATTC	250
	CAACACCAGA	ACGTGATTCT	GACAAACCAT	TCATGATGCC	AGTTGAGGAC	300
	GTATTCTCAA	TCACTGGTGC	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	350
	TGGTCAAATC	AAAGTCGGTG	AAGAAATCGA	AATCATCGGT	ATGCAAGAAG	400
45	AATCAAGCAA	AACAACGTGT	ACTGGTGTAG	AAATGTTCCG	TAAATTATTA	450
	GACTACGCTG	AAGCTGGTGA	CAACATTGGT	GCATTATTAC	GTGGTGTTTC	500
	ACGTGATGAC	GTACAACGTG	GTCAAGTTTT	AGCTGCTCCT	GGTACTATTA	550
	CACCACATAC	AAAATTCAAA	GCGGATGTTT	ACGTTTTATC	TAAAGATGAA	600
	GGTGGTCGTC	ATACACCATT	CTTCACTAAC	TACCGCCCAC	AATTCTATTT	650
50	CCGTACTACT	GACGTAAC TG	GTGTTGTTAA	CTTACCAGAA	GG	692

2) INFORMATION FOR SEQ ID NO: 11

55

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 821 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
60	(D)	TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacteroides ovatus*
(B) STRAIN: ATCC 8483

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 11

10	CGGTGCTATC	ATCGTTTGTG	CTGCAACTGA	TGGTCCGATG	CCTCAAACCTC	50
	GCGAACACAT	TCTGTTAGCT	CGTCAGGTAA	ACGTACCTCG	TCTGGTTGTA	100
	TTCTTGAACA	AATGCGATAT	GGTAGACGAC	GAAGAAATGT	TGGAACCTCGT	150
	TGAAATGGAA	ATGAGAGAAC	TCCTTTCATT	CTATGATTTT	GATGGTGACA	200
	ATACTCCTAT	CATCCGTGGT	TCTGCTCTTG	GCGCATTGAA	CGGTGTTGAA	250
15	AAATGGGAAG	ACAAAGTTAT	GGAAGTATG	GATGCAGTTG	ATAACTGGAT	300
	TCCACTGCCT	CCGCGCGATG	TTGATAAACC	ATTCTTGATG	CCGGTTGAAG	350
	ACGTGTTCTC	TATCACAGGT	CGTGGTACTG	TAGCAACAGG	TCGTATCGAA	400
	ACAGGTGTCA	TCCACGTTGG	TGATGAAGTC	GAAATTCCTG	GTTTAGGTGA	450
	AGATAAGAAA	TCAGTTGTAA	CTGGTGTGTA	AATGTTCCGT	AAACTGTTGG	500
20	ATCAAGGTGA	AGCTGGTGAC	AACGTAGGTC	TTTTGCTTCG	TGGTATTGAC	550
	AAGAACGAAA	TCAAACGTGG	TATGGTTCCT	TGTAAACCAG	GTCAGATTAA	600
	ACCGCACTCT	AAATTCAAAG	CTGAGGTTTA	TATCTTGAAG	AAAGAAGAAG	650
	GTGGTCGTCA	CACTCCGTTT	CACAACAAAT	ACCGTCCTCA	GTTCTACTTG	700
	CGTACTATGG	ACTGTACAGG	TGAAATCACT	TTGCCGGAAG	GAACAGAAAT	750
25	GGTAATGCCG	GGTGATAACG	TAAGTATTAC	AGTTGAGTTG	ATTTACCCAG	800
	TAGCATTGAA	CCCGGGCTTC	G			821

30 2) INFORMATION FOR SEQ ID NO: 12

(i)SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 838 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Bartonella henselae*
(B) STRAIN: ATCC 49882

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 12

45	TGGTGCGATT	TTGGTTGTTT	CAGCTGCTGA	TGGTCCGATG	CCTCAAACAC	50
	GTGAGCATAT	TCTTCTTGCC	CGTCAGGTTG	GTGTTCCAGC	GATTGTTGTT	100
	TTTCTTAATA	AGGTTGATCA	GGTTGATGAT	GCTGAGCTTT	TGGAGCTTGT	150
	TGAGCTTGAA	GTTCTGGGAGT	TATTGTCGAA	ATATGATTTT	CCAGGAGACG	200
50	ATATTCCGAT	CGTTAAAGGT	TCTGCTTTGG	CAGCGCTTGA	AGATAAAGAT	250
	AAAAGCATTG	GTGAAGATGC	GGTTCGTCTT	TTGATGAGTG	AAGTTGATAA	300
	TTATATACCG	ACGCCTGAAC	GTCCTGTTGA	TCAGCCGTTT	TTGATGCCAA	350
	TTGAAGATGT	TTTTTTCGATT	TCGGGTCGTG	GAAGTTGAGA	TTATCGGCAT	400
	GTTGAGCGTG	GTGTTATTAA	GGTTGGTGAA	GAAGTTGAGA	TTATCGGCAT	450
55	TCGTCCAAC	TCTAAGACAA	CAGTTACAGG	GGTTGAAATG	TTCCGCAAGC	500
	TTTTAGATCA	GGGGCAAGCG	GGTGATAATA	TTGGAGCGCT	GCTTCGTGGT	550
	ATTGATCGTG	AAGGGATTGA	GCGTGGACAA	GTTTTGGCGA	AGCCTGCTTC	600
	GGTTACACCT	CATACGAGAT	TTAAAGCAGA	GGCTTACATT	TTGACGAAAG	650
	ATGAAGGTGG	TCGTCATACT	CCATTTTTCA	CGAATTATCG	TCCTCAGTTT	700
60	TATTTCCGTA	CTACGGATGT	AACGGGAATT	GTTACGCTTC	CAGAAGGTAC	750

AGAGATGGTT ATGCCTGGTG ATAATGTTGC TATGGATGTC TCTCTGATTG 800
 TTCCAATTGC CATGGAAGAA AACTTCGTT TTGCTATC 838

5

2) INFORMATION FOR SEQ ID NO: 13

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium adolescentis*
 (B) STRAIN: ATCC 15703

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13

TGGCGCCATC CTTGTTGTGG CCGCCACCGA CGGCCCGATG GCTCAGACCC 50
 GCGAGCACGT GCTGCTCGCT CGTCAGGTGG GCGTCCCGAA GATCCTCGTC 100
 GCTCTGAACA AGTGCGATAT GGTCGACGAC GACGAGCTCA TCGAGCTCGT 150
 25 TGAGGAAGAG GTCCGTGACC TCCTCGACGA AAATGGCTTC GATCGCGATT 200
 GCCCGGTCAT CCACGTGTCC GCTTACGGCG CACTGCACGA TGACGCTCCG 250
 GACCACGAGA AGTGGGTTGA GCAGATCAAG AAGCTCATGG ACGCCGTCGA 300
 TGACTACATC CCGACCCCGG TCCACGATCT GGACAAGCCG TTCCTGATGC 350
 CGATCGAAGA TGTCTTCACC ATCTCCGGCC GTGGCACCGT GGTGACCGGC 400
 30 CGTGTGCGAGC GTGGTAAGCT CCCGGTCAAC TCCAACGTCG AGATCGTCGG 450
 CATCCGTCCG ACCCAGACCA CCACCGTCAC CTCCATCGAG ACCTTCCACA 500
 AGCAGATGGA CGAGTGCGAG GCTGGCGACA ACACCGGTCT GCTGCTCCGC 550
 GGCATCAACC GTGACCAGGT CGAGCGTGGC CAGGTTCTGG CTGCTCCGGG 600
 CTCCGTGACC CCGCACACCA AGTTCGAGGG CGAAGTCTAC GTGCTGACCA 650
 35 AGGACGAAGG CGGCCGTCAC TCGCCGTTCT TCTCCAATA CCGTCCGCAG 700
 TTCTACTTCC GTACCACCGA CGTCACCGGC GTCATCACCC TGCCGGAAGG 750
 CGTTGAGATG GTGCAGCCGG GCGATCACGC TACCTTCGGC GTTGAGCTGA 800
 TCCAGCCGAT CGCTATGGAA GAGGGCCTGA CCTTCGCAG 839

40

2) INFORMATION FOR SEQ ID NO: 14

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium dentium*
 (B) STRAIN: ATCC 27534

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

TGGCGCTATC CTCGTTGTGG CCGCCACCGA CGGCCCGATG GCTCAGACCC 50
 GCGAGCACGT GCTGCTCGCT CGTCAGGTGG GCGTGCCGCG TATCCTCGTC 100
 60 GCCCTGAACA AGTGCGATAT GGTCGACGAC GAAGAGCTCA TCGAGCTCGT 150

	TGAGGAAGAG	GTCCGTGACC	TCCTCGACGA	AAACGGCTTC	GATCGCGATT	200
	GCCCCGGTCAT	CCACACCTCC	GCCTACGGCG	CGCTGCACGA	TGACGCTCCG	250
	GACCACGACA	AGTGGGTTGA	GTCCGTCAAG	GAATCATGA	AGGCCGTCGA	300
	CGAGTACATC	CCGACCCCGA	CCCACGATCT	GGACAAGCCG	TTCCTGATGC	350
5	CGATCGAAGA	TGTGTTCAAC	ATCTCCGGCC	GTGGCACCGT	GGTTACCGGC	400
	CGTGTCGAGC	GTGGTAAGCT	CCCGGTCAAC	TCCAACGTTG	AGATCGTCGG	450
	CATCCGTCCG	ACCCAGACCA	CCACCGTCAC	CTCCATCGAG	ACCTTCCACA	500
	AGCAGATGGA	CGAGTGCAG	GCTGGCGACA	ACACCGGTCT	GCTGCTCCGC	550
	GGCATCAACC	GTGACCAGGT	CGAGCGTGGC	CAGGTTCTGG	CTGCTCCGGG	600
10	CTCCGTGACC	CCGCACACCA	AGTTCGAGGG	CGAAGTCTAC	GTGCTGACCA	650
	AGGACGAAGG	CGGCCGTCAC	TCGCCGTTCT	TCTCCAATA	CCGTCCGCAG	700
	TTCTACTTCC	GTACCACCGA	CGTCACCGGC	GTCATCACCC	TGCCGGAAGG	750
	CGTTGAGATG	GTGCAGCCGG	GCGATCACGC	TACCTTCGGC	GTTGAGCTGA	800
	TCCAGCCGAT	CGCTATGGAA	GAGGGCCTGA	CCTTCGCAG		839

15

2) INFORMATION FOR SEQ ID NO: 15

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 838 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Brucella abortus*

30 (B) STRAIN: S2308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15

	TGGCGCGATC	CTGGTGGTTT	CGGCTGCTGA	CGGCCCGATG	CCGCAGACCC	50
35	GCGAGCACAT	CCTGCTTGCC	CGTCAGGTTG	GCGTTCCGGC	GATCGTCGTG	100
	TTCCTCAACA	AGTGCGACCA	GGTTGACGAT	GCAGAACTGC	TCGAACTGGT	150
	TGAACTGGAA	GTGCGCGAAC	TTCTGTGCGA	GTACGAATTC	CCCGGCGACG	200
	AAATCCCGAT	CATCAAGGGC	TCGGCTCTTG	CTGCTCTGGA	AGATTCTTCC	250
	AAGGAACTGG	GCGAAGATGC	CATCCGCAAC	CTGATGGACG	CGGTTGACAG	300
40	CTACATTCCG	ACCCCGGAAC	GCCCGATCGA	CCAGCCGTTT	CTGATGCCGA	350
	TCGAAGACGT	GTTCTCGATC	TCCGGCCGTG	GTACGGTTGT	GACGGGTCGC	400
	GTGAGCGCG	GTATCGTTAA	GGTCGGTGAA	GAAGTTGAAA	TGTTGGGCAT	450
	CAAGGCGACG	ACGAAGACCA	CGTTTACCGG	CGTTGAAATG	TTCCGCAAGC	500
	TGCTCGACCA	GGGCCAGGCT	GGCGACAACA	TTGGCGCGCT	GATCCGCGGC	550
45	GTTGGCCGTG	AAGACGTTGA	ACGCGGCCAG	GTTCTCTGCA	AGCCGGGTTC	600
	TGTGAAGCCG	CACACCAAGT	TTAAGGCAGA	AGCCTATATT	CTGACCAAGG	650
	ACGAAGGTGG	CCGTCATACG	CCGTTCTTCA	CCAATACTCC	TCCGCAGTTC	700
	TACTTCCGTA	CGACGGACGT	GACGGGTGTT	GTGACGCTTC	CGGCTGGCAC	750
	GGAAATGGTC	ATGCCTGGCG	ATAACGTCGC	CATGGACGTT	ACCCTGATCG	800
50	TGCCGATCGC	CATGGAAGAG	AAGCTTCGCT	TCGCTATC		838

2) INFORMATION FOR SEQ ID NO: 16

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 771 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Burkholderia cepacia*
(B) STRAIN: LSPQ 2217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16

10	GGCAGCAGAC	GGCCCGATGC	CGCAAACGCG	TGAGCACATC	CTGCTGGCGC	50
	GTCAGGTTGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	GTGCGACATG	100
	GTGGACGACG	CCGAAGTGT	CGAGCTGGTC	GAGATGGAAG	TTCGCGAACT	150
	CCTGTCTGAAG	TACGACTTCC	CGGGCGACGA	CACGCCGATC	GTGAAGGGTT	200
	CGGCGAAGCT	GGCGCTGGAA	GGCGACACGG	GCGAGCTGGG	CGAAGTGGCG	250
15	ATCATGAGCC	TGGCCGACGC	GCTGGACACG	TACATCCCGA	CGCCGGAGCG	300
	TGCAGTTGAC	GGCGCGTTCC	TGATGCCGGT	GGAAGACGTG	TTCTCGATCT	350
	CGGGCCGCGG	TACGGTGGTG	ACGGGTCGTG	TCGAGCGCGG	CATCGTGAAG	400
	GTCGGCGAAG	AAATCGAAAT	CGTCGGTATC	AAGCCGACGG	TGAAGACGAC	450
	CTGCACGGGC	GTTGAAATGT	TCCGCAAGCT	GCTGGACCAA	GGTCAAGCAG	500
20	GCGACAACGT	TGGTATCCTG	CTGCGCGGCA	CGAAGCGTGA	AGACGTGGAG	550
	CGTGGCCAGG	TTCTGGCGAA	GCCGGGTTCG	ATCACGCCGC	ACACGCACTT	600
	CACGGCTGAA	GTGTACGTGC	TGAGCAAGGA	CGAAGGCGGC	CGTCACACGC	650
	CGTTCTTCAA	CAACTACCGT	CCGCAGTTCT	ACTTCCGTAC	GACGGACGTG	700
	ACGGGCTCGA	TCGAGCTGCC	GAAGGACAAG	GAAATGGTGA	TGCCGGGCGA	750
25	CAACGTGTCTG	ATCACGGTGA	A			771

2) INFORMATION FOR SEQ ID NO: 17

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Cedecea davisae*
(B) STRAIN: ATCC 33431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17

45	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAT	GGCCCAATGC	CACAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTTGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGTGAACT	TCTGTCCCAG	TACGACTTCC	CGGGCGACGA	200
	TACTCCAATC	GTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
50	AGTGGGAAGC	TAAAATCGTT	GAGCTGGCTG	GCTACCTGGA	TTCTTACATC	300
	CCTGAGCCAG	AGCGTGCTAT	CGATAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGCC	GTGGTACCGT	TGTTACCGGT	CGTGTAAGAGC	400
	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAT	450
	ACTGCGAAAT	CTACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
55	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCAGG	CTCTATCAAG	600
	CCACACACCA	AGTTCGAATC	TGAAGTGTAC	ATCCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACTGA	CGTGACCGGC	ACCATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
60	GTAATGCCTG	GCGACAACAT	CAAATGGTT	GTTACCCTGA	TCCACCCAAT	800

CGCGATGGAT GACGGTCTGC GTTTCGCAA

5 2) INFORMATION FOR SEQ ID NO: 18

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea neteri*
 (B) STRAIN: ATCC 33855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18

20 CGCTATCCTG GTTGTTGCTG CGACTGACGG CCCTATGCCT CAGACCCGTG 50
 AGCACATCCT GCTGGGTCGT CAGGTTGGCG TTCCTTACAT CATCGTGTTT 100
 CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTTGA 150
 AATGGAAGTT CGTGAAGTTC TGTCTCAGTA CGACTTCCCG GGCGATGACA 200
 25 CTCCAATCAT CCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAAGCAGAG 250
 TGGGAAGCTA AAATYGTTGA GCTGGCTGGC TTCCTGGATT CCTACATCCC 300
 AGAACCAGTA CGTGCAATCG AYCTGCCGTT CCTGCTGCCA ATCGAAGACG 350
 TATTCTCCAT CTCCGGCCGT GGTACCGTTG TTACCGGTCG TGTAGAGCGC 400
 GGTATCGTTA AAGTGGGCGA AGAAGTAGAA ATCGTTGGTA TCAAAGATAC 450
 30 TGCGAATCT ACCTGTACCG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG 500
 AAGGCCGTGC TGGTGAGAAC GTTGGTGTTT TGCTGCGTGG TATCAAACGT 550
 GAAGAAATCG AACGTGGTCA GGTTCCTGGCT AAGCCAGGCT CTATCAAGCC 600
 GCACACCAAG TTCGAATCTG AAGTGACAT CCTGTCCAAA GACGAAGGCG 650
 GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCACAGTT CTACTTCCGT 700
 35 ACAACTGACG TGACCGGTAC CATCGAAGT CCAGAAGGCG TAGAGATGGT 750
 AATGCCAGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG 800
 CGATGGACGA CCGTCTGCGT TTCG 824

40

2) INFORMATION FOR SEQ ID NO: 19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea lapagei*
 (B) STRAIN: ATCC 33432

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19

CGCTATTCTG GTTGTTGCTG CAACTGACGG CCCTATGCCT CAGACCCGTG 50
 AGCACATCCT GCTGGGTCGC CAGGTTGGCG TTCCTTACAT CATCGTGTTT 100
 CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTAGA 150
 60 AATGGAAGTT CGTGAAGTTC TGTCTCAGTA CGACTTCCCA GGCGATGATA 200

CCCCATCAT CCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAAGCAGAG 250
 TGGGAAGCTA AAATCGTTGA GCTGGCTGGC TTCCTGGATT CCTACATCCC 300
 AGAACCAGTA CGTGCAATCG ACCTGCCGTT CCTGCTGCCA ATCGAAGACG 350
 TATTCTCCAT CTCCGGCCGT GGTACCGTTG TKACCGGTCG TGTAGAGCGC 400
 5 GGTATCGTTA AAGTGGGCGA AGAAGTAGAA ATCGTTGGTA TCAAAGATAC 450
 TGCAGAAATCT ACCTGTACTG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG 500
 AAGGCCGTGC TGGTGAGAAC GTTGGTGTTC TGCTGCGTGG TATCAAACGT 550
 GAAGAAATCG AACGTGGTCA GGTCTGGCT AAGCCAGGCT CTATCAAGCC 600
 GCACACCAAG TTCGAATCTG AAGTGACAT CCTGTCCAAA GACGAAGGCG 650
 10 GCCGTCATAC TCCGTTCTTC AARGGCTACC GTCCACAGTT CTACTTCCGT 700
 ACCACTGACG TGACCGGTAC CATCGAACTG CCAGAAGGCG TAGAGATGGT 750
 AATGCCAGGT GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG 800
 CGATGGACGA CCGTCTGCGT TTCGCAA 827

15

2) INFORMATION FOR SEQ ID NO: 20

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 25 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Chlamydia pneumoniae*
 (B) STRAIN: CWL 029

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20

GCGGAGCTAT CCTAGTCGTT TCAGCTACAG ACGGAGCTAT GCCACAAACT 50
 AAAGAACATA TCTTGCTAGC TCGCCAGGTT GGAGTTCCTT ATATCGTTGT 100
 35 TTTCTTGAAT AAAGTAGATA TGATCTCTCA AGAAGATGCT GAACTTATTG 150
 ACCTTGTTGA GATGGAAGTT AGTGAGCTTC TTGAAGAAAA AGGCTACAAA 200
 GGATGCCCTA TTATCCGTGG TTCTGCTTTG AAAGCTCTTG AAGGTGATGC 250
 AAATTATATC GAAAAAGTTC GAGAACTTAT GCAAGCTGTG GATGACAACA 300
 TCCCTACACC AGAAAGAGAA ATTGATAAGC CTTTCTTAAT GCCTATCGAA 350
 40 GACGTATTCT CAATCTCTGG TCGTGGTACT GTGGTTACAG GAAGAATCGA 400
 GCGTGGAATC GTTAAAGTTT CTGATAAAGT TCAGCTCGTG GGATTAGGAG 450
 AGACTAAAGA AACAATCGTT ACTGGAGTCG AAATGTTTCAG GAAAGAACTT 500
 CCTGAAGGTC GTGCAGGAGA AAACGTTGGT TTAATCCTCA GAGGTATTGG 550
 AAAGAACGAT GTTGAAAGAG GTATGGTGGT TTGTCAGCCT AACAGCGTGA 600
 45 AGCCTCATAC GAAATTTAAG TCAGCTGTTT ACGTTCTTCA GAAAGAAGAA 650
 GGCGGACGTC ATAAGCCTTT CTTAGCGGA TACAGACCTC AGTTCTTCTT 700
 CCGTACTACA GACGTGACAG GAGTCGTAAC TCTTCCTGAA GGAAGTGAAG 750
 TGGTAATGCC TGGAGATAAC GTTGAGCTTG ATGTTGAGCT CATTGGAACA 800
 GTTGCTCTTG AAGAAGGAAT GAGATTTGCA A 831

50

2) INFORMATION FOR SEQ ID NO: 21

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chlamydia psittaci*

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21

	TGGAGCGATT	CTCGTTGTTT	CCGCTACTGA	CGGTGCGATG	CCTCAGACCA	50
	AAGAACATAT	TCTTTTGGCG	AGACAGGTTG	GTGTTCCCTA	CATCGTTGTT	100
10	TTCCTTAACA	AAATCGATAT	GATTTCTCAA	GAAGATGCTG	AGCTCGTAGA	150
	CTTAGTTGAA	ATGGAATTGT	CCGAACCTTCT	AGAAGAAAAA	GGTTATAAAG	200
	GTTGCCCAAT	TATCCGTGGT	TCTGCTTTGA	AAGCCTTAGA	AGGTGATGCA	250
	AGCTACGTTG	AAAAAATTCG	CGAGTTAATG	CAAGCAGTGG	ATGATAACAT	300
	CCCTACTCCA	GAGCGTGAAG	TTGATAAGCC	TTTCTTAATG	CCTATCGAAG	350
15	ACGTATTCTC	TATTTCTGGT	CGTGGTACTG	TGGTCACAGG	ACGTATCGAG	400
	CGTGGAATCG	TTAAAGTGGG	TGATAAAGTA	CAGATTGTTG	GTTTAAGAGA	450
	TACTAGAGAG	ACAATTGTTA	CCGGTGTGGA	AATGTTTCAGA	AAAGAACTTC	500
	CAGAAGGTCA	AGCAGGGGAA	AACGTTGGTT	TGCTCCTCAG	AGGTATCGGT	550
	AAGAATGACG	TTGAACGTGG	TATGGTTATC	TGCCAACCTA	ATAGCGTGAA	600
20	ATCTCACACA	CAATTTAAAG	GTGCTGTCTA	CATTCTACAA	AAAGAAGAGG	650
	GTGGACGTCA	TAAACCTTTC	TTTACCGGAT	ACAGACCTCA	GTTCTTCTTC	700
	CGTACAACAG	ATGTTACAGG	TGTTGTAAC	CTCCCAGAAG	GTACAGAGAT	750
	GGTTATGCCA	GGCGATAACG	TTGAATTTCG	AGTTCAATTA	ATTAGCCCAG	800
	TAGCTCTAGA	AGAAGGTATG	AGATTT			826

25

2) INFORMATION FOR SEQ ID NO: 22

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chlamydia trachomatis*

40

(B) STRAIN: LGV 12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22

	GGGGCTATTC	TAGTAGTTTC	TGCAACAGAC	GGAGCTATGC	CTCAAACCTAA	50
45	AGAGCATATT	CTTTTGGCAA	GACAAGTTGG	GGTTCCTTAC	ATCGTTGTTT	100
	TTCTCAATAA	AATTGACATG	ATTTCCGAAG	AAGACGCTGA	ATTGGTCGAC	150
	TTGGTTGAGA	TGGAGTTGGC	TGAGCTTCTT	GAAGAGAAAG	GATACAAAGG	200
	GTGTCCAATC	ATCAGAGGTT	CTGCTCTGAA	AGCTTTGGAA	GGGGATGCTG	250
	CATACATAGA	GAAAGTTCGA	GAGCTAATGC	AAGCCGTCGA	TGATAATATC	300
50	CCTACTCCAG	AAAGAGAAAT	TGACAAGCCT	TTCTTAATGC	CCATTGAGGA	350
	CGTGTTCTCT	ATCTCCGGAC	GAGGAACTGT	AGTAACTGGA	CGTATTGAGC	400
	GTGGAATTGT	TAAAGTTTCC	GATAAAGTTC	AGTTGGTCGG	TCTTAGAGAT	450
	ACTAAAGAAA	CGATTGTTAC	TGGGGTTGAA	ATGTTTCAGAA	AAGAACTCCC	500
	AGAAGGTCGT	GCAGGAGAGA	ATGTTGGATT	GCTCCTCAGA	GGTATTGGTA	550
55	AGAACGATGT	GGAAAGAGGA	ATGTTGTTT	GCTTGCCAAA	CAGTGTTAAA	600
	CCTCATACAC	GGTTTAAAGT	TGCTGTTTAC	GTTCTGCAAA	AAGAAGAAGG	650
	TGGACGACAT	AAGCCTTTCT	TCACAGGATA	TAGACCTCAA	TTCTTCTTCC	700
	GTACAACAGA	CGTTACAGGT	GTGGTAACTC	TGCCTGAGGG	AGTTGAGATG	750
	GTCATGCCTG	GGGATAACGT	TGAGTTTGAA	GTGCAGTTGA	TTAGCCCTGT	800
60	GGCTTTAGAA	GAAGGTATGA	GA			822

2) INFORMATION FOR SEQ ID NO: 23

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 835 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chryseobacterium meningosepticum*

(B) STRAIN: CDC B7681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23

20	CGGAGCTATC	TTAGTATGTG	CTGCTACAGA	TGGTCCAATG	CCTCAAACCTA	50
	GAGAACACAT	CCTACTTTGC	CGTCAGGTAA	ACGTACCTAG	AATTGTTGTG	100
	TTCATGAACA	AAGTTGACAT	GGTAGATGAT	CCAGAATTGT	TAGAGCTTGT	150
	TGAGCTTGAA	CTTAGAGATC	TATTATCTAC	TTACGAATAT	GATGGTGATA	200
	ACTCTCCAGT	AATTC AAGGT	TCTGCTCTTG	GTGCTCTTAA	CGGTGATGCT	250
25	AAGTGGGTAG	CTACTGTAGA	AGCTCTAATG	GATGCTGTTG	ATACTTGGAT	300
	CGAGCAACCA	GTAAGAGATT	CTGATAAGCC	ATTCCTTATG	CCAATCGAAG	350
	ACGTATTCTC	TATTACAGGT	AGAGGTACTG	TAGCAACTGG	TAGAATCGAG	400
	GCTGGTGTA	TCAACACAGG	TGATCCTGTT	GACATCGTAG	GTATGGGTGA	450
	CGAGAAGTTA	ACTTCTACTA	TTACAGGTGT	TGAGATGTTT	AGAAAAATCC	500
30	TAGACAGAGG	TGAAGCTGGT	GATAACGTAG	GTCTATTGTT	GAGAGGTATT	550
	GAAAAGACTG	ACATCAAGAG	AGGTATGGTT	ATCGCTAAGA	AAGATTCAGT	600
	TAAGCCACAC	AAGAAATTCA	AAGCTGAGGT	TTATATCCTT	TCTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCCACAACA	AATACCGTCC	TCAGTTCTAT	700
	GTAAGAACTA	CTGACGTTAC	AGGTGAAATC	TTCTTACCAG	AAGGTGTAGA	750
35	AATGGTAATG	CCTGGTGATA	ACTTAACTAT	CACTGTAGAA	TTGTTACAAC	800
	CAATCGCTCT	TAACGAGGGT	CTTAGATTCG	CGATC		835

2) INFORMATION FOR SEQ ID NO: 24

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 816 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter amalonaticus*

(B) STRAIN: ATCC 25405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24

55	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
60	ACACCCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250

GAGTGGGAAG CGAAAATCAT CGAACTGGCC GGCTTCCTGG ATTCTTACAT 300
 CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
 ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA 400
 CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
 5 GACTGCCAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTGTCTG 500
 ACGAAGGCCG TGCGGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA 550
 CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCWCCATCAA 600
 GCCGCACACC ATGTTCTGAAT CYGAAGTGTA CATCCTGTCC AAAGACGAAG 650
 GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
 10 CGTACAACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTTGAGAT 750
 GGTAAATGCCG GGCGACAACA TCAAATGGT TGTACCCTG ATCCACCCGA 800
 TCGCGATGGA CGACGG 816

15

2) INFORMATION FOR SEQ ID NO: 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter braakii*
 (B) STRAIN: ATCC 43162

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25

CGCGATCCTG GTTGTGCTG CAACTGACGG CCCGATGCCG CAGACTCGTG 50
 AGCACATCCT GCTGGGTCGY CAGGTAGGCG TTCCGTACAT CATCGTGTTC 100
 CTGAACAAAT GCGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTAGA 150
 35 AATGGAAGTT CGTGAAC TTC TGTCTCAGTA CGATTTCCCG GGCGACGACA 200
 CGCCGATCGT TCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAWGCAGAG 250
 TGGGAAGCGA AAATCATCGA ACTGGCTGGC TTCCTGGATT CTTACATCCC 300
 GGAACCAGAG CGTGCGATTG ACAAGCCGTT CCTGCTGCCT ATCGAAGACG 350
 TATTCTCCAT CTCTGGTCGT GGTACCGTTG TTACCGGTCG TGTAGAGCGC 400
 40 GGTATCATCA AAGTTGGTGA AGAAGTTGAA ATCGTTGGTA TCAARGACAC 450
 TGCTAAGTCT ACCTGTACTG GCGTTGAAAT GTTCCGCAA CTGCTGGACG 500
 AAGGCCGTGC TGGTGAGAAC GTTGGTGTTT TGCTGCGTGG TATCAAGCGT 550
 GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGCT CTATCAAGCC 600
 GCACACCAAG TTCGAATCTG AAGTGACAT TCTGTCCAAA GACGAAGGCG 650
 45 GCCGTCATAC TCCGTTCTTC AARGGCTACC GTCCGCAGTT CTACTTCCGT 700
 ACTACTGACG TGAAGGTGAC CATCGAAGT CCGGAAGGCG TTGAGATGGT 750
 AATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG 800
 CGATGGACGA CCGTCTGCGT TTCGC 825

50

2) INFORMATION FOR SEQ ID NO: 26

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter koseri*
 (B) STRAIN: ATCC 27156

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCGGTA	CATCATCGTG	100
10	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAGATGGAA	GTGCGTGAAC	TGCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ACACGCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAMGCT	250
	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTACCTGG	ATTCTTACAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
15	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTGCG	CGAAGAAGTT	GAAATYGTG	GTATCAAAGA	450
	GACTGCGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GYTCCATCAA	600
20	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATYCTGTCY	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAACTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
25	TCGCGATGGA	CGACGGTCTG	CGTTTCGCAA			830

2) INFORMATION FOR SEQ ID NO: 27

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter farmeri*
 (B) STRAIN: ATCC 51112

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27

	CGCGATCCTG	GTTGTTGCTG	CGACTGACGG	CCCGATGCCG	CAGACTCGTG	50
45	AGCACATCCT	GCTGGGTCGT	CAGGTAGGCG	TTCCGTACAT	CATCGTGTTT	100
	CTGAACAAAT	GCGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTAGA	150
	GATGGAAGTT	CGTGAAGTGC	TGTCTCAGTA	CGATTTCCCG	GGCGACGACA	200
	CGCCGATCGT	TCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGACGCAGAG	250
	TGGGAAGCGA	AAATCATCGA	ACTGGCAGGC	TTCTGGATT	CTTACATCCC	300
50	GGAACCAGAG	CGTGCGATTG	ACAAGCCGTT	CCTGCTGCCG	ATCGAAGACG	350
	TATTCTCCAT	CTCTGGTCGT	GGTACCGTTG	TTACCGGTCG	TGTAGAGCGC	400
	GGTATCATCA	AAGTGGGTGA	AGAAGTTGAA	ATCGTTGGTA	TCAAAGAGAC	450
	TGCCAAGTCT	ACCTGTACTG	GCGTTGAAAT	GTTCCGCAAA	CTGCTGGACG	500
	AAGGCCGTGC	TGGTGAGAAC	GTAGGTGTTC	TGCTGCGTGG	TATCAAACGT	550
55	GAAGAAATCG	AACGTGGTCA	GGTACTGGCT	AAGCCGGGCW	CCATCAAGCC	600
	RCACACTATG	TTCGAATCTG	AAGTGACAT	TCTGTCCAAA	GACGAAGGCG	650
	GCCGTCATAC	TCCGTTCTTC	AAAGGCTACC	GTCCGCAGTT	CTACTTCCGT	700
	ACGACTGACG	TGACTGGCAC	CATCGAACTG	CCGGAAGGTG	TTGAGATGGT	750
	TATGCCGGGC	GACAACATCA	AAATGGTTGT	TACCCTGATC	CACCCGATCG	800
60	CGATGGACGA	CGGTCTGCGT	TTCGCAA			827

2) INFORMATION FOR SEQ ID NO: 28

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter freundii*
 (B) STRAIN: ATCC 8090

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28

20	CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACT CGTGAGCACA	50
	TCCTGCTGGG TCGTCAGGTA GCGTTCCGT ACATCATCGT GTTCCTGAAC	100
	AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAAGTGG TAGAAATGGA	150
	AGTTCGTGAA CTTCTGTCTC AGTACGATTT CCCGGGCGAC GACACTCCGA	200
	TCGTTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGAAGC AGAGTGGGAA	250
25	GCGAAAATCA TCGAACTGGC TGGCTTCCTG GATTCTTACA TCCCAGAACC	300
	AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCTATCGAA GACGTATTCT	350
	CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC	400
	ATCAAAGTTG GTGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTGCTAA	450
	GTCTACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC	500
30	GTGCTGGTGA GAACGTTGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA	550
	ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCTCTATCA AGCCGCACAC	600
	CAAGTTCGAA TCTGAAGTGT ACATTCTGTC CAAAGACGAA GGCGGCCGTC	650
	ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACTACT	700
	GACGTGACTG GTACCATCGA ACTGCCGGAA GCGGTAGAGA TGGTAATGCC	750
35	GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCA ATCGCGA	797

2) INFORMATION FOR SEQ ID NO: 29

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter sedlakii*
 (B) STRAIN: ATCC 51115

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29

55	CGGCGCGATC CTGGTTGTTG CCGCGACTGA CGGCCCGATG CCGCAGACCC	50
	GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG	100
	TTCCTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT	150
	AGAGATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTT CCGGGCGACG	200
	ACACGCCGAT CGTTCGTGGT TCAGCTCTGA AAGCGCTGGA AGGCGACGCA	250
60	GAGTGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT	300

	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	G TTCCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTGCGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
5	ACGAAGGCCG	TGCGGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCGAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	TATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAACTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
10	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGTCTG	CGTTTC			826

15 2) INFORMATION FOR SEQ ID NO: 30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter werkmanii*
 (B) STRAIN: ATCC 51114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30

30	GCGATCCTGG	TTGTTGCTGC	GACTGACGGC	CCGATGCCGC	AGACTCGTGA	50
	GCACATCCTG	CTGGGTCGTC	AGGTAGGCGT	TCCGTACATC	ATCGTGTTCC	100
	TGAACAAATG	CGACATGGTT	GATGACGAAG	AGCTGCTGGA	ACTGGTAGAA	150
	ATGGAAGTTC	GTGAACTTCT	GTCTCAGTAC	GATTTCCCGG	GCGACGACAC	200
35	TCCGATCGTT	CGTGGTTCTG	CTCTGAAAGC	GCTGGAAGGC	GAAGCAGAGT	250
	GGGAAGCGAA	AATCATCGAA	CTGGCTGGCT	TTCTGGATTC	TTACATCCCG	300
	GAACCAGAGC	GTGCGATTGA	CAAGCCGTTC	CTGCTRCCTA	TCGAAGACGT	350
	ATTCTCCATC	TCCGGTCGTC	GTACCGTTGT	TACCGGTCGT	G TAGAGCGCG	400
	GTATCATCAA	AGTTGGTGAA	GAAGTTGAAA	TCGTTGGTAT	CAAAGACACC	450
40	GCTAAGTCTA	CCTGTACCGG	CGTTGAAATG	TTCCGCAAAC	TGCTGGACGA	500
	AGGCCGTGCT	GGTGAGAACG	TTGGTGTTC	GCTGCGTGGT	ATCAAACGTG	550
	AAGAAATCGA	ACGTGGTCAG	GTACTGGCTA	AGCCGGGGCTC	TATCAAGCCG	600
	CACACCAAGT	TCGAATCTGA	AGTGACATC	CTGTCCAAAG	ACGAAGGCGG	650
	CCGTCATACT	CCGTTCTTCA	AAGGCTACCG	TCCGCAGTTC	TACTTCCGTA	700
45	CTACTGACGT	GACTGGTACC	ATCGAACTGC	CGGAAGGCGT	AGAGATGGTA	750
	ATGCCGGGCG	ACAACATYAA	AATGGTTGTT	ACYCTGATCC	ACCCGATCGC	800
	GATGGACGAC	GGTCTGCGTT	TCG			823

50

2) INFORMATION FOR SEQ ID NO: 31

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter youngae*
 (B) STRAIN: ATCC 29935

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
10	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTCC	CGGGCGACGA	200
	TACGCCGATC	GTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
	AGTGGGAAGC	GAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTACATC	300
	CCGGAACCAG	AACGTGCTAT	CGATAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACTGGT	CGTGTAAGAC	400
15	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCCAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCTATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGACGAAGG	650
20	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACGGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
	GTAATGCCGG	GCGACAACAT	CAAATGGTT	GTTACCCTGA	TCCACCCAAT	800
	CGCGATGGAT	GACGGTCTGC	GTTTCG			826

25

2) INFORMATION FOR SEQ ID NO: 32

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
 (B) STRAIN: ATCC 13124

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32

	CGGAGCTATA	TTAGTTTGTT	CAGCAGCTGA	TGGTCCAATG	CCTCAAACAA	50
	GAGAGCACAT	CTTATTATCA	TCAAGAGTTG	GAGTTGACCA	CATCGTAGTA	100
45	TTCTTAAACA	AAGCAGATAT	GGTTGACGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTAGAGAGT	TATTAAGCGA	GTACAACCTC	CCAGGAGACG	200
	AYATTCCAGT	AATCAARGGA	TCAGCTTTAG	TAGCATTAGA	AAACCCAACT	250
	GACGAAGCTG	CAACAGCTTG	TATCAGAGAG	TTAATGGATG	CTGTAGATAG	300
	CTACATCCCA	ACACCAGAAA	GAGCAACAGA	TAAGCCATTC	TTAATGCCAG	350
50	TAGAGGACGT	ATTCACAATC	ACTGGTAGAG	GAACAGTTGC	AACAGGAAGA	400
	GTTGAAAGAG	GAGTTCTACA	TGTAGGAGAC	GAAGTAGAAG	TAATCGGATT	450
	AACTGAAGAA	AGAAGAAAAA	CTGTTGTAAC	AGGAATCGAA	ATGTTTCAGAA	500
	AGTTATTAGA	TGAAGCACAA	GCTGGAGATA	ACATCGGAGC	ATTATTAAGA	550
	GGTATCCAAA	GAAGTGAAT	CGAAAGAGGT	CAAGTTTTCAG	CTCAAGTTGG	600
55	AACAATCAAC	CCACACAAAA	AATTCGTAGG	TCAAGTATAC	GTAAGTTAAA	650
	AAGAAGAAGG	TGGAAGACAT	ACTCCATTCT	TCGATGGATA	CAGACCACAA	700
	TTCTACTTCA	GAACAACAGA	CGTTACAGGA	TCAATCAAAT	TACCAGAAGG	750
	AATGGAAATG	GTTATGCCTG	GAGACCACAT	CGACATGGAA	GTTGAATTAA	800
60	TCACAGAAAT	CGCTATGGAY	GAAGGATTAA	GATTCGCTAT	C	841

2) INFORMATION FOR SEQ ID NO: 33

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Comamonas acidovorans*
 15 (B) STRAIN: ATCC 15668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33

	CGGCGCCATC	CTGGTGTGCT	CGGCCGCTGA	CGGCCCCATG	CCCCAGACCC	50
20	GCGAGCACAT	CCTGCTGGCC	CGTCAGGTGG	GCGTGCCCTA	CATCATCGTG	100
	TTCCTGAACA	AGTGCGACAT	GGTGGACGAC	GAAGAGCTGC	TGGAACTGGT	150
	CGAAATGGAA	GTGCGCGAGC	TGCTTGCCAA	GTACGACTTC	CCCGGCGACG	200
	ACACCCCAT	CATCCGCGGC	TCGGCCAAGC	TGGCCCTGGA	AGGCGACCAG	250
	TCCGACAAGG	GCGAACCTGC	CATCCTGCGC	CTGGCTGAAG	CACTGGACTC	300
25	CTACATCCCC	ACGCCCAGAGC	GCGCTGTGGA	CGGCGCCTTT	GCAATGCCCG	350
	TGGAAGACGT	GTTCTCGATC	TCTGGCCGTG	GCACCGTGGT	GACTGGCCGT	400
	ATCGAGCGCG	GCATCATCAA	GGTCGGCGAA	GAAATCGAAA	TCGTCGGTAT	450
	CCGCGACACC	CAGAAGACCA	TCGTCACCGG	CGTGGAATG	TTCCGCAAGC	500
	TGCTGGACCA	AGGTCAAGCT	GGCGACAACG	TGGGTCTGCT	GCTGCGCGGC	550
30	ACCAAGCGTG	AAGACGTGGA	ACGCGGCCAA	GTGCTGTGCA	AGCCCGGCTC	600
	CATCAAGCCC	CACACCCACT	TCACGGCTGA	GGTGTACGTG	CTGTCCAAGG	650
	ACGAAGGTGG	TCGCCACACT	CCGTTCTTCA	ACAACCTACCG	TCCCCAGTTC	700
	TATTTCCGTA	CGACCGACGT	GACCGGCTCC	ATCGAGCTGC	CCGCCGACAA	750
	GGAAATGGTG	ATGCCTGGCG	ACAACGTGTC	GATCACCGTC	AAGCTGATCG	800
35	CCCCCATCGC	CATGGAAGAA	GG			822

2) INFORMATION FOR SEQ ID NO: 34

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 702 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Corynebacterium bovis*
 (B) STRAIN: ATCC 7715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34

55	GCCGCAGACC	CGTGAGCACG	TCCTCCTGGC	CCGTCAGGTC	GGTGTGCCCT	50
	ACATCCTCGT	CGCCCTCAAC	AAGTGCGACA	TGGTCGACGA	CGAGGACCTC	100
	ATCGAGCTCG	TCGAGATGGA	GGTCCGTGAG	CTCCTCGCCG	AGCAGGACTA	150
	CGACGAGGAC	GCCCCGATCA	TCCACATCTC	CGCCCTCAAG	GCCCTCGAGG	200
	GTGACCCGGA	GTGGACGCAG	CGCATCGTGC	ACCTCATGAA	GGCCTGCGAC	250
60	GACGCCATCC	CGGATCCGGA	GCGCGAGACG	GACAAGCCGT	TCCTCATGCC	300

GATCGAGGAC ATCTTCACGA TCACCGGCCG CGGCACCGTC GTCACGGGCC 350
 GTGTCGAGCG TGGCATCCTC AACGTCAACG AGGAGGTCGA GATCCTGGGT 400
 ATCTGCGAGA ACTCCCAGAA GACGACCGTC ACCTCCATCG AGATGTTCAA 450
 CAAGTTCCTC GACACGGCCG AGGCCGGCGA CAACGCCGCC CTGCTGCTCC 500
 5 GTGGCCTGAA GCGCGAGGAC GTCGAGCGTG GCCAGATCGT GGCCAAGCCG 550
 GGCGCCTACA CGCCGCACAC CGAGTTCGAG GGCTCCGTGT ACATCCTCTC 600
 CAAGGACGAG GGTGGCCGCC ACACGCCGTT CTTGACAAAC TACCGTCCGC 650
 AGTTCTACTT CCGGACGACC GACGTCACCG GCGTCGTCAA GCTGCCGGAG 700
 GG 702
 10

2) INFORMATION FOR SEQ ID NO: 35

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium cervicis*
 25 (B) STRAIN: NCTC 10604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35

GGCTCAGACC CGCGAGCACG TTCTGCTTGC TCGCCAGGTT GGCGTTCCGA 50
 30 CGATCCTGGT TGCCCTCAAC AAGGCCGATA TGGTCGACGA TGAGGAAATG 100
 CTGGAGCTCG TTGAGGAAGA GTGCCGCGAC CTGCTCGAGT CCCAGGACTT 150
 CGATCGTGAC GCCCCGATCA TCCAGGTTTC CGCGCTGAAG GCTCTCGAAG 200
 GTGATCCGCA GTGGGTTGCT AAGGTCGAGG AGCTCATGGA GGCAGTCGAC 250
 ACCTTCGTGC CGACTCCTGA GCGCGACATG GACAAGCCGT TCCTCATGCC 300
 35 GATCGAAGAC GTCTTCACCA TCACCGGCCG TGGCACCGTT GTTACCGGTC 350
 GTGTTGAGCG TGGCAAGCTC CCGATCAACT CTGAGGTTGA AATCCTCGGT 400
 ATCCGCGAAC CGCAGAAGAC CACCGTTACC GGTATCGAGA TGTTCCACAA 450
 GTCCATGGAT GAAGCATGGG CAGGCGAGAA CTGTGGTCTC CTCCTGCGTG 500
 GCACCAAGCG CGATGAGGTT GAGCGCGGTC AGGTCGTTGC CGTTCCCGGT 550
 40 TCGATCACCC CGCACACCAA CTTACCCGGA CAGGTCTACA TCCTCAAGAA 600
 GGAAGAAGGC GGTCGTCACA ACCCGTTCTT CTCGAAGTAC CGTCCGCAGT 650
 TCTACTTCCG CACCACGGAC GTGACCGGCG TCATCACCC 689

45

2) INFORMATION FOR SEQ ID NO: 36

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium flavescens*
 (B) STRAIN: ATCC 10340

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36

```

GGTTGTTGCT GCAACCGATG GTCCTATGCC GCAGACCCGC GAGCACGTTC      50
TTCTGGCTCG CCAGGTTGGC GTTCCTTACA TCCTCGTTGC TCTTAACAAG      100
TGCGACATGG TTGATGATGA GGAAATCATC GAGCTCGTTG AGATGGAAAT      150
5  CCGCGAACTG CTCGCTGAGC AGGACTACGA CGAGGATGCC CCCATCATCC      200
ACATCTCCGC TCTCAAGGCT CTTGAGGGTG ACGAGAAGTG GGTACAGGCC      250
ATCGTCGACC TCATGCAGGC CTGCGATGAC TCCATTCCGG ATCCGGAGCG      300
CGAGACCGAC AAGCCCTTCC TCATGCCTAT CGAGGACATC TTCACCATCA      350
CCGGCCGCGG TACCGTTGTT ACCGGCCGTG TTGAGCGTGG CGTTTTGAAG      400
10 GTCAACGAGG ATGTTGAGAT CATCGGCATC AAGGAGAAGT CCATCTCCAC      450
CACC GTTACC GGTATCGAAA TGTTCCGCAA GATGATGGAC TACACCGAGG      500
CTGGCGACAA CTGTGGTCTG CTTCTGCGTG GTACCAAGCG TGAAGAGGTC      550
GAGCGCGGCC AGGTTGTTAT CAAGCCGGGC GCCTACACCC CCCACACCAA      600
GTTTCGAGGGT TCCGTCTACG TCCTCAAGAA GGAAGAGGGC GGCCGCCACA      650
15 CCCC GTTCAT GGACA ACTAC CGTCCGCAGT TCTACTTCCG TACCACTGAC      700
GTGACCGGCG TTGTTACCT GCCTGAGGGC ACCGAGATGG TCATGCCTGG      750
CGACAACGTT GATATGACCG TTGAGCTCAT CCAGCCCGTC GCTAGGATGA      800
GGGC                                                                804

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20

2) INFORMATION FOR SEQ ID NO: 37

(i) SEQUENCE CHARACTERISTICS:

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25  (A) LENGTH: 692 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

      (A) ORGANISM: Corynebacterium kutscheri
      (B) STRAIN: ATCC 15677

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

```

TGCCTCAGAC CCGTGAGCAC GTTCTTCTTG CTCGCCAGGT TGGCGTTCCT      50
TACATCCTCG TTGCTCTTAA CAAGTGCGAC ATGGTTGACG ATGAGGAAAT      100
40 CATCGAGCTC GTTGAGATGG AAGTTCGCGA GCTTCTTGCT GAGCAGGAGT      150
ACGATGAAGA GGCTCCAATC ATCCACATCT CTGCTTTGAA GGCTCTTGAG      200
GGCGACGAGA AGTGGACTCA GGCCATCATC GACCTCATGC AGGCTTGTGA      250
TGACTCCATC CCAGATCCAG AGCGTGAGAC CGACAAGCCA TTCCTCATGC      300
CTATCGAGGA TATCTTCACC ATCACCGGTC GTGGCACCGT TGTTACCGGT      350
45 CGTGTGAGC GCGGTTCTTT GAAGGTGAAT GAGGACGTCG AGATCATCGG      400
CATCAAGGAG AAGTCCACCA CTACTACCGT TACCGGTATC GAAATGTTCC      450
GTAAGCTTCT TGATTACACC GAAGCTGGCG ATAAGTGTGG TCTGCTTCTT      500
CGTGGTATCA AGCGCGAAGA CGTTGAGCGT GGTCAGGTTG TTGTTAAGCC      550
AGGCGCTTAC ACACCTCACA CCGAGTTCGA GGGCTCTGTT TACGTTCTTT      600
50 CCAAGGACGA GGGCGGCCGC CACACCCCAT TCTTCGACAA CTACCGTCCA      650
CAGTTCTACT TCCGCACCAC TGACGTTACC GGTGTTGTGA AG              692

```

55 2) INFORMATION FOR SEQ ID NO: 38

(i) SEQUENCE CHARACTERISTICS:

```

      (A) LENGTH: 797 bases
      (B) TYPE: Nucleic acid
60  (C) STRANDEDNESS: Double

```

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium minutissimum*

(B) STRAIN: ATCC 23348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38

```

10 CCTGGTTGTT GCTGCAACCG ATGGCCCGAT GCCGCAGACC CGCGAGCACG      50
   TTCTTCTGGC CCGCCAGGTT GGCGTTCCGT ACATCCTCGT TGCACTGAAC      100
   AAGTGTGACA TGGTTGACGA TGAGGAAATC ATCGAGCTCG TTGAGATGGA      150
   GATCCGTGAG CTGCTCGCTG AGCAGGACTA CGACGAGGAA GCTCCGATCG      200
15 TTCACATCTC CGCTCTGAAG GCTCTTGAGG GCGACGAGAA GTGGGCACAG      250
   TCCATCGTTG ACCTGATGCA GGCTTGCGAT GACTCCATCC CCGATCCGGA      300
   GCGCGAGCTG GACAAGCCGT TCCTGATGCC GATCGAGGAC ATCTTCACCA      350
   TTACCGGCCG CCGTACCGTT GTTACCGGCC GTGTTGAGCG TGGCTCCCTG      400
   AACGTTAACG AGGACATCGA GATCATCGGT ATCAAGGACA AGTCCATGTC      450
20 CACCACCGTT ACCGGTATCG AGATGTTCCG CAAGATGATG GACTACACCG      500
   AGGCTGGCGA CAACTGTGGT CTGCTTCTGC GTGGTACCAA GCGTGAAGAG      550
   GTTGAGCGTG GCCAGGTTTG CATCAAGCCG GGCGCTTACA CCGCGCACAC      600
   CAAGTTCGAG GGTTCCGTCT ACGTCCTGAA GAAGGAAGAG GGCGGCCGCC      650
   ACACCCCGTT CATGGACAAC TACCGTCCGC AGTTCTACTT CCGCACCACC      700
25 GACGTCACCG GTGTCATCAA GCTGCCGGAG GGCACCGAGA TGGTCATGCC      750
   GGGCGACAAC GTTGAGATGT CCGTAGAGCT GATCCAGCCG GTCGCTA        797

```

30 2) INFORMATION FOR SEQ ID NO: 39

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 702 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium mycetoides*

(B) STRAIN: ATCC 21134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

```

45 GCCGCAGACC CGCGAGCACG TTCTTCTGGC CCGCCAGGTC GGCGTCCCCT      50
   ACATCCTCGT TGCGCTGAAC AAGTGCAGCA TGGTTGATGA TGAGGAGATC      100
   ATCGAGCTCG TGGAGATGGA GGTCCGTGAG CTGCTCGGCG AGCAGGACTA      150
   CGACGAGGAC GCCCCCATCA TCCACATCTC CGCTCTGAAG GCTCTCGAGG      200
50 GCGACGAGAA GTGGGTTTCAG TCCGTGCTCG ACCTCATGCA GGCGTGCGAC      250
   GACTCCATCC CCGATCCGGT CCGCGAGACC GACCGCGACT TCCTGATGCC      300
   GATCGAGGAC ATCTTCACCA TCTCCGGCCG CGGCACCGTG GTTACCGGTC      350
   GTGTGGAGCG CGGCGTGCTC AACCTCAACG ACGAGGTCGA GATCATCGGC      400
   ATCCGCGACA AGTCCCAGAA GACCACCGTC ACCTCCATCG AGATGTTCAA      450
55 CAAGCTGCTC GATACCGCTG AGGCAGGCGA CAACGCGGCT CTGCTGCTCC      500
   GCGGTCTGAA GCGCGAGGAC GTCGAGCGTG GCCAGGTTGT CATCAAGCCG      550
   GGCGCCTACA CCGCGCACAC CAAGTTCGAG GGTTCCGTCT ACGTCCTGTC      600
   CAAGGACGAG GGCGGCCGCC ACACCCCGTT CTTCGACAAC TACCGTCCGC      650
   AGTTCTACTT CCGCACCACC GACGTGACCG GTGTTGTGAA GCTGCCGGAG      700
60 GG                                                                702

```


2) INFORMATION FOR SEQ ID NO: 40

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Corynebacterium pseudogenitalium*
 (B) STRAIN: ATCC 33038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40

20	GCTCGCCAGG TTGGCGTTCC TTACATCCTC GTTGCGCTGA ACAAGTGCGA	50
	CATGGTTGAT GATGAGGAAA TCATCGAGCT CGTTGAGATG GAGATCCGTG	100
	AGCTGCTCGC AGAGCAGGAT TACGATGAGG AAGCTCCTAT CGTTCACATC	150
	TCCGCTCTGA AGGCCCTCGA GGGCGATGAC AAGTGGGTAC AGTCCGTCGT	200
	TGATCTGATG GAAGCCTGCG ACAACTCCAT CCCGGATCCG GAGCGCGCTA	250
25	CCGACCAGCC GTTCCTGATG CCTATCGAGG ACATCTTCAC CATTACCGGC	300
	CGCGGTACCG TTGTTACCGG CCGTGTGAG CGTGGCCGTC TGAACGTCAA	350
	CGAGGACGTT GAGATCATCG GTATCCAGGA GAAGTCCCAG ACCACCACCG	400
	TTACCGGTAT CGAGATGTTT CGCAAGATGA TGGACTACAC CGAGGCTGGC	450
	GACAACTGTG GTCTGCTTCT GCGTGGTACC AAGCGTGAGG ACGTTGAGCG	500
30	TGGCCAGGTT GTTATCAAGC CGGGCGCTTA CACCCCGCAC ACCAAGTTCG	550
	AGGGCTCCGT CTACGTCCTG AAGAAGGAAG AGGGCGGCCG CCACACCCCG	600
	TTCATGAACA ACTACCGTCC GCAGTTCTAC TTCCGTACCA CGGACGTTAC	650
	CGGTGTTGTT CACCTGCCAG AGGG	674

35

2) INFORMATION FOR SEQ ID NO: 41

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 694 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium renale*
 50 (B) STRAIN: ATCC 19412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41

	TGCCTCAGAC CCGTGAGCAC GTTCTGCTTG CTCGTCAGGT CGGCGTTCCT	50
	TACATCCTCG TTGCACTGAA CAAGTGCAGC ATGGTCGACG ACGAAGAAAT	100
55	CATCGAGCTC GTCGAGATGG AAATCCGTGA ACTGCTCGCA GAGCAGGACT	150
	ACGATGAGGA AGCTCCTATC GTTCACATCT CCGCTCTGGG CGCCCTGAAC	200
	GGCGAGCAGA AGTGGGTGTA CTCCATCGTC GAACTGATGG AAGCTTGCGA	250
	CAACTCCATC CCAGACCCAG TTCGCGACAT CGACCACCCA TTCCTGATGC	300
	CTATCGAGGA CATCTTCACC ATTACCGGTC GCGGTACCGT TGTTACCGGC	350
60	CGTGTGAGC GTGGCCGTCT CAACGTCAAC GAAGAAGTTG AGATCATCGG	400

	TATCAAGGAC	AAGTCCCAGA	AGACCACCGT	CACCGGTATC	GAGATGTTCC	450
	GCAAGATGCT	GGACTACACC	GAAGCTGGCG	ACAACTGTGG	TCTGCTGCTC	500
	CGCGGCATCG	GCCGTGAGGA	TGTCGAGCGT	GGCCAGGTTA	TCATCAAGCC	550
	AGGCGCTTAC	ACCCCTCACT	CTGAGTTCGA	GGGCTCTGTC	TACGTCCTGT	600
5	CCAAGGACGA	GGGTGGCCGC	CACACCCCAT	TCTTCGACAA	CTACCGTCCA	650
	CAGTTCTACT	TCCGCACCAC	CGACGTGACC	GGCGTTGTGC	ACCT	694

10 2) INFORMATION FOR SEQ ID NO: 42

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 687 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium ulcerans*
 (B) STRAIN: NCTC 8665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42

25	GCCGCAGACC	CGCGAGCACG	TTCTGCTGGC	TCGCCAGGTT	GGCGTTCCKT	50
	ACATCCTSGT	TGCACTGAAC	AAGTGCGACA	TGGTTGACGA	TGAGGARCTC	100
	CTSGAGCTCG	TCGAGATGGA	GGTCCGCGAG	CTGCTGGCTG	AGCAGGACTA	150
	CGACGAGGAA	GCTCCGRTCG	TTCACATCTC	CGCWCTGAAC	GCCCTGGACG	200
30	GCGACSAGAA	GTGGGCTVAC	TCCATCCTCG	AGCTGATGCA	GGCTTGCGAC	250
	GAGTCCATCC	CGGATCCGGA	GCGCGAGACC	GACAAGCCGT	TCCTGATGCC	300
	GATTGAGGAC	ATCTTCACCA	TTACCGGTCTG	CGGYACCGTT	GTTACCGGCC	350
	GTGTTGAGCG	TGGCDTCCTG	AACGTSAAACG	ACGASGTTGA	GATCATGGGY	400
	ATCCGGGAGA	AGTCCCAGAA	GACCACCGTY	ACCKSCATCG	AGATGTTCAA	450
35	CAAGMTGMTG	GACWCCGCAG	AGGCTGGCGA	CAACGCTGSW	CTGCTGCTGC	500
	GTGGTMTSAA	GCGTGAGGAC	GTTGAGCGTG	GCCAGATCAT	CGYTAAGCCG	550
	GGCGCKTACA	CCCCGCACAC	CGAGTTCGAG	GGCTCCGTCT	ACGTCCTGTC	600
	CAAGGACGAG	GGCGGCCGCC	ACACCCCGTT	CTTCGACAAC	TACCGTCCGC	650
40	AGTTCTACTT	CCGCACCACC	GACGTSACCG	GTGTTGT		687

2) INFORMATION FOR SEQ ID NO: 43

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium urealyticum*
 55 (B) STRAIN: ATCC 43042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43

	CTGGTTGTTG	CTGCAACCGA	TGGCCCGATG	CCGCAGACCC	GTGAGCACGT	50
60	TCTGCTGGCT	CGCCAGGTTG	GCGTTCCGTA	CATCCTCGTT	GCACTGAACA	100


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    AGTGCACAT  GGTGACGAT  GAGGAGCTCC  TCGAGCTCGT  CGAGATGGAG      150
    GTCCGCGAGC  TTCTGGCTGA  GCAGGACTAC  GACGAGGAGG  CTCCGGTCGT      200
    CCCGATCTCC  GCACTGGGCG  CCCTGGACGG  CGATCAGAAG  TGGGTGCGACT     250
    CCATCCTCGA  GCTCATGAAG  GCTTGCGACG  AGTCCATCCC  GGACCCGGAG      300
5   CGCGAGACCG  ACAAGCCGTT  CCTGATGCCG  GTTGAGGACA  TCTTCACCAT      350
    TACCGGTCGC  GGCACCGTCG  TTACCGGCCG  TGTGAGCGT  GCGTCCTGA      400
    ACCTGAACGA  CGAGGTCGAG  ATCCTGGGCA  TCCGCGAGAA  GTCCACCAAG      450
    ACCACCGTCA  CCTCCATCGA  GATGTTCAAC  AAGCTGCTGG  ACACCGCAGA      500
    GGCTGGCGAC  AACGCTGCAC  TGCTGCTGCG  TGGTCTGAAG  CGTGAGGACG      550
10  TCGAGCGAGG  CCAGATCATC  GCTAAGCCGG  GCGCTTACAC  CCCGCACACC      600
    GAGTTCGAGG  GCTCCGTCTA  CGTCCTGTCC  AAGGACGAGG  GCGGCCGTCA      650
    CACCCCGTTC  TTCGACAACT  ACCGTCCGCA  GTTCTACTTC  CGTACCACCG      700
    ACGTCACCGG  TGTCGTTACC  CTGCCAGAGG  GCACCGACAT  GGTCATGCCG      750
    GGCGACAACG  TTGAGATGAG  CGTCAAGC      778
15

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2) INFORMATION FOR SEQ ID NO: 44

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20  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 703 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
25
    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Corynebacterium xerosis
30  (B) STRAIN: ATCC 373

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44

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    CGCAGACCCG  TGAGCACGTC  CTCCTGGCCC  GCCAGGTCGG  CGTCCCCTAC      50
35  ATCCTCGTCG  CCCTGAACAA  GTGCGACATG  GTCGACGATG  AGGAGATCAT      100
    CGAGCTCGTG  GAGATGGAGG  TCGGTGAGCT  TCTCGCCGAG  CAGGACTACG      150
    ACGAGGAGGC  CCCGATCGTG  CACATCTCCG  CCCTGGGCGC  CCTCAATGGC      200
    GAAGAGAAGT  GGGTCGACTC  CATCGTCGAG  CTCATGAACG  CCGTCGACGA      250
    GAACGTTCCG  GACCCGGTCC  GCGAGACCGA  CAAGCCGTTC  CTGATGCCCCG      300
40  TCGAGGACAT  CTTACCATC  ACCGGCCGCG  GCACCGTCGC  CACCGGTCGC      350
    GTGGAGCGCG  GCACCCTGAA  GGTCAACGAC  GAGGTCGAGA  TCCTGGGCAT      400
    CCAGGAGAAG  TCCCAGACCA  CCACCGTCAC  CGGCATCGAG  ATGTTCCGCA      450
    AGCTGCTGGA  CTCCGCCGAG  GCCGGCGACA  ACTGTGGCCT  GCTGCTCCGC      500
    GGCATCAAGC  GCGAGGACAT  CGAGCGCGGC  CAGATCATCG  CGAAGCCGGG      550
45  CGCCTACACC  CCGCACACCG  AGTTCGAGGG  CTCCGTCTAC  ATCCTGGCCA      600
    AGGACGAGGG  CGGCCGCCAC  ACCCCGTTCT  TCGACAATA  CCGTCCGCAG      650
    TTCTACTTCC  GCACCACCGA  CGTCACCGGC  GTCGTGAAGC  TGCCGGAGGG      700
    CAC      703
50

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2) INFORMATION FOR SEQ ID NO: 45

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55  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 832 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

60  (ii) MOLECULE TYPE: Genomic DNA

```

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coxiella burnetii*
 (B) STRAIN: Nine Mile phase II

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45

GGAGCGATAT TGGTGGTGAG CGCAGCGGAC GGCCCGATGC CGCAAACGCG 50
 GGAACACATT GTATTGGCGA AGCAAGTGGG TGTTCGGAAC ATAGTGGTTT 100
 10 ACTTGAACAA AGCGGACATG GTGGATGACA AAGAGCTGTT GGAATTAGTG 150
 GAAATGGAAG TGAGGGATT TTTGAACAGT TATGATTTCC CTGGGGATGA 200
 GACGCCGATA ATAGTGGGGT CAGCGTTAAA GCGGTTAGAA GGTGACAAGA 250
 GTGAGGTTGG GGAGCCATCG ATAATCAAAT TAGTGGAAC GATGGACACG 300
 TACTTCCCGC AGCCGGAGCG AGCGATAGAC AAACCGTTTT TAATGCCGAT 350
 15 CGAAGATGTG TTTTCGATAT CGGGCCGAGG GACGGTGGTG ACGGGACGCG 400
 TAGAGCGAGG GATCATCAAA GTGGGCGACG AGATAGAGAT TGTGGGGATC 450
 AAGGACACGA CGAAGACGAC GTGCACGGGC GTTGAGATGT TTCGCAAATT 500
 ATTGGATGAA GGTCAAGCGG GTGACAACGT AGGAATTTTA TTGAGAGGGA 550
 CGAAACGCGA AGAAGTGGAG CGTGGTCAAG TATTGGCGAA ACCGGGATCG 600
 20 ATCACGCCAC ACAAGAAATT TGAGGCGGAG ATTTATGTGT TGTCGAAGGA 650
 AGAAGGGGGA CGCCACACAC CGTTTTTACA AGGCTATCGA CCGCAATTTT 700
 ATTTCCGCAC GACGGACGTG ACGGGCCAGT TATTGAGTTT ACCGGAGGGG 750
 ATAGAGATGG TGATGCCGGG AGATAACGTG AAAGTGACGG TTGAATTGAT 800
 TCGCGCCGTA GCGATGGATG AAGGGCTACG AT 832
 25

2) INFORMATION FOR SEQ ID NO: 46

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella hoshinae*
 40 (B) STRAIN: ATCC 33379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46

GGCGCTATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG 50
 45 TGAGCACATC CTGCTGGGTC GCCAGGTAGG CGTTCCGTAC ATCATCGTGT 100
 TCCTGAACAA GTGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT 150
 GAGATGGAAG TTCGCGAACT GCTGTCTCAG TACGATTTCC CGGGCGACGA 200
 TACGCCGGTA ATCCGCGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCCG 250
 AGTGGGAAGC GAAGATCATC GAACTGGCTG AAACGCTGGA CTCCTACATT 300
 50 CCGGAACCTG AGCGTGACAT CGACAAGCCG TTCCTGCTGC CGATCGAAGA 350
 CGTATTCTCA ATCTCTGGTC GTGGTACCGT TGTTACCGGT CGTGTAAGAC 400
 GCGGTATCAT CAAGGTAGGC GACGAAGTTG AAATCGTAGG TATCAAGCCG 450
 ACCACCAAGA CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
 CGAAGGCCGT GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTACCAAGC 550
 55 GTGACGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCACT 600
 CCGCACACCA AGTTCGAATC AGAAGTGATC ATCCTGAGCA AGGATGAAGG 650
 CGGCCGTCAT ACTCCGTTCT TCAAAGGTTA CCGTCCGCAG TTCTACTTCC 700
 GTACCACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG 750
 GTAATGCCGG GCGACAACAT CAAGATGGTT GTTACCCTGA TCCACCCGAT 800
 60 CGCCATGGAC GATGGT 816

2) INFORMATION FOR SEQ ID NO: 47

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella tarda*
 (B) STRAIN: ATCC 15947

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47

20 GGC GCG ATCC TGG TTG TTG C TGC GACTG AC GGC CCG ATGC CGC AGAC CCG 50
 TGAG CAC ATC CTG TTG GGT C GCC AGG TAGG CGT TCC GTAC ATC ATC GTGT 100
 TCCT GAA CAA GTG CGA CATG GTT GAT GACG AAG AGCTG CT GGA ACTGG TT 150
 GAG ATG GAAG TTC GCG AACT GCT GTCTC AG TAC GACTT CC CGG GCG AC GA 200
 CAC GCC GGT A ATCC GCG GTT CTG CGCTG AA AGC GCTG GA GGCGA AGCCG 250
 25 AGT GGG AAGC GAAG ATCATC GAA CTGG CTG AA ACTCTG GA CTC CTAC ATC 300
 CCG GAAC CTG AGC GTG ACAT CGACA AGCCG TTC CTG CTGC CGATCGA AGA 350
 CGT ATTCTCT ATCTCTGGCC GTGGT ACCGT TGT TACCGGT CGTGTAG AGC 400
 GCG GTATCAT CAAGGTAGGC GACGA AGTTG AAATCGTTGG TATCAAGCCG 450
 ACCACCA AGA CCACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
 30 CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTACTAAGC 550
 GTGACGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCACT 600
 CCGCACACCA AGTTCGAATC TGAAGTGATC ATCCTGAGCA AGGATGAAGG 650
 CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700
 GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG 750
 35 GTAATGCCGG GCGACAACAT CAAGATGGTT GTTACCCTGA TCCACCCGAT 800
 CGCCATGGAC GATGGTCTGC G 821

40 2) INFORMATION FOR SEQ ID NO: 48

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eikenella corrodens*
 (B) STRAIN: ATCC 23834

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48

55

CGGTGCCATC CTGGTGGTAT CCGCTGCTGA CGGCCCCATG CCTCAGACTC 50
 GCGAACACAT CCTGTTGGCT CGTCAGGTAG GTGTACCCTA CATCCTCGTA 100
 TTCATGAACA AATGCGACAT GG TAGATGAT GCCGAGCTGC TTGAGTTGGT 150
 TGAGATGGAA ATCCGCGACC TGCTCTCCAG CTATGACTTC CCTGGTGACG 200
 60 ACTGCCCGAT CGTACAAGGT TCCGCTCTCA AAGCCCTCGA AGGCGATGCC 250

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GGTTACAAAG AAAAAATCTT CGAACTAGCT GCTGCTTTGG ATAGCTACAT 300
CCCCACTCCT CAACGTGCTG TAGACAAACC CTTCTGTGTTG CCGATCGAAG 350
ACGTATTCTC TATCTCCGGC CGTGGTACCG TAGTAACCGG TCGTGTAGAG 400
CGCGGCATCA TCAAAGTAGG TGAAGAGATC GAAATCGTTG GTCTGAAGCC 450
5  CACTCAGAAA ACTACCTGTA CTGGCGTGGA AATGTTCCGC AAAGTGTGCTGG 500
ACGAAGGTCA GGCCGGTGAC AACGTAGGCG TACTGCTGCG CCGTACCAAA 550
CGTGAAGAAG TTGAGCGTGG TCAAGTATTG GCTAAACCCG GCACCATCAC 600
TCCGCACACC AAGTTCAAAG CCGAAGTATA CGTATTGAGC AAAGAAGAAG 650
GTGGTCGTCA CACCCCGTTC TTTGCCAACT ACCGTCCACA GTTCTACTTC 700
10 CGTACTACTG ACGTAACCGG TGCTGTAGAG CTGGAGCCTG GTGTAGAAAT 750
GGTTATGCCT GGTGAGAACG TAACCATCAC CGTAGAACTG ATTGCTCCGA 800
TTGCTATGGA AGAAGGTCTG CGCTTTGCGA 830

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15

2) INFORMATION FOR SEQ ID NO: 49

(i) SEQUENCE CHARACTERISTICS:

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20 (A) LENGTH: 808 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

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    (A) ORGANISM: Enterobacter aerogenes
    (B) STRAIN: ATCC 13048

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30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49

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GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACTCG 50
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT 150
35 GAGATGGAAG TTCGTGAACT GCTGTCTCAG TACGATTTCC CGGGCGACGA 200
CACTCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG 250
AGTGGGAAGC GAAAATCATC GAACTGGCTG GCTTCCTGGA TTCTTACATC 300
CCRGAAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA 350
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC 400
40 GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAC 450
ACCGCGAAAA CCACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
CGAAGGCCGT GCTGGTGAGA ACGTAGGYGT TCTGCTGCGT GGTATCAAAC 550
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CAGCATCAAG 600
CCGCACACCA AGTTCGAATC TGAAGTGATC ATCCTGTCCA AAGACGAAGG 650
45 CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700
GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGRTG 750
GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 800
CGCGATGG 808

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50

2) INFORMATION FOR SEQ ID NO: 50

(i) SEQUENCE CHARACTERISTICS:

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55 (A) LENGTH: 828 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter agglomerans*
 (B) STRAIN: ATCC 27989

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
10	TTCCTGAACA	AATGTGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ATACTCCGAT	CGTTCTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAMGCW	250
	GAGTGGGAAG	CGAAAATCAT	CGARCTGGCT	GGCCACCTGG	ATACCTATAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
15	ACGTATTCTC	CATCTCCGGT	CGCGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TYAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	TACYGCGAAA	TCAACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
20	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGTCGTCA	CACTCCGTTC	TTCAAAGGCT	ACCGTCCSCA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGTCTG	CGTTCGCA			828

25

2) INFORMATION FOR SEQ ID NO: 51

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter amnigenus*
 40 (B) STRAIN: ATCC 33072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51

	TGGCGCGATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCTATG	CCACAGACGC	50
45	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCAGGTGATG	200
	ACACTCCAAT	CATCCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAAGCA	250
	GAGTGGGAAG	CTAAAATCGT	TGAGCTGGCT	GGCTACCTGG	ATTCTTACAT	300
50	CCCGGAACCA	GAACGTGCTA	TCGATAAGCC	ATTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	TATCTCCGGC	CGTGGTACTG	TTGTAACCGG	TCGTGTAGAG	400
	CGCGGTATCG	TTAAAGTTGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTGCTAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
55	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCAG	GCTCAATCAA	600
	GCCGCACACC	AAATTCTGAAT	CTGAAGTTTA	TATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACCGG	CACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGCGACAACA	TTCAGATGGT	TGTTACCCTG	ATCCACCCAA	800
60	TCGCGATGGA	TGACGGTCTG	CGTTT			825

2) INFORMATION FOR SEQ ID NO: 52

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter asburiae*
 (B) STRAIN: ATCC 35953

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52

20	CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCAATG CCTCAGACTC	50
	GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCTTT CATCATCGTG	100
	TTCCTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT	150
	AGAGATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTC CCGGCGACG	200
	ATACTCCAAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA	250
25	GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT	300
	CCCAGAACCA GAGCGTGCGA TTGACAAGCC ATTCCTGCTG CCAATCGAAG	350
	ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG	400
	CGCGGTATCA TCAAAGTTGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA	450
	GACTGCTAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGCTG	500
30	ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA	550
	CGTGAAGAAA TCGAACGTGG TCAGGTTCTG GCGAAGCCAG GCTCAATCAA	600
	GCCACACACC AAGTTCGAAT CTGAAGTGTA CATCCTGTCC AAAGACGAAG	650
	GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCACA GTTCTACTTC	700
	CGTACAACCTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTTGAGAT	750
35	GGTAATGCCA GGCGACAACA TCAAGATGGT TGTGACTCTG ATCCACCCAA	800
	TCGCGATGGA CGACGGTCTG CG	822

40 2) INFORMATION FOR SEQ ID NO: 53

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cancerogenus*
 (B) STRAIN: ATCC 35317

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53

55

55	CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCAATG CCTCAGACTC	50
	GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCTTA CATCATCGTG	100
	TTCCTGAACA AGTGCACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT	150
	AGAAATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTC CCAGGCGACG	200
60	AACTCCAAT CGTTCGTGGT TCCGCGCTGA AAGCGCTGGA AGGCGAAGCT	250

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GAGTGGGAAG CAAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT 300
CCCAGAACCA GAGCGTGCGA TTGACAAGCC ATTCCTGCTG CCAATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG 400
CGCGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
5 TACTGCKAAA TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGCTGG 500
ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA 550
CGCGAAGAAA TCGAACGTGG TCAGGTTCTG GCGAAGCCAG GCTCAATCAA 600
GCCACACACC AAGTTCGAAT CTGAAGTGTA CATCCTGTCC AAAGACGAAG 650
GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCACA GTTCTACTTC 700
10 CGTACAACTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTAGAGAT 750
GGTAATGCCA GGCGACAACA TCAAGATGGT TGTGACGCTG ATCCACCCAA 800
TCGCGATGGA CGACGGTCTG CGTTTC 826

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15

2) INFORMATION FOR SEQ ID NO: 54

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
 (B) STRAIN: ATCC 13047

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54

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GATCCTGGTA GTAGCTGCGA CTGACGGCCC AATGCCTCAG ACTCGTGAGC 50
ACATCCTGCT GGGTCGTCAG GTAGGCGTTC CTTACATCAT CGTGTTCTCTG 100
AACAAATGCG ACATGGTTGA TGACGAAGAG CTGCTGGAAC TGGTAGAGAT 150
35 GGAAGTTCGT GAACTGCTGT CTCAGTACGA TTTCCCAGGC GACGATACCC 200
CAATCGTTCTG TGGTTCTGCT CTGAAAGCGC TGAAGGCGA CGCAGAGTGG 250
GAAGMGAAAA TCATCGAACT GGCTGGCTAC CTGGATTCTT ACATCCCAGA 300
ACCAGAGCGT GCGATTGAYA AGCCATTCTT GCTGCCAATC GAAGACGTAT 350
TCTCCATCTC CCGTCGTGGT ACCGTTGTTA CCGGTCGTGT AGAGCGCGGT 400
40 ATCATCAAAG TGGGTGAAGA AGTTGAAATC GTTGGTATCA AAGAGACTGC 450
GAAGTCTACC TGTACTGGCG TTGAAATGTT CCGCAAACCTG CTGGACGAAG 500
GCCGTGCTGG TGAGAACGTT GGTGTTCTGC TGCGTGGTAT CAAACGTGAA 550
GAAATCGAAC GTGGTCAGGT TCTGGCGAAG CCAGGCTCAA TCAAGCCACA 600
CACCAAGTTC GAATCTGAAG TGTACATCCT GTCCAAAGAC GAAGGCGGCC 650
45 GTCATACTCC GTTCTTCAAA GGCTACCGTC CACAGTTCTA CTTCCGTACA 700
ACTGACGTGA CCGGTACCAT CGAACTGCCA GAAGGCGTAG AGGTGGTAAT 750
GCCAGGCGAC AACATCAAGA TGGTTGTGAC TCTGATCCAC CCAATCGCGA 800
TGGACG 806

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50

2) INFORMATION FOR SEQ ID NO: 55

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter gergoviae*
 (B) STRAIN: ATCC 33028

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
10	TTCCTGAACA	AGTGCACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAGATGGAA	GTTCGTGAAC	TGCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ACACCCCGAT	CGTTCGCGGT	TCTGCGCTGA	AAGCGCTGGA	AGGCGACGCA	250
	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCCACCTGG	ATACCTAYAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
15	ACGTATTCTC	CATTTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAGGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	CACCGCGAAA	ACCACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTCGGCG	TTCTGCTGCG	TGGTATCAAG	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCTCCATCAA	600
20	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	CACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAAGTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAGATGGT	TGTTACCCTG	ATCCACCCGA	800
25	TCGCGATGGA	CGACGGTCTG	CGTTTC			826

2) INFORMATION FOR SEQ ID NO: 56

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter hormaechei*
 40 (B) STRAIN: ATCC 49162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCTATGC	CTCAGACCCG	50
45	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	GTTTCTTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAGATGGAAG	TTCGTGAACT	GCTGTCTCAG	TACGATTTC	CAGGCGACGA	200
	CACCCCAATC	GTTCGTGGTT	CCGCGCTGAA	AGCGCTGGAA	GGCGAMGCAG	250
	AGTGGAAGM	GAAAATCATC	GARCTGGCTG	GCTTCTGGA	TTCTTACATC	300
50	CCAGAACCAG	AGCGTGCGAT	TGACAAGCCA	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTWGAGC	400
	GCGGTATCAT	CAAAGTAGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCGAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
55	GTGAAGAAAT	CGAACGTGGT	CAGGTTCTGG	CGAAGCCAGG	CTCAATCAAG	600
	CCACACACCA	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAAGTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
	GTAATGCCAG	GCGACAACAT	CAAGATGGTT	GTGACGCTGA	TCCACCCAAT	800
60	CGCGATGGAC	GACGGTCTGC	GTTTCGCAA			829

2) INFORMATION FOR SEQ ID NO: 57

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter sakazakii*
(B) STRAIN: ATCC 29544

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57

20	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
	GAGATGGAAG	TGCGCGAGCT	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACCCCGATC	GTTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCTG	250
25	AGTGGGAAGC	GAAAATCATC	GAGCTGGCAG	GTCACCTGGA	TTCCTACATC	300
	CCGGAACCGG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCYGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAGGTTGGT	GAAGAAGTTG	AAATCGTGGG	CATCAAAGAC	450
	ACCGCGAAAT	CCACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
30	CGAAGGCCGT	GCGGGCGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCCATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGATGAAGG	650
	CGGCCGTCAC	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACRACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTTGAGATG	750
35	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCGATGGAC	GACGGTCTGC	GTTTCGCAAT	C		831

40 2) INFORMATION FOR SEQ ID NO: 58

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
(B) STRAIN: ATCC 25788

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58

55

	CGGCGCGATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACAC	50
	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	GTGTACCATA	CATCGTTGTT	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTGTCAGA	ATATGACTTC	CCAGGCGACG	200
60	ATGTTCCCTGT	AATCGCTGGT	TCTGCTTTGA	AAGCTCYTGA	AGGCGATGCT	250

	TCATACGAAG	AAAAAATCAT	GGAATTAATG	GCTGCAGTTG	ACGAATACGT	300
	TCCAACCTCCA	GAACGTGACA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTGCTGA	450
5	AGAAACTGCT	AAAACAACCTG	TAACCTGGTGT	TGAAATGTTC	CGTAAATTGT	500
	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	ACGTGGTGTT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAG	CTGGTACAAT	600
	CACACCTCAT	ACAAAATTTA	AAGCTGAAGT	TTACGTTTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCACACACCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
10	TTCCGTACAA	CTGACGTAAC	TGGTGTGTGT	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTAACAAT	CGACGTTGAA	TTGATCCACC	800
	CAATCGCTAT	CGAAGACGGA	ACTCGTTTCT	CAATT		835

15

2) INFORMATION FOR SEQ ID NO: 59

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus cecorum*
 (B) STRAIN: ATCC 43198

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59

	GGTGCTATCT	TAGTAGTATC	TGCTGCTGAT	GGTCCTATGC	CACAAACTCG	50
	TGAACACATT	CTTTTATCAC	GTAACGTTGG	TGTTCCATAC	ATCGTTGTTT	100
	TCTTAAACAA	AGTTGATATG	GTTGACGACG	AAGAATTATT	AGAATTAGTT	150
35	GAAATGGAAG	TACGTGACTT	ATTAAC TGAA	TACGACTTCC	CAGGAGACGA	200
	TGTTCCCTGTA	ATCGCTGGTT	CTGCATTAAA	AGCTTTAGAA	GGCGACCCAT	250
	CTTACGAAGA	AAAAATCTTA	GAATTAATGG	CTGCAGTTGA	CGAATACATC	300
	CCAACCTCCAG	AACGTGACAA	CGATAAACCA	TTCATGATGC	CAGTCGAAGA	350
	CGTATTTTCA	ATCACTGGTC	GTGGTACTGT	TGCTACAGGT	CGTGTTGAAC	400
40	GTGGACAAGT	ACGTGTTGGT	GACGAAGTTG	AAATAGTTGG	TATCCATGAT	450
	GAAATTTCTA	AAACAACAGT	TACTGGTGTT	GAAATGTTCC	GTAAATTATT	500
	AGATTACGCT	GAAGCTGGAG	ACAACATCGG	TGCATTATTA	CGTGGTGTGG	550
	CTCGTGAAGA	TATCCAACGT	GGTCAAGTAT	TAGCTAAACC	AGGTTCAATC	600
	ACTCCACATA	CAAAATTCAC	TGCTGAAGTG	TACGTTTTTA	CTAAAGAAGA	650
45	AGGTGGACGT	CATACTCCAT	TCTTCACTAA	CTACCGTCCA	CAATTCTACT	700
	TCCGTACAAC	TGACGTTACA	GGTGTAGTTA	ACTTACCAGA	AGGTACTGAA	750
	ATGGTTATGC	CTGGTGATAA	CGTAACTATG	GAAGTTGAAT	TAATCCACCC	800
	AATCGCTATC	GAAGACGGAA	CTCGTT			826

50

2) INFORMATION FOR SEQ ID NO: 60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus dispar*
 (B) STRAIN: ATCC 51266

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60

	CGGCGCGATC	TTGGTAGTAT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CCTATTGTCA	CGTAACGTTG	GTGTTCTTA	CATCGTCGTT	100
10	TTCTTGAACA	AAATGGACAT	GGTTGATGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTGTCAGA	ATACGACTTC	CCAGGCGACG	200
	ACACTCCAGT	TATCGCAGGT	TCAGCTTTGA	AAGCCTTAGA	AGGCGACGCT	250
	TCATATGAAG	AAAAAATCTT	AGAATTAATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GTTCGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
15	ATGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCAACTGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTAG	GTATCGCTGA	450
	AGAAACTGCT	AAAACTACTG	TAACAGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TGGATTACGC	TGAAGCTGGC	GACAACATTG	GTGCATTATT	ACGTGGTGTG	550
	GCTCGTGAAG	ATATCCAACG	TGGTCAAGTA	TTATCAAAAC	CAGGTTCAAT	600
20	CACTCCACAT	ACAAAATTTG	CGGCAGAAGT	TTACGTTTAA	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGCCC	ACAATTCTAC	700
	TTCCGTACAA	CTGACGTAAC	AGGTGTTGTT	GAATTACCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGATA	ACGTTACTAT	GGACGTTGAA	TTAATCCACC	800
25	CAATCGCGAT	CGAAGACGGT	ACTCGTTTCT	CAATC		835

2) INFORMATION FOR SEQ ID NO: 61

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus durans*
 40 (B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61

	CGGAGCTATC	TTAGTAGTTT	CTGCTGCTGA	TGGCCCTATG	CCTCAAACCTC	50
45	GTGAACATAT	CCTATTATCT	CGTCAAGTTG	GTGTTCTTA	CATCGTYGTA	100
	TTCTTGAACA	AAGTAGATAT	GGTCGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTAACAGA	ATACGAATTC	CCTGGTGACG	200
	ATGTTCTGT	AATCGCTGGT	TCAGCTTTGA	AAGCTTTAGA	AGGCGACGCT	250
	TCATACGAAG	AAAAAATCCT	TGAATTAATG	GCTGCAGTTG	ACGAATATAT	300
50	CCCAACTCCA	GAACGTGACA	ACGACAAACC	ATTCATGATG	CCAGTTGAAG	350
	ATGTATTCTC	RATCACTGGT	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGTTGTA	GATATCGTTG	GTATCGCAGA	450
	AGAAACAGCT	CAAACAACAG	TTACTGGTGT	TGAAATGTTT	CGTAAATTAT	500
	TAGRCTACGC	TGAAGCTGGA	GACAACATTG	GTGCTTTACT	ACGTGGTGTG	550
55	GCACGTGAAG	ACATCCAACG	TGGACAAGTT	TTAGCTAAAC	CAGGTACAAT	600
	CACKCCTCAT	ACAAAATTCT	CTGCAGAAGT	ATACGTGTTG	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACAA	CTGACGTAAC	AGGTGTTGTT	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGCGACA	ACGTAACAAT	GGAAGTTGAA	TTAATCCACC	800
60	CAATCGCTAT	CGAAAATGGT	ACTAAATTCT	CAATC		835

2) INFORMATION FOR SEQ ID NO: 62

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R610

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62

20	AGTAGTTTCT	GCTGCTGATG	GTCCTATGCC	TCAAACACGT	GAACATATCT	50
	TATTATCACG	TAACGTTGGT	GTACCATAACA	TCGTTGTATT	CTTAAACAAA	100
	ATGGATATGG	TTGATGACGA	AGAATTATTA	GAATTAGTAG	AAATGGAAGT	150
	TCGTGACTTA	TTATCAGAAT	ACGATTTCCT	AGGCGATGAT	GTTCCAGTTA	200
	TCGCAGGTTT	TGCTTTGAAA	GCTTTAGAAG	GCGACGAGTC	TTATGAAGAA	250
25	AAAATCTTAG	AATTAATGGC	TGCAGTTGAC	GAATATATCC	CAACTCCAGA	300
	ACGTGATACT	GACAAACCAT	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	350
	TCACTGGACG	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	TGGTGAAGTT	400
	CGCGTTGGTG	ACGAAGTTGA	AATCGTTGGT	ATTAAAGACG	AAACATCTAA	450
	AACAACGTGT	ACAGGTGTTG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	500
30	AAGCAGGCGA	CAACATCGGT	GCTTTATTAC	GTGGTGTAGC	ACGTGAAGAT	550
	ATCGAACGTG	GACAAGTATT	AGCTAAACCA	GCTACAATCA	CTCCACACAC	600
	AAAATTCAAA	GCTGAAGTAT	ACGTATTATC	AAAAGAAGAA	GGCGGACGTC	650
	ACACTCCATT	CTTCACTAAC	TACCGTCCTC			680

35

2) INFORMATION FOR SEQ ID NO: 63

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R487

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63

	AGTAGTTTCT	GCTGCTGATG	GTCCTATGCC	TCAAACACGT	GAACATATCT	50
	TATTATCACG	TAACGTTGGT	GTACCATAACA	TCGTTGTATT	CTTAAACAAA	100
55	ATGGATATGG	TTGATGACGA	AGAATTATTA	GAATTAGTAG	AAATGGAAGT	150
	TCGTGACTTA	TTATCAGAAT	ACGATTTCCT	AGGCGATGAT	GTTCCAGTTA	200
	TCGCAGGTTT	TGCTTTGAAA	GCTTTAGAAG	GCGACGAGTC	TTATGAAGAA	250
	AAAATCTTAG	AATTAATGGC	TGCAGTTGAC	GAATATATCC	CAACTCCAGA	300
	ACGTGATACT	GACAAACCAT	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	350
60	TCACTGGACG	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	TGGTGAAGTT	400

	CGCGTTGGTG	ACGAAGTTGA	AATCGTTGGT	ATTAAAGACG	AAACATCTAA	450
	AACAACTGTT	ACAGGTGTTG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	500
	AAGCAGGCGA	CAACATCGGT	GCTTTATTAC	GTGGTGTAGC	ACGTGAAGAT	550
	ATCGAACGTG	GACAAGTATT	AGCTAAACCA	GCTACAATCA	CTCCACACAC	600
5	AAAATTCAAA	GCTGAAGTAT	ACGTATTATC	AAAAGAAGAA	GGCGGACGTC	650
	ACACTCCATT	CTTCACTAAC	TACCGTCCTC			680

10 2) INFORMATION FOR SEQ ID NO: 64

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64

25	AGTAGTTTCT	GCTGCTGACG	GCCCAATGCC	TCAAACCTCGT	GAACACATCC	50
	TATTGTCTCG	TCAAGTTGGT	GTTCCCTTACA	TCGTTGTATT	CTTGAACAAA	100
	GTAGACATGG	TTGATGACGA	AGAATTACTA	GAATTAGTTG	AAATGGAAGT	150
	TCGTGACCTA	TTAACAGAAT	ACGAATTCCC	TGGTGACGAT	GTTCCCTGTAG	200
30	TTGCTGGATC	AGCTTTGAAA	GCTCTAGAAG	GCGACGCTTC	ATACGAAGAA	250
	AAAATTCTTG	AATTAATGGC	TGCAGTTGAC	GAATACATCC	CAACTCCAGA	300
	ACGTGACAAC	GACAAACCAT	TCATGATGCC	AGTTGAAGAC	GTGTTCTCAA	350
	TTACTGGACG	TGGTACTGTT	GCTACAGGTC	GTGTTGAACG	TGGACAAGTT	400
	CGCGTTGGTG	ACGAAGTTGA	AGTTGTTGGT	ATTGCTGAAG	AAACTTCAAA	450
35	AACAACAGTT	ACTGGTGTTG	AAATGTTCCG	TAAATTGTTA	GACTACGCTG	500
	AAGCTGGAGA	CAACATTGGT	GCTTTACTAC	GTGGTGTTGC	ACGTGAAGAC	550
	ATCCAACGTG	GACAAGTTTT	AGCTAAACCA	GGTACAATCA	CACCTCATA	600
	AAAATTCTCT	GCAGAAGTAT	ACGTGTTGAC	AAAAGAAGAA	GGTGGACGTC	650
40	ATACTCCATT	CTTCACTAAC	TACCGTCCTC	AATTT		685

2) INFORMATION FOR SEQ ID NO: 65

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 55 (B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65

60	CGGCGCGATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCTAYG	CCTCAAACAC	50
	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	GTGTACCATA	CATCGTTGTT	100

	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTGTCAGA	ATATGACTTC	CCAGGCGACG	200
	ATGTTCTGT	AATCGCTGGT	TCTGCTTTGA	AAGCTCTTGA	AGGCGATGCT	250
	TCATACGAAG	AAAAAATCAT	GGAATTAATG	GCTGCAGTTG	ACGAATACGT	300
5	TCCAACCTCA	GAACGTGACA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTGCTGA	450
	AGAAACTGCT	AAAACAACCTG	TAACCTGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	ACGTGGGGTT	550
10	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTAGCTAAAG	CTGGTACAAT	600
	CACACCTCAT	ACAAAATTTA	AAGCTGAAGT	TTACGTTTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTGTGT	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGTGATA	AMGTAACAAT	CGACGTTGAA	TTGATCCACC	800
15	CAATCGCTAT	CGAAGACGGA	ACTCG			825

2) INFORMATION FOR SEQ ID NO: 66

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66

35	TCCTATGCCT	CAAACCTCGTG	AACACATCTT	GTTATCACGT	AACGTTGGCG	50
	TACCATACAT	CGTTGTTTTT	TTGAACAAAA	TGGATATGGT	TGATGACGAA	100
	GAATTGCTAG	AATTAGTTGA	AATGGAAGTT	CGTGACCTAT	TGTCTGAGTA	150
	TGACTTCCCA	GGCGACGATG	TTCCTGTAAT	CGCCGTTTCT	GCTTTGAAAG	200
	CTCTTGAAGG	AGATCCTTCA	TACGAAGAAA	AAATCATGGA	ATTGATGGCT	250
40	GCAGTTGACG	AATACGTTCC	AACTCCAGAA	CGTGATACTG	ACAAACCATT	300
	CATGATGCCA	GTCGAAGACG	TATTCTCAAT	CACTGGACGT	GGTACTGTTG	350
	CTACAGGCCG	TGTTGAACGT	GGACAAGTTC	GCGTTGGTGA	TGAAGTAGAA	400
	ATCGTTGGTA	TTGCTGACGA	AACTGCTAAA	ACAACTGTAA	CAGGTGTTGA	450
	AATGTTCCGT	AAATTGTTAG	ACTATGCTGA	AGCAGGGGAT	AACATTGGTG	500
45	CATTGCTACG	TGGGGTTGCT	CGTGAAGACA	TCCAACGTGG	ACAAGTATTG	550
	GCTAAAGCTG	GTACAATCAC	ACCTCATACA	AAATTCAAAG	CTGAAGTTTA	600
	TGTTTTGACA	AAAGAAGAAG	GTGGACGTCA	CACTCC		636

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2) INFORMATION FOR SEQ ID NO: 67

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus hirae*

(B) STRAIN: ATCC 8043

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67

	CGGAGCTATC	TTAGTAGTTT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACCTC	50
	GTGAACATAT	CCTAYTATCT	CGTCAAGTTG	GTGTTCCATA	CATCGTTGTA	100
	TTCTTGAACA	AAGTAGATAT	GGTTGACGAC	GAAGAATTAC	TAGAATTAGT	150
10	TGAAATGGAA	GTTCGTGACT	TATTAACAGA	ATACGAATTC	CCTGGTGACG	200
	ATGTTCCCTGT	AGTTGCTGGT	YCAGCTTTGA	AAGCTTTAGA	AGGCGACGCT	250
	TCATACGAAG	AAAAAATCCT	TGAATTGATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGACA	ACGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
15	CGTGGACAAG	TTCGCGTTGG	TGACGTTGTA	GATATCGTTG	GTATCGCAGA	450
	AGAAACAGCT	CAAACAACAG	TTACTGGTGT	TGAAATGTTT	CGTAAATTAT	500
	TAGACTACGC	TGAAGCTGGA	GACAACATTG	GTGCTTTACT	ACGTGGTGTT	550
	GCACGTGAAG	ACATCCAACG	TGGACAAGTT	TTAGCTAAAC	CAGGTACAAT	600
	CACACCTCAT	ACAAAATTCT	CTGCAGAAGT	ATACGTGTTG	ACAAAAGAAG	650
20	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACRA	CTGACGTAAC	AGGTGTTGTT	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGCGACA	ACGTAACAAT	GGAAGTTGAA	TTAATCCACC	800
	CAATCGCTAT	CGAAAACGGT	ACTAAATTCT	CAATC		835

25

2) INFORMATION FOR SEQ ID NO: 68

(i).SEQUENCE CHARACTERISTICS:

30	(A)	LENGTH: 835 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus mundtii*

(B) STRAIN: ATCC 43186

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68

	CGGAGCAATC	TTAGTTGTTT	CTGCTGCTGA	CGGCCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CCTATTATCT	CGTCAAGTTG	GTGTACCATA	CATCGTTGTA	100
45	TTCTTGAACA	AAGTAGATAT	GGTTGATGAC	GAAGAATTAC	TTGAATTAGT	150
	TGAAATGGAA	GTTCGTGACC	TATTAACAGA	ATACGAATTC	CCTGGTGACG	200
	ATGTTCCCTGT	AATCGCTGGT	TCAGCTTTAA	GAGCTTTAGA	AGGCGACGCT	250
	KCATACGAAG	AAAAAATTCT	TGAATTGATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGATA	ACGACAAACC	ATTCATGATG	CCAGTTGAGG	350
50	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	ACGTGTTGAA	400
	CGTGGACAAG	YTCGTGTTGG	TGACGTTATC	GATATCGTTG	GTATCGCAGA	450
	AGAAACAGCT	CAAACAACCTG	TAACCTGGTGT	TGAAATGTTT	CGTAAATTAT	500
	TAGACTACGC	TGAAGCAGGC	GATAACATTG	GTGCGTTACT	ACGTGGTGTT	550
	TCACGTGAAG	ACATCCAACG	TGGTCAAGTT	TTAGCTAAAC	CAGGTACAAT	600
55	CACACCTCAT	ACAAAATTCT	CTGCAGAAGT	ATACGTGTTG	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	ACAATTCTAC	700
	TTCYGTACGA	CTGACGTAAC	TRGTGTTGTY	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGCGACA	ACGTAACAAT	GGAAGTTGAA	TTAATCCACC	800
	CAATCGCTAT	CGAAAATGGT	ACTAAATTCT	CAATC		835

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2) INFORMATION FOR SEQ ID NO: 69

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus pseudoavium*
 15 (B) STRAIN: ATCC 49372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69

	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCTATG	CCTCAAACAC	50
20	GTGAACACAT	CTTGTTATCT	CGTAACGTTG	GTGTTTCCTTA	CATCGYTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTGTCAGA	ATACGATTTC	CCAGGCGACG	200
	ACACTCYAGT	TATCGCTGGT	TCAGCYTTGA	AAGCTTTAGA	AGGCGACCCT	250
	TCATACRAAG	AAAAAATCTT	AGAATTAATG	SCTGCTGTTG	ACGAATACAT	300
25	CCCAACACCA	GTTCGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCAACTGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTAG	GTATCGCTGA	450
	AGAAACTGCT	AAAACAACCTG	TTACAGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACTACGC	TGAAGCAGGC	GATAACATCG	GTGCATTATT	ACGTGGTGTT	550
30	GCACGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAC	CAGCTTCAAT	600
	CACTCCACAT	ACAAAATTCT	CTGCAGAAGT	TTACGTTTTA	ACTAAAGAAG	650
	AAGGCGGGCG	TCACACTCCG	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTGTGT	GATCTACCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACAT	GGAAGTTGAA	TTAATCCACC	800
35	CAATCGCGAT	CGAAGACGGA	ACTCGTTTCT	CTATTC		836

2) INFORMATION FOR SEQ ID NO: 70

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus raffinosus*
 50 (B) STRAIN: ATCC 49427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70

55	CGGAGCTRTC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CTTGTTATCT	CGTAACGTTG	GTGTTTCCTTA	CATCGTTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGACGAT	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTAACCTGA	ATACGACTTC	CCAGGCGACG	200
	ACACTCCAGT	TATCGCAGGT	TCAGCTTTGA	AAGCCTTAGA	AGGCGACGCT	250
60	TCATACGAAG	AAAAAATCTT	AGAATTAATG	GCTGCTGTTG	ATGAATACAT	300

	CCCAACACCA	GTTCGTGATA	CTGACAAACC	ATTCATGATG	CCAGYGGAAG	350
	ACGTAYTCTC	AATCACTGGT	CGTGGAAGT	TTGCAACTGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTAG	GTATTGCTGA	450
	AGAAACTGCT	AAAACAACTG	TTACAGGTGT	TGAAATGTTT	CGTAAATTGT	500
5	TGGATTACGC	TGAAGCGGGC	GACAACATTG	GTGCATTATT	ACGTGGTGTT	550
	GCACGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAC	CAGCTTCAAT	600
	CACTCCACAT	ACAAAATTCT	CTGCAGAAGT	TTACGTTTTA	ACTAAAGAAG	650
	AAGGCGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTAGTT	GATCTACCAG	AAGGTACTGA	750
10	AATGGTAATG	CCTGGTGATA	ACGTAACAT	GGAAGTTGAA	TTAATCCACC	800
	CAATCGCGAT	CGAAGACGGA	ACTCGTTTCT	CTATT		835

15 2) INFORMATION FOR SEQ ID NO: 71

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus saccharolyticus*
 (B) STRAIN: ATCC 43076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71

30	CGGCGCGATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CTTGTTATCT	CGTAACGTAG	GTGTTCTTGA	CATCGTTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCGTGACT	TATTATCAGA	ATACGATTTC	CCAGGCGATG	200
35	ACACTCCAGT	TATTGCAGGT	TCTGCTTTGA	AAGCTTTAGA	AGGCGATCCA	250
	GTTTACGAAG	AAAAAATCTT	CGAATTAATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGATA	CTGAAAACCC	ATTCATGATG	CCAGTTGAGG	350
	ATGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGTTGTA	GAAATCGTTG	GTATCGACGA	450
40	AGAAACAGCT	CAAACTACTG	TAACAGGTGT	TGAAATGTTT	CGTAAATTAT	500
	TAGACTACGC	TGAAGCAGGC	GATAACATCG	GTGCTTTATT	ACGTGGGGTT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTAGCTAAAC	CAGGAACAAT	600
	CACTCCTCAT	ACAAAATTCT	TAGCTGAAGT	TTACGTTTTA	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	TCAATTCTAC	700
45	TTCCGTACAA	CTGACGTAAC	TGGTGTGTTA	GAATTACGCG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGACA	ACGTAACAT	CGACGTTGAA	TTAATCCACC	800
	CAATCGCTAT	CGAAGACGGA	ACTCGTTTCT	CTATT		835

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2) INFORMATION FOR SEQ ID NO: 72

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus solitarius*
 (B) STRAIN: ATCC 49428

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72

	GAGCTATCTT	GGTAGTTTCT	GCAGCTGATG	GCCCAATGCC	ACAAACTCGT	50
	GAACATATTT	TGTTGTCACG	TAATGTAGGT	GTACCTTACA	TCGTTGTGTT	100
	CTTGAACAAA	ATGGATATGG	TTGATGACGA	AGAATTACTT	GAGTTAGTTG	150
10	AAATGGAAGT	ACGTGATCTA	TTATCTGAAT	ACGACTTCCC	AGGAGATGAT	200
	ACTCCAGTTA	TTTCCGGTTC	AGCTTTGAAA	GCTTTAGAAG	GCGACGAAGA	250
	ATATGAACAA	AAAATTATGG	ACTTAATGGA	TGCAGTTGAT	GACTACATTC	300
	CAACTCCTGA	ACGTGACCAT	GACAAACCAT	TCATGATGCC	AATTGAAGAT	350
	GTATTTTCAA	TTACAGGCCG	TGGTACTGTT	GCTACAGGAC	GTGTTGAACG	400
15	CGGGACTATC	AAAGTCGGCG	ATGAAGTTGA	CATTATTGGT	ATTCATGAAG	450
	ACGTTAAAAA	GACAACAGTT	ACTGGTGTAG	AAATGTTCCG	TAAATTGTTG	500
	GACTACGCTG	AAGCAGGCCG	TAACATTGGT	ACTTTGTTAC	GTGGTGTTC	550
	TCGTGATGAT	ATCGAACGTG	GTCAAGTATT	AGCTAAACCA	GGTTCAATCA	600
	CACCACATAC	AAGATTCTCT	GCTGAAGTTT	ATGTTTTGAC	TAAAGAAGAA	650
20	GGCGGACGTC	ATACTCCATT	CTTCTCAAAC	TATCGTCCTC	AATTCTACTT	700
	CCGTACAAC	GATATCACTG	GTGTCATTGA	ATTGCCAGAA	GGTACTGAAA	750
	TGGTAATGCC	AGGTGATAAT	GTAACAATGG	ATGTTGAATT	AATCCACCCA	800
	GTCGCTATCG	AAGAAGGAAC	TCG			823

25

2) INFORMATION FOR SEQ ID NO: 73

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73

	CGGTGCAATC	TTGGTCGTAT	CAGCGACAGA	TGGCCCAATG	CCACAAACAC	50
	GGGAGCATAT	TTTGCTTTCT	CGTCAAGTGG	GTGTGAAACA	TTTGATCGTC	100
45	TTTTTGAATA	AGACGGACCT	TGTCGATGAT	GACGAGTTGA	TCGATTTAGT	150
	TGAAATGGAA	GTCAGAGAAT	TGCTGACTGA	ATATGATTTT	CCTGGCGACG	200
	ACATTCCTGT	GATCAAGGGC	TCTGCGTTAA	AAGCCTTGGA	AGGGGACCCA	250
	GATGCTGAAG	CAGCGATCTT	AACGCTGATG	GATACAGTAG	ATGAATATAT	300
	CCCAACGCCA	GAACGTGATA	CTGACAAACC	ATTGTTGTTA	CCGATCGAAG	350
50	ATGTCTTTTC	GATCACAGGA	CGGGGGACCG	TTGCTTCTGG	TCGGATCGAT	400
	CGCGGCATGG	TAAAAGTCGG	GGATGAAGTA	GAAATCGTCG	GAATCAAACC	450
	TGAAACACAA	AAAGCAGTCG	TGACAGGGGT	AGAAATGTTC	CGCAAAACGA	500
	TGGACTTCGG	AGAAGCTGGC	GATAACGTAG	GGGTATTGTT	ACGGGGCATC	550
	ACCCGTGATG	AAATTGAACG	TGGCCAAGTG	TTAGCAAAAC	CAGGTTCTAT	600
55	CACACCGCAT	ACGAAATTCC	AAGCGGAAGT	CTATGTGTTG	ACAAAAGAAG	650
	AAGGCGGTCG	CCATACCCCA	TTCTTTAATA	ATTATCGCCC	ACAATTTTAC	700
	TTCCGTACAA	CGGACGTAAC	TGGGAATATC	GTTTACCAG	AAGGAACGGA	750
	AATGGTGATG	CCTGGTGACA	ACGTAACGAT	CGATGTGGAA	TTGATCCATC	800
	CGATCGCTGT	AGAAAATGGA	ACGACCTTCT	CGATT		835

60

2) INFORMATION FOR SEQ ID NO: 74

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus saprophyticus*
 15 (B) STRAIN: ATCC 15305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74

20	TAACGGGCGT CTCGATAGAA AAACACGTGA AAATCCCAAT GATTATAAAC	50
	AATCAATATA CGATTTTGCT GAAGCTGTAA CAAAAGGTAT TAAGGAACAA	100
	ACAAATAAAA ATTAATAGGC AACTTAACCA GAATCGTTAA AACTATATGA	150
	AGATTCTGGT TTTTAAATT CAAAAGTTT TCTAAAAAAT TTAATTGCTT	200
	TTTAAAGTAT AGGTATAAAA TACGATTGAT TAAAACAGTA AAGGAAATGA	250
	ATCATGAAAC AATTAATAA GCCTTTATAC TTTTACCTAT TACTTTTAT	300
25	TACAACAACG CTGATTGGCG CGTTACTATT ATATTGCCA ATCACAGGTA	350
	AACATCCTAT TGATTTTGTG GACGCCCGTT	380

30 2) INFORMATION FOR SEQ ID NO: 75

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 666 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus flavescens*
 40 (B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75

45	GCAATCTTGG TCGTATCAGC GACAGATGGC CCAATGCCAC AAACACGGGA	50
	GCATATTTTG CTTTCTCGTC AAGTGGGTGT GAAACATTTG ATCGTCTTTT	100
	TGAATAAGAC GGACCTTGTC GATGATGACG AGTTGATCGA TTAGTTGAA	150
	ATGGAAGTCA GAGAATTGCT GACTGAATAT GATTTTCCTG GCGACGACAT	200
50	TCCTGTGATC AAGGGCTCTG CGTTAAAAGC CTTGGAAGGG GACCCAGATG	250
	CTGAAGCAGC GATCTTAACG CTGATGGATA CGGTAGATGA ATATATCCCA	300
	ACGCCAGAAC GTGATACTGA CAAACCATTG TTGTTACCGA TCGAAGATGT	350
	CTTTTCGATC ACAGGACGGG GGACCGTTGC TTCTGGTCGG ATCGATCGCG	400
	GCATGGTAAA AGTCGGGGAT GAAGTAGAAA TCGTCGGAAT CAAACCTGAA	450
55	ACACAAAAG CAGTCGTGAC AGGGGTAGAA ATGTTCCGCA AAACGATGGA	500
	CTTCGGAGAA GCTGGCGATA ACGTAGGGGT ATTGTTACGG GGCATCACCC	550
	GTGATGAAAT TGAACGTGGC CAAGTGTTAG CAAAACCAGG TTCTATCACA	600
	CCGCATACGA AATTCCAAGC GGAAGTCTAT GTGTTGACAA AAGAAGAAGG	650
60	CGGTCGCCAT ACCCCA	666

2) INFORMATION FOR SEQ ID NO: 76

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus gallinarum*
 15 (B) STRAIN: ATCC 49573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76

	TGGTGCGATT	TTAGTTGTAT	CCGCAACAGA	TGGTCCAATG	CCTCAAACCC	50
20	GGGAACATAT	CTTGCTTTTCG	AGACAAGTTG	GTGTGAAACA	TCTGATTGTT	100
	TTCTTGAACA	AAATCGATTT	AGTCGATGAC	GAAGAATTGA	TTGATTTAGT	150
	AGAAATGGAA	GTAAGAGAAC	TGCTATCTGA	ATATAATTTT	CCAGGGGATG	200
	ACATTCCTGT	TATCAAAGGT	TCGGCATTAA	AAGCGTTGGA	AGGAGACCCT	250
	GATGCAGAAG	CTGCCATCAT	GGAATTAATG	GATACAGTAG	ACAGCTATAT	300
25	CCCAACACCT	GAGCGTGATA	CAGACAAACC	ATTACTCTTG	CCAGTTGAAG	350
	ATGTCTTTTC	GATTACTGGA	CGAGGAACAG	TTGCTTCCGG	ACGGATCGAT	400
	CGGGGAACAG	TTCGGGTAGG	CGATGAAGTA	GAAATCGTCG	GTATCAAACC	450
	TGAAACCCAA	AAAGCTGTAG	TGACAGGCGT	CGAAATGTTC	CGCAAGACGA	500
	TGGACTTTGG	GGAAGCCGGT	GACAATGTAG	GTGTCTTGCT	GAGAGGGATC	550
30	ACTCGTGACG	AAATTGAACG	AGGACAAGTG	TTGGCTAAAC	CAGGTTCGAT	600
	CACACCACAT	ACAAAATTCC	AAGCAGAAGT	TTATGTATTG	ACGAAAGAAG	650
	AAGGTGGTCG	TCATACACCA	TTCTTCAACA	ACTATCGTCC	ACAATTTTAT	700
	TTCCGTACAA	CGGATGTGAC	AGGGAACATT	ACATTGCCTG	AAGGAACAGA	750
	A					751

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2) INFORMATION FOR SEQ ID NO: 77

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 45 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Ehrlichia canis*
 50 (B) STRAIN: Florida

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77

	TGCAGCAATA	TTAGTAGTGT	CTGCAACTGA	TGGAGCAATG	CCACAAACAA	50
55	GAGAACATAT	ATTATTAGCA	AAGCAAGTAG	GTGTAAAAGA	TATAGTAGTG	100
	TGGATGAATA	AGTGTGATGT	TGTAGATGAT	GAAGAAATGT	TGTCATTAGT	150
	TGAAATGGAA	ATAAGGGAAT	TGTTATCAAA	ATATGGGTAT	CCTGGGGATG	200
	ATATAGATGT	AGTTAGAGGA	TCTGCAGTTA	AAGCATTAGA	AGAAGAAACA	250
	GGCTCAGGTG	TGTGGAGTGA	AAAAATAATG	GAATTGATGA	ATGCTTTAGA	300
60	AAAAATAAGT	TTACCAGTAA	GAGAAAAAGA	TAAGCCATTT	TTAATGTCAA	350

	TAGAAGATGT	GTTTTCAATA	CCTGGAAGAG	GTACAGTAGT	AACAGGAAGA	400
	ATAGAAAGAG	GAGTAATTAG	AGTAGGGGAT	AAAATAGAGA	TAGTAGGATT	450
	GCGTGAGATA	CAAAGTACAG	TATGTACAGG	TGTTGAAATG	TTTCATAAAG	500
	CATTAGATGC	AGGAGAAGCA	GGGGATAATG	CTGGAATATT	GTTAAGAGGG	550
5	ATAAAAAAAG	AAGATGTAGA	AAGAGGGCAA	GTATTGAGTG	CACCTGGACA	600
	GATACATTCA	TATAAGAGAT	TTAAGGCAGA	GGTATATATA	TTGAAAAAAG	650
	AAGAAGGAGG	AAGACATACT	CCATTTTTCT	CAAATTACCA	GCCGCAATTT	700
	TATGTTAGAA	CAACAGATGT	AACAGGGAAT	ATAAAGTTAC	CAGAAGGAGT	750
	AGAAATGGTA	ATGCCAGGGG	ATAATATAAA	TATCGAAGTG	AGTTTGGATA	800
10	AGCCTGTTGC	TATTGATCAA	GGATTGAGAT	TTGC		834

2) INFORMATION FOR SEQ ID NO: 78

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 23511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78

30	CGGCGCGATC	CTGGTAGTTG	CTGCGACTGA	CGGCCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ACACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
35	GAGTGGGAAG	CGAAAATCCT	GGAAGTGGCT	GGCTTCCTGG	ATTCTTAYAT	300
	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
40	ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
45	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGT				817

50 2) INFORMATION FOR SEQ ID NO: 79

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia fergusonii*
 (B) STRAIN: ATCC 35469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79

5
 CGATCCTGGT AGTTGCTGCG ACTGACGGCC CGATGCCGCA GACTCGTGAG 50
 CACATCCTGC TGGGTCGTCA GGTAGGCGTT CCGTACATCA TCGTGTTCCCT 100
 GAACAAGTGC GACATGGTTG ATGACGAAGA GCTGCTGGAA CTGGTTGAAA 150
 TGGAAAGTTCG TGAACCTCTG TCTCAGTACG ACTTCCC GGG CGACGACACT 200
 10 CCGATCGTTC GTGGTTCTGC TCTGAAAGCG CTGGAAGGCG ACGCAGAGTG 250
 GGAAGCGAAA ATCCTGGAAC TGGCTGGCTT CCTGGATTCT TACATTCCGG 300
 AACCAGAGCG TGCGATTGAC AAGCCGTTCC TGCTGCCGAT CGAAGACGTG 350
 TTCTCCATCT CCGGTCGTGG TACCGTTGTT ACCGGTCGTG TAGAACGCGG 400
 TATCATCAAA GTTGGTGAAG AAGTTGAAAT CGTTGGTATC AAAGAGACTC 450
 15 AGAAGTCTAC CTGTACTGGC GTTGAAATGT TCCGCAAAC TCTGGACGAA 500
 GGCCGTGCTG GTGAGAACGT AGGTGTTCTG CTGCGTGGTA TCAAACGTGA 550
 AGAAATCGAA CGTGGTCAGG TACTGGCTAA GCCGGGCACC ATCAAGCCGC 600
 ACACCAAGTT CGAATCTGAA GTGTACATTC TGTCCAAAGA TGAAGGCGGT 650
 CGTCATACTC CGTTCCTTCAA AGGCTACCGT CCGCAGTTCT ACTTCCGTAC 700
 20 TACTGACGTG ACTGGTACCA TCGAACTGCC GGAAGGCGTA GAGATGGTAA 750
 TGCCGGGCGA CAACATCAAA ATGGTTGTTA CCCTGATCCA CCCGATCGCG 800
 ATGGACGACG GTCTGCGTTT CGCAA 825

25

2) INFORMATION FOR SEQ ID NO: 80

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 829 bases
 30 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia hermannii*
 (B) STRAIN: ATCC 33650

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80

GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG 50
 TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 100
 TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT 150
 45 GAGATGGAAG TTCGCGAACT GCTGTCCCAG TACGATTTCC CGGGCGACGA 200
 CACCCCGATC GTTCGTGGTT CCGCGCTGAA AGCGCTGGAA GGCGAAGCAG 250
 AGTGGGAAGA GAAAATCATC GAACTGGCTG GCTACCTGGA TTCCTATATC 300
 CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CTATCGAAGA 350
 CGTATTCTCC ATCTCCGGCC GTGGTACCGT TGTTACCGGT CGTGTAAGC 400
 50 GCGGTATCAT CAAAGTGGGT GAAGAAGTTG AAATCGTGGG TATCAAAGAT 450
 ACTGCGAAAT CAACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
 CGAAGGCCGT GCGGGCGAGA ACGTGGGTGT TCTGCTGCGT GGTATCAAAC 550
 GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG TTCCATCAAG 600
 CCKCACACCA AGTTCGAATC TGAAGTGATC ATTCTGTCCA AAGACGAAGG 650
 55 CGGCCGTAC ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700
 GTACAAGTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTTGAGATG 750
 GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 800
 CGCGATGGAC GACGGTCTGC GTTTCGCAA 829

60

2) INFORMATION FOR SEQ ID NO: 81

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia vulneris*
 (B) STRAIN: ATCC 33821

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81

CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC 50
 GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
 20 TTCCTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT 150
 TGAGATGGAA GTGCGTGAAC TTCTGTCCCA GTACGACTTC CCGGGCGACG 200
 ACACCCCGAT CATTCGTGGT TCTGCGCTGA AAGCGCTGGA AGGCGAAGCT 250
 GAGTGGGAAG AGAAAATCGT TGAGCTGGCT GGCTACCTGG ATTCCTACAT 300
 CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
 25 ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG 400
 CGCGGTATCA TCAARGTKGG TGAAGAAGTT GAAATCGTGG GTATCAAAGA 450
 TACTGCGAAA TCTACCTGTA CCGGCGTTGA AATGTTCCGC AAAGTGTGCTG 500
 ACGAAGGTCG TGCAGGCGAG AACTGCGGCG TTCTGCTGCG TGGTATCAAG 550
 CGTGAAGAGA TCCAGCGTGG CCAGGTTCTG GCTAAGCCGG GCTCAATCAA 600
 30 GCCGCACACC AAGTTCGAAT CCGAAGTGTA CATCCTGTCC AAAGACGAAG 650
 GCGGCCGTCA CACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
 CGTACAACCTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
 GGTAATGCCG GGCGACAACA TCAAATGGT TGTTACCCTG ATCCATCCGA 800
 TCGCGATGGA CGACGG 816

35

2) INFORMATION FOR SEQ ID NO: 82

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eubacterium lentum*
 50 (B) STRAIN: ATCC 43055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82

CGGCGCCTCC TCGTTATCGC CGCCACCGAC GGCCCGATGG CCCAGACCCG 50
 55 CGAGCACATC CTGCTCGCCC GTCAGGTCGG CGTGCCCTAC ATCGTGGTCT 100
 TCCTGAACAA GTGCGACATG GTCGACGACG AGGAGCTCCT CGAGCTCGTC 150
 GAGATGGAAG TTCGCGAGCT GCTCGACTCT TACGAGTTCC CCGGCGACGA 200
 CACCCCGATC ATCCGCGGCT CCGCTTTGAA GGCCCTCGAG GGCGACAAAG 250
 AGTGGCAGGA GAAGGTCTGG GAGCTCATGG ACGCCGTCGA CTCCTACATC 300
 60 CCGACGCCGG AGCGCATGGT CGACAAGCCG TTCCTGATGG CCGTCGAGGA 350

50

	CACGATGACC	ATCACCGGCC	GCGGCACCGT	TGCCACCGGT	CGTGTGGAGC	400
	GTGGTACGCT	GCATGTCAAC	GACCCGCTGG	AGATCGTCGG	TATCAAGGAG	450
	ACCCAGAACA	CGGTCTGCAC	CGGTATCGAG	ATGTTCCGCA	AGCTGCTCGA	500
	CGAGGCTCAG	GCCGGCGACA	ACATCGGCTG	CCTGCTCCGC	GGTGTCAAGC	550
5	GCGAGGAGAT	CGTTCGCGGC	CAGGTTCTCT	GCAAGCCCGG	TAGCGTGACC	600
	CCGCACACCG	AGTTCGAGGG	TCAGGTCTAC	ATCCTGACGA	AGGAAGAGGG	650
	CGGCCGCCAC	ACGCCGTTCT	TCGACGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GCACGACGGA	CGTGACGGGT	GTTGCCCACC	TTCCCGAGGG	CACCGAGATG	750
	GTCATGCCCG	GCGACAACGT	GGAGATCAAG	GGCGAGCTCA	TTCACCCGAT	800
10	CGCCAGGAAG	AGGGCTGCGT	TCGCTAAC			828

2) INFORMATION FOR SEQ ID NO: 83

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Eubacterium nodatum*
 (B) STRAIN: ATCC 33099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83

30	GGAGCAATTC	TGGTTTGTGC	AGCAACKGAC	GGACCAATGC	CTCAGACAAG	50
	AGAACATATC	CTTTTGTCAA	GGCAGGTAGG	AGTGCCATAT	ATCATCGTAT	100
	TCCTGAATAA	ATGTGACATG	GTGGATGAYG	AAGAGCTTCT	GGACTTGGTA	150
	GAGATGGAAG	TAAGAGAACT	TCTCAGTGAG	TATGAATTCC	CGGGAGATGA	200
	TACCCCGATA	GTAAGAGGTT	CAGCCCTGAA	GGCACTGGAA	GAACCCAATG	250
35	GAGAATGGGC	AGACAAGATT	GTAGAGCTGA	TGGAGGAAGT	AGATAAATAC	300
	ATTCTGAAC	CAAAGAGAGA	TAACGACAAA	CCGTTCTCTGA	TGCCTGTAGA	350
	GGACGTATTC	TCAATAACAG	GAAGAGGAAC	AGTAGCGACA	GGAAGRGTG	400
	AAAGAGGAAT	CCTGAAGGTC	GGTGATGAAG	TAGAAATCGT	GGGAATGAGC	450
	GAAGAGAGAA	GAAAGGTAGT	AGTAACGGGA	GTTGAAATGT	TCAGAAAGCT	500
40	TCTGGATGAA	GCAGAGACAG	GAGACAACAT	CGGAGCACTG	CTGAGAGGAG	550
	TTCAGAGAAC	RGAGATCCAG	AGAGGTCAGG	TATTGGCRGC	ACCTGGAACG	600
	ATCAACCCAC	ATACAAAGTT	CAAGGGTCAG	GTATATGTAC	TGAAGAAGGA	650
	AGAAGGAGGA	AGGCATACGC	CGTTCTTCAA	YGGATACAGW	CCACAGTTCT	700
	ACTTCAGAAC	AACAGACGTA	ACAGGAGATT	TGCAGCTGCC	GGAAGGARCA	750
45	GAGATGTGCA	TGCCGGGAGA	TAATGTGGTA	ATGAACRTCA	GCCTGATCAC	800
	TCCGATTGCT	ATAGAAGAGG	GWCTGAGATT	TGCCA		835

50 2) INFORMATION FOR SEQ ID NO: 84

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Ewingella americana*
 (B) STRAIN: ATCC 33852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84

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5      GCGATCCTGG TTGTTGCTGC AACTGATGGC CCTATGCCAC AGACTCGTGA      50
      GCACATCCTG TTGGGTCGYC AGGTTGGCGT TCCATTCATG ATCGTATTCA      100
      TGAACAAATG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTAGAA      150
      ATGGAAGTTC GYGAAGTTCT GTCTGCTTAC GATTTCCCAG GCGACGACAT      200
10     CCCAGTTGTT AAAGGTTTCAG CGCTGAAAGC ACTGGAAGGC GAAGCAGAGT      250
      GGGAAAGCTAA GATCATCGAG CTGGCTGGCC ACCTGGATAG CTACATCCCA      300
      GAACCAGAGC GTGCGATTGA CAAGCCATTC CTGCTGCCAA TCGAAGACGT      350
      ATTCTCCATC TCCGGTCGTG GTACCGTTGT TACCGGTCGT GTAGAGCGCG      400
      GTATCATCAA AGTTGGCGAA GAAGTTGAAA TCGTTGGTAT CAAGGACACT      450
15     GTTAAGTCTA CTTGTACTGG CGTTGAAATG TTCCGCAAAC TGCTGGACGA      500
      AGGCCGTGCT GGTGAGAACG TTGGTGTCTT GCTGCGTGGT ATCAAGCGTG      550
      AAGACATCGA ACGTGGTCAG GTTCTGGCTA AACCAGGTTC AATCAAACCA      600
      CACACCACWT TYGACTCAGA AGTTTATATC CTGAGCAAAG ATGAAGGCGG      650
      CCGTCATACT CCGTTCTTCA AAGGCTACCG TCCACAGTTC TACTTCCGTA      700
20     CAACTGACGT GACCGGTACC ATCGAACTGC CAGAAGGCGT AGAGATGGTA      750
      ATGCCAGGTG ACAACATCAA CATGRTAGTT ACCCTGATCC ACCCAATCGC      800
      GATGGATGAC GGTCTGCGTT TCGCAA      826
  
```

25

2) INFORMATION FOR SEQ ID NO: 85

(i) SEQUENCE CHARACTERISTICS:

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      (A) LENGTH: 828 bases
30     (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Francisella tularensis*
 (B) STRAIN: LVS

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85

```

      TGGTGCTATT CTAGTATGTT CTGCTGCGGA TGGTCCTATG CCACAAACTC      50
      GTGAGCACAT TCTGCTTTCT CGTCAAGTTG GTGTACCAA AATCGTTGTT      100
      TTCTTAAACA AGTGTGACAT GGTTGATGAT GAAGAGTTAT TAGAGCTAGT      150
45     TGAGATGGAA GTTCGTGAGC TTTTAGATCA GTATGAGTTC CCAGGTGATG      200
      ACACTCCAGT TATTATGGGT TCAGCTCTTA GAGCTATTGA AGGTGACGAA      250
      GCTTACGTTG AGAAAATTGT TGAGCTAGTT CAAGCTATGG ATGACTATAT      300
      TCCTGCTCCT GAGCGTGATA CTGAGAAGCC ATTTATTCTT CCGATCGAAG      350
      ATGTATTCTC AATTTTCAGGT CGTGGTACTG TTGTAAGTGG TCGTATTGAG      400
50     CGCGGTGTAG TTAACGTTGG TGATGAAGTT GAAGTTGTTG GTATTCGTCC      450
      AACTCAAAAA ACTACAGTAA CTGGTGTGGA AATGTTCCGT AAGCTTTTAG      500
      ATAGAGGGGA AGCTGGTGAT AACGTTGGTA TCCTAGTTTC TGGACTTAAG      550
      AGAGATGATG TTGAGCGTGG ACAAGTATTA TGTAAGCCAG GTTCAATTAA      600
      GCCACATACT AAGTTTGAAG CTGAGGTTTA TGTATTATCT AAAGAAGAGG      650
55     GTGGTAGACA TACTCCATTC TTCAAGGGAT ATAGACCACA ATTCTACTTC      700
      CGTACTACAG ACATTACTGG AGCTGTTGAG CTTCCAGAGG GTGTAGAAAT      750
      GGTATGCCTT GGTGATAACG TTAAGATGAC TATCACTCTA ATTAACCCAA      800
      TCGCTAGGAT GAAGGGTTAC GTTTTGCA      828
  
```

60

2) INFORMATION FOR SEQ ID NO: 86

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*
(B) STRAIN: ATCC 10953

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86

	CGGTGCTATC ATCGTAGKTG CTGCTACTGA TGGTCCGATG CCTCARACTC	50
	GTGAGCAYAT CYTGCTGGCT CGTCAGGTAA ACGTWCKAG ACTGGTTGTA	100
20	TTCATGAACA AGTGYGACAT GGTAGACGAC GCTGAAATGY TGGAACCTCGT	150
	TGAAATGGAA ATGCGTGAAC TGCTTTCAGC YTACGAATTC GAYGGYGACA	200
	ACACTCCKTT CATTTCAGGGT TCTGCTCTTG GTGCRTTGAA YGGCGTTGAA	250
	AAGTGGGAAG AGAAGGTTAT GGANCTGATG GATGCTTGCG ACACTTGGAT	300
	TCCTTTGCCT CCGCGTGATA TTGAYAAACC GTTCTTGATG CCGGTTGAAG	350
25	ACGTATTCTC AATCACTGGT CGTGGTACTG TAGCTACTGG TCGTATCGAA	400
	GCTGGTGTTA TCCATGTAGG TGACGAAGTT GAAATCCTCG GTTTGGGTGA	450
	AGACAAGAAG TCTGTTGTAA CTGGTGTGTA AATGTTCCGC AAGTTGCTGG	500
	ATCAAGGTGA AGCTGGTGAC AACGTAGGTY TGTGCTCCG TGGTATCGAC	550
	AAGAACGAAA TCAAACGTGG TATGGTTCTT TGTAAGCCCG GTCAGATTAA	600
30	ACCTCACTCT AAGTTCAAAG CTTCTATCTA CGTTTTGAAG AAAGAAGAAG	650
	GTGGTCGTCA CACTCCGTTT CACAACAAAT ACCGTCCTCA GTTCTATCTG	700
	CGTACTATGG ACTGTACAGG TGAAATCWCT CTTCCGGAAG GAACTGAAAT	750
	GGTAATGCCT GGTGATAACG TAGAAATCAC TGTAGAACTG ATCTACCCGG	800
	TAGCATTGAA CGTAGGTTTG CGTTTCGCT	829

35

2) INFORMATION FOR SEQ ID NO: 87

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Gemella haemolysans*
(B) STRAIN: ATCC 10379

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87

	CTATCTTAGT AATCGCTGCT ACAGATGGAC CAATGGCTCA AACTCGTGAG	50
55	CACATCCTAT TATCTCGTAA CGTTGGAGTA CCAAAAATCG TTGTATTCTT	100
	AAACAAATGT GATATGGTTG ATGACGAAGA GTTATTAGAA TTAGTTGAAA	150
	TGGAAGTTTCG TGAACCTATTA TCTGAATACG GATTCGACGG AGATGAACTA	200
	CCAGTAATCA AAGGTTCTGC TCTTAAAGCT CTTGAAGGAG ATGCAGATGC	250
	AGAAAAAGCT ATCATCGAAT TAATGGAAAC AGTTGACGAA TACATCCCAA	300
60	CTCCAGAACG TGATAACGCT AAACCATTC A TGATGCCAGT TGAGGACGTA	350

	TTCTCAATCA	CAGGTCGTGG	TACAGTTGCT	ACTGGACGTG	TTGAACGTGG	400
	ACAAGTTAAA	GTTGGAGACG	TAGTAGAAAT	CGTTGGATTA	ACTGAAGAAC	450
	CAGCTTCAAC	TACTGTAACA	GGTGTTGAAA	TGTTCCGTAA	ATTATTAGAT	500
	TACGCTGAAG	CAGGAGATAA	CATCGGTGCA	TTATTACGTG	GTGTTGCTCG	550
5	TGAAGACATC	GAACGTGGAC	AAGTTTTAGC	AGCTCCTAAA	ACAATCACTC	600
	CACACACTCA	ATTCGTAGCT	GACGTGTACG	TATTATCTAA	AGAAGAAGGT	650
	GGACGTCACA	CTCCATTCTT	CACAACTAC	CGTCCTCAAT	TCTACTTCCG	700
	TACTACTGAC	GTAAGTGGTG	TAGTTACTTT	ACCAGAAGGT	ACTGAAATGG	750
	TAATGCCTGG	GGATAACGTA	TCAATCAACG	TAGAACTTAT	TTCTCCAATC	800
10	GCGATCGAAG	AAGGAACTCG	TTTCTCAA			828

2) INFORMATION FOR SEQ ID NO: 88

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Gemella morbillorum*
 (B) STRAIN: ATCC 27824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88

30	TCTTAGTAAT	CGCTGCTACA	GATGGTCCTA	TGGCTCAAAC	TCGTGAACAC	50
	ATCCTATTAT	CTCGTAACGT	TGGAGTACCT	AAAATTGTTG	TATTCTTAAA	100
	CAAATGTGAT	ATGGTTGATG	ACGAAGAGTT	ATTAGAATTA	GTAAGAAATGG	150
	AAGTTCGTGA	ACTATTATCT	GAATACGGAT	TTGATGGAGA	TGAACTACCA	200
	GTAATCAAAG	GTTTCAGCTCT	TAAAGCTCTT	GAAGGAGATG	CAGATGCTGA	250
35	AAAAGCTATC	ATCGAATTAA	TGGAAACAGT	TGACGAGTAC	ATCCCAACTC	300
	CAGAACGTGA	TAACGCTAAA	CCATTTATGA	TGCCAGTTGA	GGACGTGTTT	350
	TCAATCACAG	GTCGTGGTAC	AGTTGCTACT	GGACGTGTTG	AACGTGGACA	400
	AGTTAAAGTT	GGTGACGTAG	TAGAAATCGT	TGGATTAACT	GAAGAACCAG	450
	CTTCAACTAC	TGTAACAGGT	GTTGAAATGT	TCCGTAAATT	ATTAGATTAC	500
40	GCTGAAGCAG	GAGATAACAT	CGGTGCATTA	TTACGTGGTG	TTGCTCGTGA	550
	AGATATCGAA	CGTGGACAAG	TTTTAGCAGC	TCCTAAAACA	ATCACTCCAC	600
	ATACTCAATT	CGTAGCTGAT	GTGTACGTAT	TATCTAAAGA	AGAAGGTGGA	650
	CGTCACACTC	CATTCTTCAC	AACTACCGT	CCACAATTCT	ACTTCCGTAC	700
	TACTGACGTA	ACTGGTGTAG	TTACTTTACC	AGAAGGTACT	GAAATGGTAA	750
45	TGCCTGGGGA	CAACGTATCA	ATCAACGTAG	AACTTATTTC	TCCAATCGCT	800
	ATCGAAGAAG	GAAGTCGTTT	CTC			823

50 2) INFORMATION FOR SEQ ID NO: 89

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60

(A) ORGANISM: *Haemophilus actinomycetemcomitans*
(B) STRAIN: ATCC 33384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89

5
GCTATCTTAG TAGTAGCAGC AACCGACGGT CCTATGCCAC AAACCTCGTGA 50
GCACATCTTA TTAGGTCGCC AAGTAGGTGT TCCTTACATC ATCGTATTCT 100
TAAACAAATG CGACATGGTA GATGACGAAG AGTTATTAGA ATTAGTTGAA 150
ATGGAAGTTC GTGAACTTCT TTCTCAATAT GACTTCCCGG GCGATGACAC 200
10 CCCAATCGTA CGCGGTTCTG CATTAAAAGC GCTTGAAGGC GATGCCGCAT 250
GGGAAGAAAA AATCCTTGAA TTAGCAAACC ATTTAGATAC TTACATCCCG 300
GAACCTGAGC GTGCTATCGA CCAACCGTTC CTTCTTCCAA TTGAAGATGT 350
GTTCTCTATC TCCGGTCGTG GTACCGTAGT AACGGGTCGT GTTGAGCGCG 400
GTATCATCCG TACCGGTGAT GAAGTTGAAA TCGTGGGTAT CAAACCGACT 450
15 GCAAAAACCA CCGTAACCGG TGTGAAATG TTCCGTAAAT TACTTGACGA 500
AGGTCGTGCG GGTGAAAACA TCGGTGCATT ATTGCGTGGT ACTAAACGTG 550
AAGAAATCGA ACGTGGTCAG GTATTGGCGA AACCGGGGTC AATCACCCCG 600
CACACTGACT TCGAATCTGA AGTGTACGTA TTGTCCAAAG AAGAAGGTGG 650
TCGTCATACT CCATTCTTCA AAGGTTACCG TCCACAATTC TATTTCCGTA 700
20 CAACTGACGT AACCGGTACT ATCGAGTTAC CTGAAGGCGT GGAAATGGTT 750
ATGCCTGGCG ATAACATCAA AATGACCGTA TCCTTAATTC ACCCAATTGC 800
GATGGACCAA GGTTTACGTT TCGCTATCG 829

25

2) INFORMATION FOR SEQ ID NO: 90

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus aphrophilus*
(B) STRAIN: ATCC 33389

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90

TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC 50
GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCTTA CATCATCGTA 100
TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT 150
45 TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGATG 200
ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTTGCA 250
GAATGGGAAG AAAAAATCCT TGAATTAGCA AACCACTTAG ATACTTACAT 300
TCCTGAGCCA CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATTGAAG 350
ACGTGTTCTC TATCTCCGGT CGTGGTACTG TAGTAACAGG TCGTGTTGAG 400
50 CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC 450
GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG 500
ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGCACTAAA 550
CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GCTCAATCAC 600
TCCGCACACT GATTTCGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG 650
55 GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTC 700
CGTACAACCTG ACGTAACCGG TACTATCGAG TTACCGGAAG GCGTGGAAT 750
GGTTATGCCT GGCGATAACA TCAAAATGAC TGTATCCTTA ATCCACCCAA 800
TCGCGATGGA CCAAGGTTTA CGTTTCGCTA TCG 833

60

2) INFORMATION FOR SEQ ID NO: 91

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 815 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus ducreyi*
 (B) STRAIN: DSM 8925

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91

CGGCGCTATC TTAGTTGTAG CAGCAACTGA TGGTCCTATG CCTCAAACCTC 50
 GTGAACACAT CTTATTAGGC CGCCAAGTTG GTGTTCCCTA CATCATCGTA 100
 20 TTCTTAAATA AATGCGATAT GGTAGATGAT GAAGAATTAT TAGAATTAGT 150
 TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGATTTC CCAGGTGACG 200
 ATACTCCTAT CGTTCGTGGT TCAGCATTAC AAGCATTAAA TGGTGTGCCT 250
 GAGTGGGAAG AAAAAATCAT TGAATTAGCA CAACACTTAG ATTCTTATAT 300
 CCCTGAGCCT GAGCGTGCGA TTGATAAACCT TTTCTTATTA CCAATCGAAG 350
 25 ACGTATTCTC AATTTTCAGGT CGTGGTACAG TAGTAACCGG TCGTGTTGAG 400
 CGTGGTATCA TCAAATCAGG TGAAGAAGTT GAAATCGTAG GGATTAAAGA 450
 AACGACAAA ACAACAGTAA CCGGTGTTGA GATGTTCCGT AAACCTATTAG 500
 ACGAAGGTCG TCGGGGTGAA AACGTAGGTG CCTTATTACG TGGTACTAAA 550
 CGTGAAGAAA TCGAACGTGG TCAAGTATTA GCGAAACCAG GTACAATTAC 600
 30 ACCACACACT GATTTTGAAT CAGAAGTTTA TGTATTATCA AAAGAAGAAG 650
 GTGGTCGTCA TACTCCATTC TTCAAAGGTT ATCGTCCTCA GTTCTACTTC 700
 CGYACAACGG ACGTAACAGG AACGATTGAA TTACCTGAAG ATGTTGAGAT 750
 GGTAATGCCT GGTGATAATA TCAAGATGAC AGTAAGCTTA ATTCACCCTA 800
 TCGCGATGGA CGAAG 815

35

2) INFORMATION FOR SEQ ID NO: 92

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus haemolyticus*
 50 (B) STRAIN: ATCC 33390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92

TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCAATG CCACAAACTC 50
 55 GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCCATA CATCATCGTA 100
 TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT 150
 AGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCAGGTGACG 200
 ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCATTAAA TGGCGTAGCA 250
 GAATGGGAAG AAAAAATCCT TGAGTTAGCA AACCCTTAG ATACTTACAT 300
 60 CCCAGAACCA GAGCGTGCAA TTGACCAACC GTTCCTTCTT CCAATCGAAG 350

	ATGTGTTCTC	AATCTCAGGT	CGTGGTACAG	TAGTAACTGG	TCGTGTAGAA	400
	CGTGGTATCA	TCCGTACTGG	TGATGAAGTA	GAAATCGTAG	GTATCAAAGA	450
	TACAGCAAAA	ACTACTGTAA	CGGGTGTGTA	AATGTTCCGT	AAATTACTTG	500
	ACGAAGGTCG	TGCAGGTGAA	AACATCGGTG	CATTATTACG	TGGTACCAAA	550
5	CGTGAAGAAA	TCGAACGTGG	TCAAGTATTA	GCGAAACCAG	GTTCAATCAC	600
	GCCACACACT	GACTTCGAAT	CAGAAGTTTA	TGTATTATCA	AAAGAAGAAG	650
	GTGGTCGTCA	TACTCCATTC	TTCAAAGGTT	ACCGTCCACA	ATTCTATTTC	700
	CGTACAACTG	ACGTAACCTG	TACTATCGAG	TTACCAGAAG	GCGTAGAAAT	750
	GGTAATGCCA	GGCGATAACA	TCAAGATGAC	AGTAAGCTTA	ATCCACCCAA	800
10	TCGCGATGGA	CCAAGGTTTA	CGTTTCGCAA			830

2) INFORMATION FOR SEQ ID NO: 93

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Haemophilus parahaemolyticus*
 (B) STRAIN: ATCC 10014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93

30	TCTTAGTAGT	AGCAGCAACA	GACGGTCCAA	TGCCACAAAC	TCGTGAGCAC	50
	ATCTTATTAG	GTCGCCAAGT	AGGTGTTCCA	TACATCATCG	TATTCTTAAA	100
	CAAATGCGAT	ATGGTTGACG	ATGAAGAATT	ATTAGAATTA	GTTGAAATGG	150
	AAGTGCGTGA	ACTTCTTTCA	CAATATGACT	TCCCAGGTGA	TGACACGCCA	200
	GTAGTACGTG	GTTCAGCGTT	ACAAGCGTTA	AACGGCGTAG	CAGAGTGGGA	250
35	AGAAAAAATT	CTTGAATTAG	CAAACCACTT	AGATACATAC	ATCCCAGAGC	300
	CAGAGCGTGC	GATTGATAAA	CCATTCTTAT	TACCAATCGA	AGACGTATTTC	350
	TCAATCTCAG	GTCGTGGTAC	AGTAGTAACA	GGTCGTGTTG	AGCGTGGTAT	400
	CATCAAAGCG	GGTGAAGAAG	TTGAAATCGT	AGGTATCAAA	GACACTGCGA	450
	AAACAACAGT	AACTGGCGTG	GAAATGTTCC	GTAAATTATT	AGACGAAGGT	500
40	CGTGCGGGTG	AAAACGTTGG	TGCATTATTA	CGTGGTACAA	AACGTGAAGA	550
	AATCGAACGT	GGTCAAGTGT	TAGCGAAACC	AGGTACAATT	ACACCACACA	600
	CAGACTTCGA	ATCAGAAGTG	TACGTATTAT	CAAAAGAAGA	AGGTGGTCGT	650
	CACACTCCAT	TCTTCAAAGG	TTACCGTCCA	CAATTCTACT	TCCGTACAAC	700
	TGACGTAAC	GGTACTATTG	AATTACCAGA	AGGCGTAGAA	ATGGTAATGC	750
45	CAGGCGATAA	CATCAAAATG	ACAGTATCAT	TAATCCACCC	AATCGCGATG	800
	GACGAAGGTT	TACGTTTTGC	GATT			824

50 2) INFORMATION FOR SEQ ID NO: 94

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus parainfluenzae*
 (B) STRAIN: ATCC 7901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94

5
 TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC 50
 GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCTTA CATCATCGTG 100
 TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT 150
 TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGACG 200
 10 ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTWGCA 250
 GAATGGGAAG AAAAAATCCT TGAATTAGCT AGCCACTTAG ATTCTTACAT 300
 TCCTGAGCCT CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATCGAAG 350
 ACGTGTTCTC TATCTCCGGT CGTGGTACAG TAGTAACAGG TCGTGTTGAG 400
 CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC 450
 15 GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG 500
 ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGTACYAAA 550
 CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GTTCAATCAC 600
 TCCACACACT GATTTCTGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG 650
 GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTC 700
 20 CGTACAACCTG ACGTAACCGG AACTATCGAA TTACCGGAAG GCGTGGAAT 750
 GGTATGCCT GGTGATAACA TCAAATGAC TGTATCCTTA ATCCACCCAA 800
 TCGCGATGGA CCAAGGTTTA CGTTTCGCTA TCG 833

25

2) INFORMATION FOR SEQ ID NO: 95

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 824 bases
 30 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus paraphrophilus*
 (B) STRAIN: ATCC 29241

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95

TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC 50
 GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCTTA CATCATCGTA 100
 TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT 150
 45 TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGACG 200
 ATACGCCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTTGCA 250
 GAATGGGAAG AAAAAATCCT TGAATTAGCA AACCCTTGG ATACTTACAT 300
 TCCTGAGCCA CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATCGAAG 350
 ACGTGTTCTC TATCTCCGGT CGTGGTACAG TAGTAACAGG TCGTGTTGAG 400
 50 CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC 450
 GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG 500
 ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGTACCAA 550
 CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GTTCAATCAC 600
 TCCACACACT GATTTCTGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG 650
 55 GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTC 700
 CGTACAACCTG ACGTAACCGG TACTATCGAG TTACCGGAAG GTGTGGAAAT 750
 GGTAAATGCCT GCGGATAACA TCAAATGAC CGTATCCTTA ATCCACCCAA 800
 TCGCGATGGA CCAAGGTTTA CGTT 824

60

2) INFORMATION FOR SEQ ID NO: 96

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus segnis*
 (B) STRAIN: ATCC 33393

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96

20 GCTATCTTAG TAGTAGCAGC AACTGATGGT CCTATGCCAC AAACCTCGTGA 50
 GCACATCTTA TTAGGTCGCC AAGTAGGTGT TCCTTACATC ATCGTATTCT 100
 TAAACAAATG CGACATGGTA GATGACGAAG AGTTATTAGA ATTAGTTGAA 150
 ATGGAAGTTC GTGAACTTCT TTCTCAATAT GACTTCCCAG GTGATGATAC 200
 TCCAATCATT CGTGGTTCTG CATTACAAGC GTTAAACGGC GTAGCAGAAT 250
 GGGAAGAAAA AATCCTTGAA TTAGCTCAAG CATTAGATAC TTACATTCTT 300
 GAACCTGAGC GTGCAATCGA CCAACCGTTC CTTCTTCCAA TTGAAGACGT 350
 25 GTTCTCAATC TCTGGTCGTG GTACTGTAGT AACAGGTCGT GTAGAGCGTG 400
 GTATCATCCG TACCGGTGAT GAAGTTGAAA TCGTTGGTAT CAAACCAACT 450
 GCGAAAACAA CCGTAACCGG TGTGAAATG TTCCGTAAAT TACTTGACGA 500
 AGGTCGTGCA GGTGAAAACA TCGGTGCATT ATTACGTGGT ACTAAACGTG 550
 AAGAAATCGA ACGTGGTCAA GTATTAGCGA AACC GG GTTC AATCACTCCA 600
 30 CACACTGACT TCGAATCTGA AGTGTACGTA TTATCTAAAG AAGAAGGTGG 650
 TCGTCATACT CCATTCTTCA AAGGTTACCG TCCACAATTC TATTTCCGTA 700
 CAACTGACGT AACC GG TACT ATCGAGTTAC CGGAAGGCGT GGAAATGGTT 750
 ATGCCTGGCG ATAACATCAA AATGACCGTA TCCTTAATCC ACCCAATCGC 800
 GATGGACCAA GGT TTACG 818

35

2) INFORMATION FOR SEQ ID NO: 97

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 763 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Hafnia alvei*
 50 (B) STRAIN: ATCC 13337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97

55 CGGCGCTATC CTGGTTGTTG CTGCGACTGA CGGCCCTATG CCTCAGACTC 50
 GTGAGCACAT CCTGCTGGGT CGTCAGGTTG GCGTTCCTTW CATCATCGTR 100
 TTCCTGAACA AATGCGACAT GGTGATGAT GAAGAGCTGC TGGAAC TGGT 150
 AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCWGGYGATG 200
 ATACTCCAAT CATCCGTGGT TCTGCTCTGA AAGCGCTGGA AGGYGMACCT 250
 GAGTGGGAAG CTAAGATCGT AGAACTGGCT GAAACTCTGG ATTCTTACAT 300
 60 YCCACARCCA GAACGTGCTA TCGAYAAGCC ATTCCTGCTG CCAATCGAAG 350

	ACGTATTCTC	TATCTCTGGC	CGTGGTACWG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCG	TTAAAGTTGG	TGAAGAAGTT	GARATCGTTG	GTATCAAAGA	450
	TACCGTTAAA	TCAACTTGTA	CCGGCGTTGA	AATGTTCCGT	AAACTGCTGG	500
	ACGAAGGTCG	TGCAGGCGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAG	550
5	CGTGAAGACA	TCGAACGTGG	TCAGGTTCTG	GCTAAACCAG	GYTCYATCAA	600
	GCCACACACC	AAGTTCGAAT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GCGGYCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACTG	ACGTGACCGG	TACCATCGAA	TTGCCAGAAG	GCGTGGAAT	750
	GGTAATGCCA	GGC				763

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2) INFORMATION FOR SEQ ID NO: 98

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 828 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kingella kingae*

25 (B) STRAIN: ATCC 23330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98

	CGGCGCAATC	TTGGTATGTT	CAGCAGCTGA	CGGTCCTATG	CCACAAACTC	50
30	GCGAACACAT	CTTGTTGGCT	CGCCAAGTAG	GTGTACCTTA	TATCATCGTA	100
	TTCATGAACA	AATGCGACAT	GGTCGATGAT	GCTGAGTTGT	TGGAATTGGT	150
	TGAAATGGAA	ATCCGTGACT	TGTTGTCTAG	CTACGATTTT	CCAGGCGACG	200
	ATTGCCCAAT	CGTTCAAGGT	TCTGCATTGC	GYGCATTGGA	AGGCGACGCT	250
	GCATACAAAG	AAAAAATCTT	TGAATTGGCT	GCTGCTTTGG	ATAGCTACAT	300
35	TCCTACTCCA	GAACGTGCTG	TTGATAAACC	ATTCTTGTTG	CCAATCGAAG	350
	ATGTATTCTC	TATCTCTGGT	CGTGGTACAG	TAGTTACTGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTAGG	CGAAGAGATT	GAAATCGTTG	GTTTGAAAGA	450
	CACGCAAAAA	ACCACTTGTA	CTGGCGTGGA	AATGTTCCGC	AAATTGTTGG	500
	ACGAAGGTCA	AGCTGGTGAT	AACGTTGGTG	TATTATTGCG	TGGTACGAAG	550
40	CGTGAAGACG	TTGAACGTGG	TCAGGTATTG	GCTAAACCAG	GTTCTATCAC	600
	TCCGCACACT	AAATTGGAAG	CTGAAGTGTA	TGTGTTGAGC	AAAGAAGAAG	650
	GTGGCCGTCA	TACGCCATTC	TTGCTAAC	ACCGCCACA	ATTCATCTC	700
	CGTACGACTG	ACGTAACTGG	TGCAGTTACT	TTGTCTGAGG	GTGTGGAAAT	750
	GGTTATGCCA	GGCGAAAACG	TGAAAATCAC	TGTTGAGTTG	ATTGCACCTA	800
45	TCGCTAGGAA	AACGGTTTGC	GTTTTGCG			828

2) INFORMATION FOR SEQ ID NO: 99

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 828 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella ornithinolytica*

(B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99

5	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAGCTGGTT	150
	GAAATGGAAG	TCCGTGAGCT	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACGCCGATC	GTTCTGTGGT	CCGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
10	ACTGGGAAGC	GAAAATCATC	GAAGTGGCTG	GCTACCTGGA	TTCTTACATC	300
	CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAAGAGC	400
	GCGGTATCAT	CAAAGTGGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCGAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
15	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCTATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACAACCTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
20	GTCATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TTCACCCGAT	800
	CGCGATGGAC	GATGGTCTGC	GTTTCGCA			828

25 2) INFORMATION FOR SEQ ID NO: 100

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 749 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Klebsiella oxytoca</i>
	(B)	STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100

40	GATGCCGCAG	ACTCGTGAGC	ACATCCTGCT	GGGTCGTCAG	GTAGGCGTTC	50
	CGTACATCAT	CGTGTTCTCT	AACAAGTGCG	ACATGGTTGA	TGACGAAGAG	100
	CTGCTGGAAC	TGGTTGAAAT	GGAAGTTCGT	GAAGTTCTGT	CTCAGTACGA	150
	TTTCCCGGGC	GACGACACTC	CGATCGTTCG	TGGTTCTGCT	CTGAAAGCGC	200
45	TGGAAGGCGA	CGCWGAGTGG	GAACKKAAAA	TCATCGAACT	GGCTGGCTTC	250
	CTGGATTCTT	ACATTCCGGA	ACCAGAGCGT	GCGATTGACA	AGCCGTTTCCT	300
	GCTGCCGATC	GAAGACGTAT	TCTCCATCTC	CGGTCGTGGT	ACCGTTGTTA	350
	CCGGTCGTGT	AGAGCGCGGT	ATCATCAAAG	TTGGCGAAGA	AGTTGAAATY	400
	GTTGGTATYA	AAGACACTGC	TAAGTCTACC	TGTACTGGCG	TTGAAATGTT	450
50	CCGCAAACTG	CTGGACGAAG	GCCGYGCTGG	TGAGAACGTT	GGTGTTCTGC	500
	TGCGTGGTAT	CAAACGTGAA	GAAATCGAAC	GTGGTCAGGT	ACTGGCTAAG	550
	CCGGGCTCTA	TCAAGCCGCA	CACCAAGTTC	GAATCTGAAG	TTTATATCCT	600
	GTCCAAAGAC	GAAGGCGGCC	GTCACACTCC	GTTCTTCAAA	GGCTACCGTC	650
	CGCAGTTCTA	CTTCCGTACA	ACTGACGTGA	CTGGCACCAT	CGAACTGCCG	700
55	GAAGGCGTAG	AGATGGTTAT	GCCGGGCGAC	AACATCAAAA	TGGTTGTTA	749

2) INFORMATION FOR SEQ ID NO: 101

60

61

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Klebsiella planticola*
 (B) STRAIN: ATCC 33531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101

15	TGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTCGTGAGC	TGCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ACACTCCGAT	CGTTCGTGGT	TCCGCTCTGA	AAGCGCTGGA	AGGCGAAGCA	250
20	GACTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTACCTGG	ATTCTTACAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCCTGCTG	CCTATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	TACTGCTAAR	TCWACCTGTA	CYGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
25	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCTCTATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAACTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
30	GGTAATGCCG	GCGGACAACA	TCAAATGGT	TGTTACCCTG	ATTCACCCRA	800
	TCGCGATGGA	CGACGGTCTG	CGTTTCGCAA			830

35 2) INFORMATION FOR SEQ ID NO: 102

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
 (B) STRAIN: ATCC 11296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102

50	CCTGGTTGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACT	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCCGT	ACATCATCGT	GTTCTGAAC	100
	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TTGAGATGGA	150
	AGTTCGTGAA	CTGCTGTCTC	AGTACGATTT	CCCGGGCGAC	GACACCCCGA	200
55	TCGTTTCGTGG	TTCTGCTCTG	AAAGCGCTGG	AAGGCGACGC	AGAGTGGGAA	250
	GCGAAAATCA	TCGAAGTGGC	TGGCCACCTG	GATACCTATA	TCCCGGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCGATCGAA	GACGTATTCT	350
	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	GCGCGGTATC	400
	ATCAAAGTAG	GTGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AAACCGCGAA	450
60	AACCACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAACTGCTG	GACGAAGGCC	500

GTGCTGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA 550
 ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA ACCCGCACAC 600
 CAAGTTCGAA TCTGAAGTGT ACATCCTGTC CAAAGACGAA GGCGGCCGTC 650
 ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACTACT 700
 5 GACGTGACTG GCACCATCGA ACTGCCGGAA GGCGTAGAGA TGGTAATGCC 750
 GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
 ACGACG 806

10

2) INFORMATION FOR SEQ ID NO: 103

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 743 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103

GCAGACTCGT GAGCACATCC TGCTGGGTCG TCAGGTAGGC GTTCCGTACA 50
 TCATCGTGTT CCTGAACAAA TGCGACATGG TTGATGACGA AGAGCTGCTG 100
 GAACTGGTTG AGATGGAAGT TCGTGAACTG CTGTCTCAGT ACGATTTCCC 150
 30 GGGCGACGAC ACTCCGATCG TTCGTGGTTC TGCTCTGAAA GCGCTGGAAG 200
 GCGACGCAGA GTGGGAAGCG AAAATCATCG AACTGGCTGG CCACCTGGAT 250
 ACCTATATCC CGGAACCAGA GCGTGCGATT GACAAGCCGT TCCTGCTGCC 300
 GATCGAAGAC GTATTCTCCA TCTCCGGTCG TGGTACCGTT GTTACCGGTC 350
 GTGTAGAGCG CCGTATCATC AAAGTAGGTG AAGAAGTTGA AATCGTTGGT 400
 35 ATCAAAGAAA CCGCGAAAAC CACCTGTACT GCGGTTGAAA TGTTCCGCAA 450
 ACTGCTGGAC GAAGGCCGTG CTGGTGAGAA CGTAGGTGTT CTGCTGCGTG 500
 GTATCAAACG TGAAGAAATC GAACGTGGTC AGGTACTGGC TAAGCCGGGC 550
 ACCATCAACC CGCACACCAA GTTCGAATCT GAAGTGATCA TCCTGTCCAA 600
 AGACGAAGGC GGCCGTCACA CTCCGTTCTT CAAAGGCTAC CGTCCGCAGT 650
 40 TCTACTTCCG TACTACTGAC GTGACTGGCA CCATCGAACT GCCGGAAGGC 700
 GTAGAGATGG TAATGCCGGG CGACAACATC AAAATGGTTG TTA 743

45 2) INFORMATION FOR SEQ ID NO: 104

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp.
rhinoscleromatis
 (B) STRAIN: ATCC 13884

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104

	TGGTTGTTGC	TGCGACTGAC	GGCCCCGATGC	CGCAGACTCG	TGAGCACATC	50
	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	100
	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	GAGATGGAAG	150
5	TTCGTGAACT	RCTGTCTCAG	TACGATTTCC	CGGGCGACGA	CACCCCGATC	200
	GTTCTGTTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	250
	GAAAATCATC	GAAGTGGCTG	GCCACCTGGA	TACCTATATC	CCGGAACCAG	300
	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	CGTATTCTCC	350
	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	GCGGTATCAT	400
10	CAAAGTAGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAA	ACCGCGAAAA	450
	CCACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	500
	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	550
	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAC	CCGCACACCA	600
	AGTTCGAATC	TGAAGTGTAC	ATCCTGTCCA	AAGACGAAGG	CGGCCGTCAC	650
15	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	GTACTACTGA	700
	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	GTAATGCCGG	750
	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCATCCGAT	CGCGATGGAC	800
	GACGGTCTGC	GTTTCGCAA				819

20

2) INFORMATION FOR SEQ ID NO: 105

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 832 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kluyvera ascorbata*

(B) STRAIN: ATCC 33433

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	TGGCCCTATG	CCACAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
40	TTCCTGAACA	AATGYGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCAGGCGACG	200
	ATACTCCAAT	CATCCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGATGCA	250
	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAACGTGCTA	TCGATAAGCC	GTTCTGCTG	CCAATCGAAG	350
45	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTTGG	YGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	CACCGCTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCTAAGCCAG	GCTCTATCAA	600
50	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTTGAGAT	750
	GGTAATGCCA	GGCGACAACA	TCAAGATGGT	TGTGACTCTG	ATCCACCCAA	800
	TCGCGATGGA	CGACGGCCTG	CGTTTCGCAA	CC		832

55

2) INFORMATION FOR SEQ ID NO: 106

60 (i) SEQUENCE CHARACTERISTICS:

64

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera cryocrescens*
 (B) STRAIN: ATCC 33435

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106

	TGGCGCGATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCTATG	CCACAGACTC	50
15	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
	TTCCTGAACA	AATGTGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCAGGCGACG	200
	ACACTCCTAT	CGTTCGTGGT	TCCGCGCTGA	AAGCGCTGGA	AGGCGACGCT	250
	GAGTGGGAAG	CAAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
20	CCCAGAACCA	GAGCGTGCGA	TTGATAAGCC	GTTCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTGG	GTATCAAAGA	450
	CACTGCTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
25	CGTGAAGAAA	TCGAACGTGG	TCAGGTCTCTG	GCTAAGCCAG	GCTCCATCAA	600
	GCCGCACACC	AAATTCGAAT	CTGAAGTTTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCAA	800
30	TCGCGATGGA	CGACGGTCTG	CGTTTCGCAA			830

2) INFORMATION FOR SEQ ID NO: 107

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera georgiana*
 (B) STRAIN: ATCC 51603

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107

50	CGCGATCCTG	GTTGTTGCTG	CGACTGACGG	CCCGATGCCG	CAGACTCGTG	50
	AGCACATCCT	GCTGGGTCGT	CAGGTTGGCG	TTCCGTACAT	CATCGTGTTT	100
	CTGAACAAAT	GCGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTTGA	150
	AATGGAAGTT	CGTGAACCTT	TGTCTCAGTA	CGACTTCCCG	GGCGACGACA	200
	CGCCGATCGT	TCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGACGCTGAG	250
55	TGGGAAGCGA	AAATCATCGA	ACTGGCGGGC	TTCCTGGATT	CTTACATCCC	300
	GGAACCAGAG	CGTGCGATTG	ACAAGCCGTT	CCTGCTGCCG	ATCGAAGACG	350
	TATTCTCCAT	CTCCGGTCGT	GGTACCGTTG	TTACCGGTCG	TGTAGAACGC	400
	GGTATCATCA	AAGTTGGCGA	AGAAGTTGAA	ATCGTTGGTA	TCAAAGACAC	450
	CGCTAAGTCT	ACCTGTACTG	GCGTTGAAAT	GTTCCGCAAA	CTGCTGGACG	500
60	AAGGCCGTGC	TGGTGAGAAC	GTTGGTGTTT	TGCTGCGTGG	TATCAAACGT	550

	GAAGAAATCG	AACGTGGTCA	GGTACTGGCT	AAGCCGGGTT	CTATCAAGCC	600
	GCACACCAAG	TTCGAATCTG	AAGTGTACAT	TCTGTCCAAA	GACGAAGGCG	650
	GCCGTCATAC	TCCGTTCTTC	AAAGGCTACC	GTCCGCAGTT	CTACTTCCGT	700
	ACTACTGACG	TGACTGGCAC	CATCGAACTG	CCGGAAGGCG	TTGAGATGGT	750
5	AATGCCGGGC	GACAACATCA	AAATGGTTGT	TACCCTGATC	CACCCGATCG	800
	CGAAGGACGA	AGGTCTGCGT	TTCGCA			826

10 2) INFORMATION FOR SEQ ID NO: 108

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactobacillus casei* subsp. *casei*
 (B) STRAIN: ATCC 393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108

25	GCTGCTGATG	GCCCAATGCC	ACAAACTCGT	GAACATATCT	TACTTTCACG	50
	TCAAGTTGGT	GTTCCATACA	TCGTTGTATT	CATGAACAAA	TGTGACATGG	100
	TTGACGATGA	AGAATTACTA	GAATTAGTTG	AAATGGAAAT	TCGTGATCTA	150
	TTAACTGAAT	ATGAATTCCC	TGGCGATGAC	ATTCCTGTAA	TCAAAGGTTC	200
30	AGCTCTTAAA	GCACTTCAAG	GTGAAGCTGA	CTGGGAAGCT	AAAATTGACG	250
	AGTTAATGGA	AGCTGTAGAT	TCTTACATTC	CAACTCCAGA	ACGTGATACT	300
	GACAAACCAT	TCATGATGCC	AGTTGAGGAT	GTATTCTCAA	TCACTGGTCG	350
	TGGAACAGTT	GCAACTGGAC	GTGTTGAACG	TGGACAAGTT	AAAGTTGGTG	400
	ACGAAGTAGA	AGTTATCGGT	ATTGAAGAAG	AGAGCAAAAA	AGTAGTAGTA	450
35	ACTGGAGTAG	AAATGTTCCG	TAAATYACTA	GATTACGCTG	AAGCTGGCGA	500
	CAACATTGGC	GCACTTCTAC	GTGGTGTTGC	TCGTGAAGAT	ATCCAACGTG	550
	GTCAAGTATT	AGCTAAACCA	GGTTCGATTA	CTCCACACAC	TAAGTTCAAA	600
	GCTGAAACTT	ATGTTTTAAC	TAAAGAAGAA	GGTGGACGTC	ACACTCCATT	650
	CTTCAACAAC	TACCGCCCAC	AATTCTATTT	CCGTACTACT	GACGTAAGTG	700
40	GTATTGTTAC	ACTTCCAGAA	GGTACTGAAA	TGGTAATGCC	TGGTGATAAC	750
	ATTGAGCTTG	CAGTTGANCT	AATTGCACCA	ATCGCTATCG	AAGACGGTAC	800
	TAA					803

45

2) INFORMATION FOR SEQ ID NO: 109

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactococcus lactis* subsp. *lactis*
 (B) STRAIN: ATCC 19435

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109

	CGGTGCAATC	CTCGTTGTTG	CTGCAACTGA	TGGACCAATG	CCACAAACTC	50
	GTGAACACAT	CTTGCTTTCA	CGTCAAGTTG	GTGTTAAATA	CCTTATCGTC	100
	TTCCTTAACA	AGGCTGACCT	TGTTGATGAT	GAAGAATTGA	TGGAACTCGT	150
5	TGAAATGGAA	GTTCGTGACC	TCTTGAGCGA	ATACGACTTC	CCAGGTGACG	200
	ATATTCCTGT	AATCGCTGGT	TCAGCACTTG	GTGCTTTGAA	CGGTGAACCA	250
	CAATGGGTTG	CTAAAGTTGA	AGAATTGATG	GACATCGTTG	ATGAATACAT	300
	CCCAACTCCA	GAACGCGACA	CTGACAAACC	ACTCCTTCTT	CCAGTCGAAG	350
	ACGTATTCTC	TATCACTGGT	CGTGGTACAG	TTGCTTCAGG	ACGTATCGAA	400
10	CGTGGTACTG	TTAAAGTTGG	TGACGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	AGAAACTAAA	AAAGCTGTTG	TTACTGGTAT	CGAAATGTTT	CGTAAAACAC	500
	TTACTGAAGG	TCTTGCTGGT	GATAACGTCG	GTGCACTTCT	CCGTGGTATC	550
	CAACGTGACG	AAATCGAACG	TGGTCAAGTT	ATTGCTAAAC	CAGGTTCAAT	600
	CACTCCACAC	AAACTTTTCG	AAGGTGAAGT	TTACGTATTG	AGCAAAGAAG	650
15	AAGGCGGACG	TCACACTCCA	TTCTTCGACA	ACTACCGTCC	TCAATTCTAC	700
	TTCCACACAA	CTGACGTTAC	TGGTTCAGTT	AAACTTCCAG	AAGGAACTGA	750
	AATGGTAATG	CCTGGTGACA	ACGTGCATAT	CGACGTTGAA	TTGATCCACC	800
	CAGTTGCGAT	CGAACAAGGT	ACTAC			825

20

2) INFORMATION FOR SEQ ID NO: 110

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 824 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leclercia adecarboxylata*

(B) STRAIN: ATCC 23216

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCAATGC	CTCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCTTTC	ATCATCGTGT	100
40	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
	GAGATGGAAG	TTCGTGAACT	YCTGTCCCAG	TACGACTTCC	CGGGCGACGA	200
	CACCCCAATC	GTTCGTGGTT	CTGCGCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
	AGTGGGAAGA	GAAAATCATC	GARCTGGCTG	GCTACCTGGA	TTCCTACATC	300
	CCAGAGCCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CTATCGAAGA	350
45	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAAGAGC	400
	GCGGTATCAT	CAARGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAGGAC	450
	ACTGCTAAGT	CTACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCCGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTTCTGG	CTAAGCCAGG	CTCYATCAAG	600
50	CCGCACACCA	AGTTCGAATC	TGAAGTGATC	ATCCTGTCYA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACKACTGA	CGTGACCGGT	ACCATCGARC	TGCCAGAAGG	CGTTGAGATG	750
	GTAATGCCAG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCAAT	800
	CGCAATGGAC	GATGGTCTGC	GTTC			824

55

2) INFORMATION FOR SEQ ID NO: 111

60 (i) SEQUENCE CHARACTERISTICS:

67

(A) LENGTH: 838 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Legionella micdadei*
 (B) STRAIN: ATCC 33218

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111

	CGGAGCGATA	TTAGTAGTAT	CAGCAGCGGA	TGGCCCAATG	CCTCAAACGA	50
15	GAGAGCACAT	ACTYTTATCC	CGSCAGGTAG	GTGTTCCCTA	TATAGTAGTG	100
	TTCTTAAACA	AAGCTGACAT	GGTGGATGAT	GCGGAGTTAT	TAGAATTAGT	150
	TGAAATGGAA	GTACGCGAYT	TGTTGAGCAG	CTATGAATTT	CCAGGAGATG	200
	AGATCCCGAT	TGTAGTTGGT	TCAGCATTA	AAGCATTGGA	AGGCGATACG	250
	AGTGATATAG	GTGTACCAGC	GATTGAGAAG	TTAGTTGAGA	CGATGGATTC	300
20	TTATATACCT	GAGCCGGTAA	GAAACATCGA	TAAAAGTTTC	TTGTTACCGA	350
	TCGAAGACGT	GTTCTCAATA	TCTGGACGAG	GAACAGTAGT	AACAGGACGT	400
	ATCGAAAGCG	GGATCATCAA	AGTTGGTGAG	GAAGTCGAGA	TTGTTGGTAT	450
	ACGTGACACT	CAAAGACGA	CATGCACAGG	CGTTGAAATG	TTCCGTAAAT	500
	TACTTGACGA	AGGTCGAGCT	GGAGACAACG	TTGGTATATT	GCTACGTGGT	550
25	ACGAAGCGGG	ATGAAGTTGA	ACGCGGACAA	GTATTAGCTA	AGCCGGGAAG	600
	CATTAAACCG	CATACTAAAT	TTGAAGCTGA	AGTGTATGTG	TTGTCAAAG	650
	ATGAAGGTGG	ACGTCATACC	CCATTCTTTA	ACGGATATCG	GCCTCAATTT	700
	TACTTCAGGA	CCACAGACGT	AACTGGTTCT	TGTGATTTAC	CTGARGGTAT	750
	AGAAATGGTA	ATGCCAGGTG	ATAACGTCAA	GCTGATTGTT	AGCTTACACT	800
30	CACCGATTGC	TATGGACGAA	GGTTTGCGTT	TTGCAATC		838

2) INFORMATION FOR SEQ ID NO: 112

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 838 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
 (B) STRAIN: ATCC 33152

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112

50	CGGAGCGATA	CTGGTTGTAT	CAGCAGCTGA	TGGTCCTATG	CCACAAACGA	50
	GGGAACACAT	TCTATTGTCT	CGCCAGGTAG	GTGTTCCATA	TATTGTTGTG	100
	TTCATGAACA	AAGCGGATAT	GGTTGATGAC	CCTGAGTTAT	TAGAGTTAGT	150
	GGAAATGGAA	GTGCGAGATT	TATTAAGCAG	TTACGATTTT	CCAGGGGATG	200
	ACATACCTAT	TGTTGTTGGT	TCAGCTTTGA	AAGCATTGGA	AGGTGAAGAC	250
55	AGTGATATAG	GCGTTAAGGC	TATTGAGAAA	TTGGTTGAAA	CAATGGATTC	300
	ATACATTCCT	GAGCCAGTTA	GAAACATAGA	CAAGCCATTT	TTGTTGCCGA	350
	TTGAAGACGT	ATTTTCAATT	TCTGGACGCG	GAACAGTGGT	AACTGGTCGT	400
	GTAGAGAGTG	GAATTGTTAA	AGTTGGTGAG	GAAGTTGAAA	TTGTTGGAAT	450
	AAGAGACACC	CAAAGACGA	CTTGACGGG	TGTTGAGATG	TTCCGTAAAT	500
60	TACTTGATGA	AGGTCGAGCT	GGTGATAACG	TTGGTGTGTT	ATTACGAGGT	550

	ACGAAGCGAG	ATGAAGTGG	GCGTGGACAG	GTATTGGCGA	AGCCAGGAAC	600
	CATCAAGCCA	CACACCAAGT	TTGAAGCAGA	AGTGTATGTA	TTATCCAAGG	650
	AAGAAGGCGG	ACGTCACACT	CCATTCTTTA	ATGGATACCG	TCCACAATTC	700
	TATTTTCAGAA	CCACTGACGT	GACAGGTACT	TGTGACTTGC	CATCAGGAGT	750
5	TGAAATGGTA	ATGCCTGGAG	ATAATGTGCA	ATTAGTTGTT	AGCTTGCATG	800
	CTCCGATTGC	GATGGATGAA	GGTTTAAGAT	TCGCAATT		838

10 2) INFORMATION FOR SEQ ID NO: 113

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leminorella grimontii*
 (B) STRAIN: ATCC 33999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113

25	GTGCAATCCT	GGTAGTAGCA	GCGACTGACG	GCCCGATGCC	TCAGACTCGC	50
	GAGCACATCC	TGCTGGGTCG	TCAGGTAGGC	GTTCCGTACA	TCATCGTATT	100
	CCTGAACAAG	TGCGATATGG	TTGATGACGA	AGAGCTGCTG	GAGCTGGTTG	150
	ARATGGAAGT	TCGCGAACTG	CTGTCTCAGT	ACGACTTCCC	GGGCGACGAC	200
30	ACTCCGGTAG	TCCGCGGTTC	AGCGCTGAAA	GCGCTGGAAG	GCGAAGCCGA	250
	GTGGGAARCG	AAAATCATCG	AGCTGGCAGG	CCMTCTGGAT	ACTTATATCC	300
	CAGAACCTGA	GCGTGCGATT	GACAAGCCGT	TCCTGCTGCC	KATCGAAGAC	350
	GTATTCTCTA	TCTCCGGCCG	TGGTACCGTT	GTTACCGGTC	GTGTAGAGCG	400
	CGGCATCATC	AAAGTCGGTG	AAGAAGTGGA	AATCGTCGGT	ATCAAAGATA	450
35	CCACCAAGAC	CACCTGTACC	GGCGTTGAAA	TGTTCCGTAA	GCTGCTGGAC	500
	GAAGGCCGTG	CGGGCGAGAA	CGTGGGCGTT	CTGCTGCGCG	GTACCAAGCG	550
	TGACGAAATC	GAACGTGGTC	AAGTTCTGGC	CAAGCCGGGC	ACCATCACTC	600
	CTCACACCCA	GTTTCGTGTCA	GAAGTGTATA	TCCTGAGCAA	GGATGAAGGC	650
	GGCCGTCATA	CTCCGTTCTT	CAAAGGCTAC	CGTCCTCAGT	TCTACTTCCG	700
40	TACGACTGAC	GTGACAGGCA	CCATCGAACT	GCCGGAAGGC	GTAGAGATGG	750
	TAATGCCAGG	CGACAACATT	CAGATGACCG	TAAGTCTGAT	TGCGCCGATC	800
	GCAATGGACG	AAGGTCTGCG	CTTCGCAA			828

45

2) INFORMATION FOR SEQ ID NO: 114

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leminorella richardii*
 (B) STRAIN: ATCC 33998

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114

	GCTATCCTGG	TTGTTGCTGC	GACTGACGGC	CCAATGCCTC	AGACTCGTGA	50
	GCACATCCTG	CTGGGTCGCC	AGGTAGGCGT	TCCTTACATC	ATCGTGTTCC	100
	TGAACAAGTG	CGACATGGTT	GATGACGAAG	AGCTGCTGGA	ACTGGTAGAA	150
5	ATGGAAGTTC	GTGAACTTCT	GTCTCAATAC	GACTTCCCGG	GCGACGATAC	200
	GCCGGTTGTT	CGCGGTTTCAG	CGCTGAAAGC	GCTGGAAGGT	GACGCYGAGT	250
	GGGAARCGAA	AATCATTGAA	CTGGCGGAAT	CCTTRGATAC	TTAYATTCCA	300
	GAGCCAGAGC	GTGCGATTGA	CAAGCCGTTC	CTGCTGCCTA	TCGAAGACGT	350
	TTTCTCTATC	TCTGGCCGTG	GTACTGTAGT	CACCGGTCGT	GTAGAGCGCG	400
10	GCATCATCAA	AGTTGGTGAA	GAAGTGGAAG	TCGTGGGAAT	CAAAGACACC	450
	ACCAAGACCA	CCTGTACTGG	CGTTGAAATG	TTCCGTAAGC	TGCTGGACGA	500
	AGGCCGTGCA	GGTGAGAACG	TTGGTGTTCT	GCTGCGYGGT	ACTAAGCGTG	550
	ACGAAATCGA	ACGTGGTCAG	GTACTGGCTA	AGCCAGGCAC	CATCACTCCT	600
	CACACAGAAT	TCGTGTCAGA	AGTGTATATC	CTGAGCAAGG	ATGAAGGCGG	650
15	YCGTCATACT	CCGTTCTTCA	AAGGCTACCG	TCCTCAGTTC	TACTTCCGTA	700
	CGACTGACGT	GACCGGCACC	ATCGAACTGC	CAGAAGGCGT	AGAGATGGTA	750
	ATGCCAGGCG	ATAACATCCA	GATGGTAGTT	ACGCTGATTG	CCCCAATCGC	800
	GATGGACGAA	GGTCTGCGCT	TCGCAA			826

20

2) INFORMATION FOR SEQ ID NO: 115

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 843 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leptospira interrogans*

(B) STRAIN: ATCC 23581

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115

	TGCGGCGATT	CTTGTAGTAT	CCGCAACTGA	CGGACCTATG	CCACAAACAA	50
	AAGAACATAT	CCTTCTTGCT	CGTCAGGTAG	GTGTTCCATA	TGTAATTGTA	100
40	TTCATTAACA	AAGCAGATAT	GCTTGCTGCT	GACGAAAGAG	CAGAAATGAT	150
	CGAAATGGTT	GAGATGGACG	TTCGTGAACT	TCTCAATAAG	TATAGCTTCC	200
	CAGGAGATAC	AACTCCTATC	GTTCAATGGT	CTGCGGTAAA	AGCACATTGAG	250
	GGCGATGAAT	CTGAAATTGG	GATGCCTGCA	ATTCTCAAAT	TGATGGAAGC	300
	TCTGGATACT	TTCGTTCCAA	ATCCAAAACG	TGTAATCGAC	AAACCTTTCC	350
45	TTATGCCAGT	AGAAGACGTT	TTCTCGATCA	CTGGTCGTGG	AACTGTTGCA	400
	ACTGGAAGAG	TGGAACAAGG	TGTTTTGAAA	GTGAACGACG	AAGTTGAAAT	450
	TATCGGTATC	CGCCCAACAA	CAAAAACGTG	TGTTACCGGT	ATCGAAATGT	500
	TCAGAAAAC	TCTCGATCAA	GCGGAAGCTG	GCGACAACAT	CGGCGCTCTT	550
	CTTCGTGGAA	CTAAAAAAGA	AGAAATCGAA	AGAGGGCAAG	TTCTTGCGAA	600
50	GCCAGGTTCT	ATCACTCCTC	ACAAAAAGTT	TGCCGCTGAG	GTGTATGTAT	650
	TAATAAGGA	TGAAGGCGGA	CGTCATACTC	CGTTTATCAA	TAATAACCGT	700
	CCTCAGTTTT	ACTTTAGAAC	AACTGACGTA	ACCGGAGTTT	GTAACCTTCC	750
	TAATGGTGTC	GAAATGGTTA	TGCCTGGTGA	TAACGTTTCT	TTGACGGTTG	800
55	AATTGATTAG	CCCGATCGCA	ATGGACAAGG	GTCTTAAGTT	CGC	843

2) INFORMATION FOR SEQ ID NO: 116

60 (i) SEQUENCE CHARACTERISTICS:

70

(A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Megamonas hypermegale*
 (B) STRAIN: ATCC 25560

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116

	CGGTGCTATC	CTCGTTGTTA	GTGCTGCTGA	TGGTCCTATG	CCTCAGACTC	50
15	GTGAACACAT	CCTTCTCGCT	CGTCAGGTTG	GTGTTCCAGC	TATCGTTGTA	100
	TTCCTCAACA	AAGCTGACCA	GGTTGATGAC	CCTGAACTTC	TCGAACTTGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTTTCCAG	CTATGACTTC	CCAGGCGATG	200
	ACGTTCCAGT	AATCACTGGT	TCCGCTCTTC	AGGCTCTCGA	AGGCGACGAA	250
	GAAGCTAAAA	AGAAAATTCT	TGAATTAATG	GATGCTGTTG	ATGATTACAT	300
20	CCCAACTCCA	ACACGTGACA	CTGATAAACC	TTTCTTAATG	CCAGTTGAAG	350
	ACGTATTCAC	AATTACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGCGAAC	TTAAACTTGG	TGACAGCGTT	GAAATCGTTG	GTCTTTCCGA	450
	TGAAAAGAAA	TCCACTACTG	TAAGTGGTAT	CGAAATGTTC	CGCAAAATGC	500
	TTGATAGCGC	TGTTGCTGGT	GATAACATCG	GTGCACTTCT	TCGTGGTATT	550
25	GACCGTAAAG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CTGGCACAAT	600
	TCATCCACAC	AAAAAATTCA	AAGCTCAGGT	TTACGTATTA	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCTCCA	ACTATCGTCC	ACAGTTCTAT	700
	TTCCGTACTA	CTGACGTTAC	TGGTGTGTTA	ACTCTTCCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGATA	ACATTGAAAT	GAGCATCGAA	CTCATCACTC	800
30	CAATCGCTAT	TGAAAAGGT	CTTCGCTTCG	CT		832

2) INFORMATION FOR SEQ ID NO: 117

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mitsuokella multacida*
 (B) STRAIN: ATCC 27723

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117

50	TGGTGCTATC	CTCGTCGTTT	CCGCTGCTGA	TGGCCCGATG	CCGCAGACGC	50
	GTGAGCACAT	CCTGCTCGCT	CGCCAGGTCG	GTGTTCCGGC	AATCGTTGTC	100
	TTCCTCAACA	AGGTTGACCA	GGTTGACGAT	CCGGAGCTCC	TCGAGCTCGT	150
	CGAGATGGAA	GTTCGCGAGC	TGCTCTCCAG	CTACGACTTC	CCGGGCGATG	200
	ACATCCCTGT	AATCGCTGGT	TCCGCTCTGA	AGGCCCTCGA	AGGCGACGAA	250
55	GAGCAGAAGA	AGAACATCCT	CAAGCTCATG	GAAGCTGTCG	ATGAGTACAT	300
	CCCGACGCCG	GTCCGCGACA	ACGCTAAGCC	GTTCTTGATG	CCGGTTCGAGG	350
	ATGTCTTCAC	GATCACGGGC	CGTGGTACGG	TTGCAACGGG	CCGCGTTGAG	400
	CGTGGTGAGC	TCAAGATGAA	CGATACGGTT	GAGATCGTTG	GTCTGCAGGA	450
	CGAGCCGCGT	CAGACGGTTG	TCACGGGCAT	CGAGATGTTC	CGCAAGATGC	500
60	TTGATTTCGC	TGAGGCTGGC	GATAACATCG	GTGCTCTGCT	CCGTGGTATC	550

```

GACCGCAAGG AGATCGAGCG TGGCCAGGTT CTCGCAAAGC CGGGCACGAT 600
TCATCCGCAC ACGAAGTTCA AGGCTCAGGT CTATGTCCTG ACGAAAGAAG 650
AAGGCGGCCG TCATACGCCG TTCTTCACGA ACTATCGCCC GCAGTTCTAC 700
TTCCGCACGA CGGACGTAAC TGGCGTAGTC AAAGTGCCGG AAGGCACGGA 750
5 GATGGTTATG CCTGGCGATA ACGTCGAGAT GGAAGTTGAG CTCATCACCC 800
CGATCGCTAT CGAGAAGGGC 820

```

10 2) INFORMATION FOR SEQ ID NO: 118

(i) SEQUENCE CHARACTERISTICS:

```

15 (A) LENGTH: 831 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Mobiluncus curtisii subsp. holmesii
    (B) STRAIN: ATCC 35242

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118

```

25 CGGCGCTATC CTCGTGGTGG CTGCTACTGA CGGTCCGATG GCTCAGACCA 50
   AGGAACACAT CCTGTTGGCT AAGCAGGTTG GCGTGCCCTC CATCCTGGTC 100
   GCTCTGAACA AGTGCGATTC TTCCGATGTG GACGAAGACA TGCTCGAAAT 150
   CGTCGAGGAC GAAATCCGCG ATGACCTGGA GAAGCAGGGC TTCGATCGTG 200
30 ACTGCCCCGAT TATCCACGTT TCCGCTCTGA AGGCCCTGGA AGGCGACCCC 250
   GAGTGGACCA AGAAGATTGA AGAGCTCATG GAAGCGGTCTG ATACCTACAT 300
   TCCTGAGCCT GTTCGTGACC TCGACAAGCC GTTCTTGATG CCTATCGAAG 350
   ACGTCTTCAC CATTACTGGT CGCGGTACCG TAGTGACCGG TCGTGTGGAA 400
   CGCGGCAAGC TACCGTTGAA CGCCGAAGTG GAAATCGTAG GTATTCTGTC 450
35 TACGCAAAG ACCACCGTTA CCGGTATCGA AATGTTCCAC AAGTCCATGG 500
   ACGAAGCCTA CGCCGGCGAG AACTGTGGTC TGTGCTGCG TGGCACCAG 550
   CGTGAGGACG TTGAGCGCGG TCAGGTTGTC TGCATTCTG GCTCCGTGAC 600
   CCCGCACACC AAGTTCGAGG GCAAGGTCTA CATCTTGAAG AAGGACGAAG 650
   GTGGACGTCA CAAGTCGTTT TACGACGGCT ACCGCCCGCA GTTCTTCTTC 700
40 CGCACCACCG ACGTGACCGG TGTTATTAC CTGCCCAGAG GCACCGAAAT 750
   GGTATGCCT GCGACACCA CCGAAATTAG CGTTGAGCTG ATTCAGCCTA 800
   TCGCTATGGA GGAAGGTCTC GGCTTCGCTA 831

```

45

2) INFORMATION FOR SEQ ID NO: 119

(i) SEQUENCE CHARACTERISTICS:

```

50 (A) LENGTH: 825 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Moellerella wisconsinensis
    (B) STRAIN: ATCC 35017

```

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119

```

      GGTGCAATTC TGGTTGTTGC TGCAACTGAT GGCCCTATGC CACAGACTCG      50
      TGAGCACATC CTGTTAGGTC GTCAGGTTGG CGTTCCATAC ATCATCGTTT      100
      TCCTGAACAA ATGTGACATG GTAGACGACG AAGAGCTGTT AGAACTGGTT      150
5     GAAATGGAAG TCCGTGAGCT GCTGTCTCAG TACGATTTCC CAGGCGATGA      200
      CACTCCAGTA ATCCGTGGTT CAGCGCTGAA AGCTCTGGAA GGCGAAGCTG      250
      AGTGGGAAGC TAAAATCATT GAACTGGCAG AAGCACTGGA TTCTTATATC      300
      CCAGAGCCAG AGCGTGACAT TGATAAGCCA TTCCTGTTAC CAATCGAAGA      350
      CGTATTCTCA ATTTCAGGCC GTGGTACAGT TGTTACTGGT CGTGTTGAGC      400
10    GTGGTATCGT TAAAGTCGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAT      450
      ACCGTGAAAA CAACATGTAC TGGCGTTGAA ATGTTCCGTA AACTGCTGGA      500
      CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTAATAAAC      550
      GTGATGATAT CGAACGTGGT CAAGTATTGG CTAAACCAGG TTCAATCACT      600
      CCGCATACAA CTTTCGAATC AGAAGTTTAC ATCCTGAGCA AAGATGAAGG      650
15    TGGCCGTCAT ACTCCATTCT TCAAAGGTTA CCGTCCACAG TTCTACTTCC      700
      GTACAACTGA CGTAACCGGT ACTATCGAAC TGCCAGAAGG CGTTGAGATG      750
      GTAATGCCAG GTGATAACAT CAAAATGATC GTTACTCTGA TCCACCCAAT      800
      TGCAATGGAT GCAGGTCTGC GTTTTT      825

```

20

2) INFORMATION FOR SEQ ID NO:120

```

      (i) SEQUENCE CHARACTERISTICS:
25      (A) LENGTH: 827 bases
          (B) TYPE: Nucleic acid
          (C) STRANDEDNESS: Double
          (D) TOPOLOGY: Linear

```

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

      (A) ORGANISM: Branhamella catarrhalis
      (B) STRAIN: ATCC 43628

```

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120

```

      TGGTGCTATC TTGGTTGTTT CTGCAACTGA TGGTCCTATG CCACAAACTC      50
      GTGAGCATAT CCTACTATCT CGTCAGGTTG GTGTACCATA CATCATGGTA      100
40    TTCATGAACA AGTGCGATAT GGTGATGAT GAAGAGCTAC TAGAATTGGT      150
      TGAAATGGAA GTTCGTGAAC TTCTATCTGA CTATGATTTC CCTGGTGATG      200
      ATACCCCAAT CATCAAAGGT TCAGCACTAG AAGCATTGAA TGGTTCCTGAT      250
      GGTAATATG GCGAGCCTGC AGTTCTAGAA CTGCTAGACA CACTAGACAG      300
      CTATATCCCA GAGCCTGAGC GTGATATCGA TAAGTCATTC TTGATGCCAA      350
45    TTGAAGATGT CTTCTCGATC TCAGGTCGTG GTACAGTTGT GACTGGTCGT      400
      GTTGAATCAG GTATTATTAA AGTTGGTGAT GAAATTGAAA TCATCGGTAT      450
      CAAACCAACT GCTAAAACCA CCTGTACTGG TGTGAAATG TTCCGTAAAC      500
      TGTTAGACGA AGGTCGTGCA GGTGAGAACT GTGGTATCTT GTTGCGTGGT      550
      ACTAAGCGTG AAGAAGTTCA ACGCGGTCAA GTACTTGCAA AACCAGGTTC      600
50    AATCACCCCA CATACTAAGT TTGATGCTGA AGTTTATGTA CTGTCAAAG      650
      AAGAAGGTGG TCGTCACACC CCATTCTTAA ATGGCTATCG CCCACAGTTC      700
      TACTTCCGTA CCACAGATGT GACTGGTGCC ATCACTCTAC AAGAAGGTAC      750
      CGAAATGGTT ATGCCTGGTG ACAATGTTGA GATGAGTGTT GAGCTTATCC      800
      ACCCAATCGC CAGGATAAAG GTCTACG      827

```

55

2) INFORMATION FOR SEQ ID NO: 121

60 (i) SEQUENCE CHARACTERISTICS:

73

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Morganella morganii* subsp. *morganii*
 (B) STRAIN: ATCC 25830

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121

	CGGCGCTATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCTATG	CCACAGACCC	50
15	GTGAGCACAT	CCTGTTAGGT	CGTCAGGTTG	GCGTTCCTTA	CATCATCGTA	100
	TTCCTGAACA	AATGTGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCTGGCGACG	200
	ACACGCCAAT	CGTTCGCGGT	TCAGCGCTGA	AAGCACTGGA	AGGCGAGCCA	250
	GAGTGGGAAG	CTAARATCGT	TGAACTGGCA	GGTTTCCTGG	ATTCTTACAT	300
20	CCCTGAGCCA	GAGCGTGCAA	TTGACAAGCC	GTTCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	AATCTCCGGC	CGTGGTACCG	TTGTTACCGG	TCGTGTTGAG	400
	CGCGGTATCA	TCAAGGTTGG	TGAGGAAGTT	GAAATCGTGG	GTATCAAAGA	450
	TACTGCGAAA	ACCACCTGTA	CCGGTGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCMGGTGAG	AACGTCGGTG	TTCTGCTGCG	TGGTACCAAG	550
25	CGTGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCTAAACCAG	GTTCAATCAA	600
	ACCACAYACC	AAATTTGAAT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	TACTCCATTC	TTCAAAGGYT	ACCGTCCACA	GTTCTACTTC	700
	CGTACCACAG	ACGTAACAGG	TACTATCGAA	CTGCCGGAAG	GCGTTGAAAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGAT	CGTCACCCTG	ATCCACCCAA	800
30	TCGCAA					806

2) INFORMATION FOR SEQ ID NO: 122

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
 (B) STRAIN: TB 299

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122

50	GGTGCGATCC	TGGTGGTCGC	CGCCACCGAC	GGCCCGATGC	CCCAGACCCG	50
	CGAGCACGTT	CTGCTGGCGC	GTCAAGTGGG	TGTGCCCTAC	ATCCTGGTAG	100
	CGCTGAACAA	GGCCGACGCA	GTGGACGACG	AGGAGCTGCT	CGAACTCGTC	150
	GAGATGGAGG	TCCGCGAGCT	GCTGGCTGCC	CAGGAATTCT	ACGAGGACGC	200
	CCCGGTTGTG	CGGGTCTCGG	CGCTCAAGGC	GCTCGAGGGT	GACGCGAAGT	250
55	GGGTTGCCTC	TGTCGAGGAA	CTGATGAACG	CGGTCGACGA	GTCGATTCCG	300
	GACCCGGTCC	GCGAGACCGA	CAAGCCGTTC	CTGATGCCGG	TCGAGGACGT	350
	CTTCACCATT	ACCGGCCGCG	GAACCGTGGT	CACCGGACGT	GTGGAGCGCG	400
	GCGTGATCAA	CGTGAACGAG	GAAGTTGAGA	TCGTCGGCAT	TCGCCCATCG	450
	ACCACCAAGA	CCACCGTCAC	CGGTGTGGAG	ATGTTCCGCA	AGCTGCTCGA	500
60	CCAGGGCCAG	GCGGGCGACA	ACGTTGGTTT	GCTGCTGCGG	GGCGTCAAGC	550

	GCGAGGACGT	CGAGCGTGGC	CAGGTTGTCA	CCAAGCCCGG	CACCACCACG	600
	CCGCACACCG	AGTTCGAAGG	CCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	650
	CGGCCGGCAC	ACGCCGTTCT	TCAACAATA	CCGTCCGCAG	TTCTACTTCC	700
	GCACCACCGA	CGTGACCGGT	GTGGTGACAC	TGCCGGAGGG	CACCGAGATG	750
5	GTGATGCCCG	GTGACAACAC	CAACATCTCG	GTGAAGTTGA	TCCAGCCCGT	800
	CGCCATGGAC	GAAGGTCTGC	GTTTC			825

10 2) INFORMATION FOR SEQ ID NO: 123

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria cinerea*
 (B) STRAIN: ATCC 14685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123

25	CGGTGCGATC	TTGGTATGTT	CCGCAGCTGA	CGGTCCTATG	CCGCAAACCTC	50
	GCGAACACAT	CCTGTTGGCC	CGCCAAGTAG	GTGTACCTTA	CATCATCGTG	100
	TTCATGAACA	AATGCGACAT	GGTTGACGAT	GCCGAGCTGT	TGGAGCTGGT	150
	TGAAATGGAA	ATCCGTGACT	TGCTGTCAAG	CTACGACTTC	CCAGGTGACG	200
30	ACTGCCCGAT	CGTACAAGGT	TCTGCACTGA	AAGCCTTGGA	AGGCGACGCA	250
	GCTTACGAAG	AAAAAATCTT	CGAATTGGCT	GCTGCATTGG	ACAGCTACAT	300
	CCCAACACCT	GAGCGTGCAG	TGGACAAACC	TTTCTTGTTG	CCTATCGAAG	350
	ACGTATTCTC	TATTTCCGGT	CGCGGTACAG	TAGTAACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCCACGTTGG	TGACGAGATC	GAAATCGTAG	GTCTGAAAGA	450
35	AACTCAAAAA	ACCACTTGTA	CCGGTGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGTCA	AGCTGGTGAC	AACGTAGGTG	TATTGCTGCG	TGGTACTAAA	550
	CGTGAAGACG	TAGAGCGTGG	TCAAGTATTG	GCTAAACCGG	GTACTATCAC	600
	TCCTCACACC	AAGTTCAAAG	CAGAAGTATA	CGTACTGAGC	AAAGAAGAGG	650
	GTGGTCGTCA	CACTCCGTTT	TTCGCTAACT	ACCGTCCACA	ATTCTACTTC	700
40	CGTACTACCG	ACGTAACCGG	CGCGGTTACT	TTGGAAGAAG	GTGTAGAAAT	750
	GGTAATGCCG	GGTGAGAACG	TAACCATTAC	TGTAGAACTG	ATTGCGCCTA	800
	TCGCTA					806

45

2) INFORMATION FOR SEQ ID NO: 124

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria elongata* subsp. *elongata*
 (B) STRAIN: ATCC 25295

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124


```

      CGGCGCAATC TTGGTATGTT CCGCTGCTGA CCGTCCTATG CCGCAAACCTC      50
      GCGAACACAT CCTGTTGGCC CGCCAAGTAG GCGTACCTTA CATCATCGTG      100
      TTCATGAATA AATGCGACAT GGTGAYGAT GCCGAACTGC TGGAAGTGGT      150
5     TGAAATGGAA ATCCGTGACT TGCTGTCAAG CTACGACTTC CCAGGCGACG      200
      ACTGCCCCGAT CGTACAAGGT TCCGCACTGA AAGCCTTGGA AGGCGACGCA      250
      GCTTACGAAG AAAAAATCTT CGAACTGGCT GCTGCATTGG ACAGCTACAT      300
      CCCGACACCT GAGCGTGCCG TGGACAAACC GTTCCTGTTG CCTATCGAAG      350
      ACGTATTCTC TATCTCCGGC CGTGGTACAG TAGTAACCGG TCGTGTAGAG      400
10    CGCGGTATCA TCCACGTCGG TGACGAGATC GAAATCGTAG GTCTGAAAGA      450
      AACCCTAAAA ACCACTTGTA CCGGTGTTGA AATGTTCCGC AAAGTGTGCTG      500
      ACGAAGGTCA AGCAGGTGAC AACGTAGGCG TATTGCTGCG CCGTACCAAA      550
      CGTGAAGAAG TGGAACGCGG TCAAGTATTG GCTAAACCGG GTACCATCAC      600
      TCCTCACACC AAATTCAAAG CAGAAGTTTA CGTATTGAGC AAAGAAGAGG      650
15    GTGGTCGTCA TACTCCGTTT TTCGCTAACT ACCGTCCACA ATTCTACTTC      700
      CGTACTACCG ACGTAACCGG TCGGGTACTT TTGGAAGAAG GTGTAGAAAT      750
      GGTATGCCT GGTGAGAACG TGGCCATCAC TGTAGAACTG ATTGCACCTA      800
      TCGCTATGGA AGAAGGTCTG CG                                822

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20

2) INFORMATION FOR SEQ ID NO: 125

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      (i) SEQUENCE CHARACTERISTICS:
25      (A) LENGTH: 820 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

30      (ii) MOLECULE TYPE: Genomic DNA

      (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Neisseria flavescens
      (B) STRAIN: ATCC 13120

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125

```

      CGGCGCGACT TGGTATGTTT CGCAGCTGAC GGTCTTATGC CGCAAACCCG      50
      CGAACACATC CTGTTGGCTC GCCAAGTAGG TGTACCTTAC ATCATCGTAT      100
40    TCATGAACAA ATGCGACATG GTAGACGATG CCGAGCTGTT GGAAGTGGTT      150
      GAAATGGAAA TTCGTGACTT GTTGTCAGC TACGACTTCC CAGGCGACGA      200
      CTGCCCAATC GTACAAGGTT CTGCACTGAA AGCTTTGGAA GTTGATGCTG      250
      CTTACGAAGA AAAAATCTTC GAATTGGCTG CTGCCTTGGA CAGCTACATC      300
      CCAACACCTG AGCGTGCTGT GGACAAACCT TTCTTGTTGC CTATCGAAGA      350
45    CGTATTCTCT ATCTCTGGTC GTGGTACAGT AGTAACCGGT CGCGTAGAGC      400
      GCGGTATCAT CCACGTTGGT GACGAGATCG AAATCGTAGG TCTGAAAGAA      450
      ACTCAAAAAA CCACTTGTA CCGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
      CGAAGGTCAA GCAGGTGACA ACGTAGGCGT ATTGCTGCGT GGTACTAAAC      550
      GTGAAGACGT AGAGCGTGGT CAAGTATTGG CTAAACCAGG TACCATCACT      600
50    CCTCACACCA AATTCAAAGC AGAAGTATAC GTACTGAGCA AAGAAGAGGG      650
      TGGTCGTCAC ACTCCATTTT TCGCTAACTA CCGTCCACAA TTCTACTTCC      700
      GTACTACCGA CGTAACCTGGT GCAGTTACTT TGGAAGAAGG CGTAGAAATG      750
      GTAATGCCAG GTGAGAACGT AACCATTACT GTAGAACTGA TTGCGCCAAT      800
      CGCTATGGAA GAAGTCTGCG                                820

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55

2) INFORMATION FOR SEQ ID NO: 126

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60      (i) SEQUENCE CHARACTERISTICS:

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76

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria gonorrhoeae*
 (B) STRAIN: ATCC 49226

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126

	GGTGCAATCC	TGGTATGTTT	TGCTGCCGAC	GGCCCTATGC	CGCAAACCCG	50
15	CGAACACATC	CTGCTGGCCC	GTCAAGTAGG	CGTACCTTAC	ATCATCGTGT	100
	TCATGAACAA	ATGCGACATG	GTCGACGATG	CCGAGCTGTT	GGAAGTGGTT	150
	GAAATGGAAA	TCCGCGACCT	GCTGTCCAGC	TACGACTTCC	CCGGCGACGA	200
	CTGCCCCGATC	GTACAAGGTT	CCGCACTGAA	AGCCTTGGAA	GGCGATGCCG	250
	CTTACGAAGA	AAAAATCTTC	GAAGTGGCTA	CCGCATTGGA	CAGCTACATC	300
20	CCGACTCCCG	AGCGTGCCGT	GGACAAACCA	TTCCTGCTGC	CTATCGAAGA	350
	CGTGTCTCTC	ATTTCGGGCC	GCGGTACCGT	AGTCACCGGC	CGTGTAGAGC	400
	GAGGTATCAT	CCACGTTGGT	GACGAGATTG	AAATCGTCGG	TCTGAAAGAA	450
	ACCCAAAAAA	CCACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGTCAG	GCGGGCGACA	ACGTAGGCGT	ATTGCTGCGC	GGTACCAAAC	550
25	GTGAAGACGT	AGAACGCGGT	CAGGTATTGG	CCAAACCGGG	TACTATCACT	600
	CCTCACACCA	AGTTCAAAGC	AGAAGTGTAC	GTATTGAGCA	AAGAAGAGGG	650
	CGGCCGCCAT	ACCCCGTTTT	TCGCCAACTA	CCGTCCCCAA	TTCTACTTCC	700
	GTACCACTGA	CGTAACCGGC	GCGGTTACTT	TGGAAAAAGG	TGTGGAAATG	750
	GTAATGCCGG	GTGAGAACGT	AACCATTACT	GTAGAACTGA	TTGCGCCTAT	800
30	CGCTATGGAA	GAAGGTCTGC	GCTTTGCGAT			830

2) INFORMATION FOR SEQ ID NO: 127

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria lactamica*
 (B) STRAIN: ATCC 23970

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127

50	CGGCGCAATC	TTGGTATGTT	CCGCCGCCGA	CGGCCCTATG	CCGCAAACCC	50
	GCGAACACAT	TCTGTTGGCC	CGCCAAGTAG	GTGTACCTTA	CATCATCGTA	100
	TTCATGAACA	AATGCGATAT	GGTCGACGAT	GCCGAGCTGT	TGGAAGTGGT	150
	TGAAATGGAA	ATCCGCGACC	TGCTGTCAAG	CTACGACTTC	CCAGGCGACG	200
	ACTGCCCAAT	CGTACAAGGT	TCCGCACTGA	AAGCTTTGGA	AGGCGATGCC	250
55	GCTTACGAAG	AAAAAATCTT	CGAACTGGCT	GCCGCATTGG	ACAGCTACAT	300
	CCCGACTCCC	GAGCGTGCCG	TGGACAAACC	GTTCTGCTG	CCTATCGAAG	350
	ACGTATTCTC	CATCTCCGGC	CGCGGTACGG	TAGTAACCGG	CCGTGTAGAG	400
	CGCGGTGTCA	TCCACGTTGG	CGACGAGATC	GAAATCGTCG	GTCTGAAAGA	450
	AACCCAAAAA	ACCACCTGTA	CCGGTGTGCA	GATGTTCCGC	AAACTGCTGG	500
60	ACGAAGGTCA	GGCAGGCGAC	AACGTAGGCG	TATTGCTGCG	CGGTACCAAA	550

	CGTGAAGAAG	TGGAACGCGG	TCAGGTATTA	GCCAAACCGG	GTACCATCAC	600
	TCCGCACACC	AAGTTCAAAG	CAGAAGTGTA	TGTATTGAGC	AAAGAAGAGG	650
	GCGGTCGTCA	CACTCCGTTC	TTCGCCAACT	ACCGTCCGCA	ATTCTACTTC	700
	CGTACCACCG	ACGTAACCGG	CGCGGTTACT	TTGGAAGAAG	GCGTGGAAT	750
5	GGTAATGCCC	GGTGAGAACG	TAACCATTAC	TGTAGAAGT	ATTGCGCCTA	800
	TCGCTATGGA	AGAAGG				816

10 2) INFORMATION FOR SEQ ID NO: 128

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*
 (B) STRAIN: ATCC 13077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128

25	CGGTGCAATC	CTGGTATGTT	CCGCAGCCGA	CGGTCCTATG	CCGCAAACCC	50
	GCGAACACAT	CCTGCTGGCC	CGTCAAGTAG	GCGTACCTTA	CATCATCGTG	100
	TTCATGAACA	AATGCGACAT	GGTCGACGAT	GCCGAGCTGT	TGGAAGTGGT	150
	TGAAATGGAA	ATCCGCGACC	TGCTGTCCAG	CTACGACTTC	CCCGGCGACG	200
30	ACTGCCCCGAT	CGTACAAGGT	TCCGCACTGA	AAGCCTTGGA	AGGCGATGCC	250
	GCTTACGAAG	AAAAAATCTT	CGAATTGGCT	GCTGCATTGG	ACAGCTACAT	300
	CCCGACTCCC	GAGCGTGCCG	TGGACAAACC	TTTCTTGTTG	CCTATCGAAG	350
	ACGTATTCTC	TATTTCCGGT	CGTGGTACAG	TAGTAACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCCACGTCGG	TGACGAGATC	GAAATCGTCG	GTCTGAAAGA	450
35	AACTCAAAA	ACCACTTGTA	CCGGTGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGTCA	AGCAGGCGAC	AACGTAGGCG	TATTGCTGCG	CGGTACCAA	550
	CGTGAAGACG	TAGAGCGTGG	TCAAGTATTG	GCTAAACCGG	GTACAATCAC	600
	TCCTCACACC	AAGTTCAAAG	CAGAAGTATA	CGTACTGAGC	AAAGAAGAGG	650
	GCGGCCGCCA	TACCCCGTTC	TTCGCCAACT	ACCGTCCCCA	ATTCTACTTC	700
40	CGTACCACCG	ACGTAACCGG	CGCGGTTACT	TTGGAAGAAG	GTGTGGAAAT	750
	GGTAATGCCG	GGCGAGAACG	TAACCATCAC	CGTAGAAGT	ATTGCGCCTA	800
	TCGCTATGGA	AGAAGGTTTG	CGCTTTGCGA	T		831

45

2) INFORMATION FOR SEQ ID NO: 129

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria mucosa*
 (B) STRAIN: ATCC 19696

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129

	CGGCGCAATC	TTGGTATGTT	CTGCTGCTGAC	GGTCCTATGC	CGCAAACCCG	50
	GYGAACACAT	CCTGTTGGCC	CGTCAAGTAG	GYGTACCTTA	CATCATCGTG	100
	TTCATGAACA	AATGCGACAT	GGTTGACGAT	GCCGAAYTGT	TGGAACCTGGT	150
5	TGAAATGGAA	ATCCGTGACT	TGCTGTCAAG	CTACGACTTC	CCTGGYGACG	200
	ACTGCCCCGAT	TGTACAAGGT	TCTGCACTGA	AAGCCTTGGA	AGGCGATGCC	250
	GCTTACGAAG	AAAAAATCTT	CGAACTGGCT	GCCGCATTGG	ACAGCTACAT	300
	CCCGACTCCC	GAGCGTGCCG	TAGACAAACC	GTTCTCTGTTG	CCTATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACAG	TAGTAACCGG	CCGTGTAGAG	400
10	CGCGGTGTTA	TCCACGTTGG	TGACGAGATC	GAAATCGTAG	GTCTGAAAGA	450
	AACCCAAAAA	ACCACATGTA	CCGGTGTGTA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGTCA	AGCCGGTGAC	AACGTAGGCG	TATTGCTGCG	CGGTACCAAA	550
	CGTGAAGAAG	TGGAACGCGG	TCAAGTATTG	GCTAAACCGG	GTACCATCAC	600
	TCCGCACACC	AAATTCAAAG	CAGAAGTGTA	CGTATTGAGC	AAAGAAGAGG	650
15	GTGGTCGTCA	TACTCCGTTT	TTCGCTAACT	ACCGTCCTCA	ATTCTACTTC	700
	CGTACTACCG	ACGTAACCGG	TGCGGTTACT	TTGGAAGAAG	GTGTAGAAAT	750
	GGTTATGCCT	GGTGAGAAYG	TAGCCATYAC	TGTAGAAGTG	ATTGCGCCTA	800
	TYGCTATGGA	AGAAG				815

20

2) INFORMATION FOR SEQ ID NO: 130

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 829 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria sicca*

(B) STRAIN: ATCC 9913

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130

	GGCGCAATCT	TGGTATGTTT	CGCTGCTGAC	GGTCCTATGC	CGCAAACCCG	50
	CGAACACATC	CTGTTGGCCC	GCCAAGTAGG	CGTACCTTAC	ATCATCGTGT	100
40	TCATGAACAA	ATGCGACATG	GTTGACGATG	CCGAGCTGTT	GGAACCTGGT	150
	GAAATGGAAA	TCCGTGACTT	GCTGTCAAGC	TACGACTTCC	CTGGTGACGA	200
	CTGCCCCGATC	GTACAAGGTT	CTGCACTGAA	AGCCTTGGA	GGCGACGCCG	250
	CTTACGAAGA	AAAAATCTTC	GAAGTGGCTG	CTGCATTGGA	CAGCTACATC	300
	CCGACTCCTG	AGCGTGCCGT	GGACAAACCG	TTCCTGTTGC	CTATTGAAGA	350
45	CGTATTCTCC	ATCTCCGGTC	GCGGTACCGT	AGTAACCGGC	CGTGTAGAGC	400
	GCGGTGTTAT	CCACGTTGGT	GACGAGATTG	AAATCGTAGG	TCTGAAAGAA	450
	ACCCAAAAAA	CACTTGTAC	CGGTGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGTCAA	GCCGGTGACA	ACGTAGGCGT	ATTGCTGCGC	GGTACCAAAC	550
	GTGAAGAAGT	GGAACGCGGT	CAAGTATTGG	CTAAACCGGG	TACCATCACT	600
50	CCTCACACTA	AATTCAAAGC	AGAAGTTTAC	GTATTGAGTA	AAGAAGAGGG	650
	TGGTCGTCAT	ACTCCGTTCT	TCGCTAACTA	CCGTCCTCAA	TTCTACTTCC	700
	GTACTACCGA	CGTAACCGGC	GCGGTTACTT	TGGAAGAAGG	TGTAGAAATG	750
	GTTATGCCTG	GTGAGAACGT	AGCCATCACT	GTAGAAGTGA	TTGCACCGAT	800
	CGCTATGGAA	GAAGGTCTGC	GCTTTGCGA			829

55

2) INFORMATION FOR SEQ ID NO: 131

60 (i) SEQUENCE CHARACTERISTICS:

79

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria subflava*
 (B) STRAIN: ATCC 14221

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131

	CGGCGCGACT	TGGTATGTTT	CGCAGCTGAT	GGTCCTATGC	CTCAAACCTCG	50
15	CGAACACATC	CTGTTGGCTC	GCCAAGTAGG	TGTACCTTAC	ATCATCGTAT	100
	TCATGAACAA	ATGCGACATG	GTTGACGATG	CCGAGCTGTT	GGAACCTGGTT	150
	GAAATGGAAA	TCCGTGACCT	GTTGTCAAGC	TACGACTTCC	CAGGCGACGA	200
	CTGCCCAATC	GTACAAGGTT	CTGCACTGAA	AGCTTTGGAA	GGTGACGCTG	250
	GTTACGAAGA	GAAAATCTTC	GAATTGGCTG	CTGCTCTGGA	CAGCTACATC	300
20	CCAACACCTG	AGCGTGCTGT	GGACAAACCT	TTCTTGTTGC	CTATCGAAGA	350
	CGTATTCTCT	ATCTCTGGCC	GTGGTACAGT	AGTAACTGGT	CGTGTAGAGC	400
	GCGGTATCAT	CCACGTTGGT	GACGAGATCG	AAATCGTAGG	TCTGAAAGAA	450
	ACCCAAAAAA	CCACTTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGTCAA	GCTGGTGACA	ACGTAGGCGT	ATTGCTGCGT	GGTACCAAAC	550
25	GTGAAGACGT	AGAGCGTGGT	CAAGTATTGG	CTAAACCAGG	TACCATTACT	600
	CCTCACACCA	AATTCAAAGC	AGAAGTATAC	GTACTGAGCA	AAGAAGAGGG	650
	TGGTCGTCAC	ACTCCATTCT	TCGCTAACTA	CCGTCCACAA	TTCTACTTCC	700
	GTACTACTGA	CGTAACTGGT	GCAGTTACTT	TGGAAGAAGG	CGTAGAAATG	750
	GTAATGCCAG	GTGAGAACGT	AACCATTACT	GTAGAACTGA	TTGCGCCTAT	800
30	CGCTATGGAA	GAAG				814

2) INFORMATION FOR SEQ ID NO: 132

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria weaveri*
 (B) STRAIN: ATCC 51223

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132

50	GCCATCTTGG	TATGTTCTGC	TGCTGACGGT	CCTATGCCGC	AAACCCGTGA	50
	GCACATCCTG	TTGGCTCGTC	AAGTAGGTGT	ACCCTACATC	ATCGTATTCA	100
	TGAACAAATG	CGATATGGTT	GATGATGCAG	AGCTGCTGGA	ATTGGTAGAA	150
	ATGGAAATCC	GTGATCTGCT	GAGCAGCTAC	GATTTCCCTG	GCGATGATTG	200
	YCCAATCGTG	CAAGGTTCTG	CTTTGAAAGC	TTTGGAAGGT	GATGCCGCTT	250
55	ACGAAGAAAA	AATCTTTGAA	TTAGCTGCTG	CATTGGATAG	CTATATTCCA	300
	ACWCCTGAGC	GYGCTGTTGA	TAAACCATTG	CTGTTGCCGA	TTGAAGATGT	350
	ATTCTCAATT	TCAGGTCGTG	GTACAGTAGT	AACTGGTCGT	GTAGAGCGCG	400
	GTATTATTCA	CGTAGGCGAT	GAAATTGAAA	TTGTAGGTTT	GAAAGARACY	450
	CAAAAACTA	CTTGTAACCG	CGTTGAAATG	TTCCGTAAAT	TGCTGGATSA	500
60	AGGTCAGGCT	GGTGATAACG	TAGGCGTATT	GTTGCGTGGT	ACCAAACGTG	550

	AAGACGTTGA	GCGTGGTCAA	GTATTGGCTA	AGCCTGGTWC	TATTACTCCG	600
	CAYACCAAAT	TCAAAGCAGA	RGTKTATGTW	TTGAGYAAGG	AAGAAGGCGG	650
	TCGTCATACT	CCGTTCTTCG	CTAACTATCG	TCCGCAATTC	TATTTCCGTA	700
	CTACAGACGT	TACCGGTGCK	GTRACTTTAG	AAGAAGGTGT	GGAAATGGTA	750
5	ATGCCTGGTG	AGAAYGTTGC	CATTACTGTW	GARYTGATYG	CTCCGATTGC	800
	KATGGAAGAA	GGYTGCGT				818

10 2) INFORMATION FOR SEQ ID NO: 133

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ochrobactrum anthropi*
 (B) STRAIN: ATCC 49188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133

25	CGGCGCAATT	CTGGTTGTTT	CGGCCGCTGA	CGGCCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTCGCT	CGTCAGGTTG	GCGTTCCGGC	AATCGTCGTG	100
	TTCCTGAACA	AGTGCGACCA	GGTTGACGAT	GCAGAACTGC	TCGAACTGGT	150
	TGAACTGGAA	GTTCGCGAAC	TTCTGTCGAA	ATACGATTTC	CCGGGCGACG	200
30	AAGTTCCGAT	CATCAAGGGC	TCGGCTCTTG	CTGCTCTGGA	AGATTCTTCG	250
	AAGGAACTGG	GCGAAGACGC	CGTTCGTTTC	CTGATGGCCG	CTGTTGACGA	300
	CTACATTCCG	ACCCCGGAAC	GTCCGATCGA	CCAGCCGTTC	CTGATGCCGA	350
	TCGAAGACGT	TTTCTCGATC	TCGGGCCGTG	GTACGGTTGT	GACGGGTCGC	400
	GTTGAGCGCG	GTATCGTCAA	GGTTGGTGAA	GAAGTTGAAA	TCGTCGGCAT	450
35	CAAGGCGACG	GCGAAGACGA	CGGTAACCGG	CGTTGAAATG	TTCCGCAAGC	500
	TGCTCGAYCA	GGGCCAGGCT	GGCGACAACA	TCGGCGCTCT	GATCCGCGGC	550
	GTTGGCCGTG	AAGACGTTGA	ACGCGGCCAG	GTTCTCTGCA	AGCCGGGTTC	600
	TGTGAAGCCG	CACACCAAGT	TCAAGGCAGA	AGCCTACATT	CTGACCAAGG	650
	ACGAAGGTGG	CCGTCATACG	CCGTTCTTTA	CGAACTACCG	TCCGCAGTTC	700
40	TACTTCCGCA	CGACGGACGT	GACCGGTGTT	GTCACGCTGC	CGGAAGGCAC	750
	GGAAATGGTT	ATGCCTGGCG	ACAACGTCCG	TATGGACGTC	ACCCTGATCG	800
	TGCCGATCGC	CATGGAAGAG	AAGCTCCGCT	TCGCTA		836

45

2) INFORMATION FOR SEQ ID NO: 134

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pantoea agglomerans*
 (B) STRAIN: ATCC 27155

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134

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      CCTGGTTGTT GCTGCGACTG ATGGCCCAAT GCCACAGACC CGTGAGCACA      50
      TCCTGCTGGG TCGTCAGGTT GGC GTTCCTT ACATCATCGT GTTCCTGAAC      100
      AAGTGTGACA TGGTTGATGA TGAAGAGCTG CTGGAAGTGG TAGAGATGGA      150
5     AGTACGTGAC CTGCTGTCAC AGTACGACTT CCCAGGCGAT GACACCCCGA      200
      TCGTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGTTCC TGAGTGGGAA      250
      GCAAAAATCG TTGAGCTGGC TGAACACCTG GACAACTACA TCCCGGATCC      300
      AGTCCGTGCG ATCGACATGC CGTTCCTGCT GCCAATCGAA GACGTATTCT      350
      CAATCTCTGG CCGTGGTACC GTTGTTACCG GTCGTGTTGA GCGCGGCATC      400
10    GTTAAAGTCG GCGACGAAGT TGAAATCGTG GGTATCAAAG ATACTGCGAA      450
      ATCAACCTGT ACCGGTGTGT AGATGTTCCG TAAGCTGCTG GACCAGGGTC      500
      AGGCAGGCGA AAAGTGTGGT GTTCTGCTGC GCGGTATCAA GCGTGAAGAC      550
      ATCCAGCGTG GCCAGGTTCCT GGCTAAGCCA GGCTCAATCA AGCCGCACAC      600
      CCAGTTCGAG TCAGAAGTTT ACGTTCTGTC TAAAGACGAA GGTGGCCGCC      650
15    ATACTCCGTT CTTCAAAGGC TATCGTCCAC AGTTCTACTT CCGTACAAC      700
      GATGTAACCG GTTCAGTAGA GCTGCCAGAA GGC GTTGAGA TGGTCATGCC      750
      AGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCA ATCGCAATGG      800
      ACGAA      805

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20

2) INFORMATION FOR SEQ ID NO: 135

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      (i) SEQUENCE CHARACTERISTICS:
25      (A) LENGTH: 825 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

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30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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      (A) ORGANISM: Pantoea dispersa
      (B) STRAIN: ATCC 14589

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135

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      CGCGATCCTG GTTGTGCTG CGACTGATGG CCCAATGCCT CAGACCCGTG      50
      AGCACATCCT GCTGGGCCGT CAGGTTGGCG TTCCTTACAT CATCGTGTTT      100
40    CTGAACAAGT GTGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTTGA      150
      GATGGAAGTT CGCGATCTGC TGTCTCAGTA CGACTTCCCA GGCGACGATA      200
      -----
      CCCCAATCGT ACGCGGTTCI GCGCTGAAAG CGCTGGAAGG CGACGCTGAG      250
      TGGGAAGCGA AAGTCGTTGA GCTGGCTGGT CACCTGGATA CTTACATTCC      300
      AGATCCAGTA CGTGCTATCG ATCTGCCGTT CCTGCTGCCA ATCGAAGACG      350
45    TATTCTCAAT CTCTGGCCGT GGTACCGTTG TTACCGGTCG TGTTGAGCGC      400
      GGCATCGTGA AAGTGGGCGA CGAAGTAGAA ATCGTTGGTA TCAAAGCGAC      450
      TGCCAAGTCT ACCTGTACCG GTGTTGAAAT GTTCCGCAA CTGCTGGACC      500
      AGGGTCAGGC AGGCGAGAAC TGTGGTGTTT TGCTGCGCGG TATCAAGCGT      550
      GAAGAGATCC AGCGTGGTCA GGTTCCTGGT AAGCCAGGCA CCATCAAGCC      600
50    ACACACCAAG TTCGTATCAG AAGTGTACGT ACTGTCTAAA GACGAAGGCG      650
      GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCACAGTT CTACTTCCGT      700
      ACYACTGATG TGACCGGCAM CATMGAAGT CCAGAAGGCG TTGAGATGGT      750
      AATGCCAGGC GACAACATCA AAATGRCCGT TGAGCTGATC CACCCAATCG      800
      CGATGGACCA GGTCTGCGT TTCGC      825

```

55

2) INFORMATION FOR SEQ ID NO: 136

60 (i) SEQUENCE CHARACTERISTICS:

82

(A) LENGTH: 762 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pasteurella multocida*
 (B) STRAIN: NCTC 10322

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136

	CACAAACACG	TGAGCACATC	CTTTTAGGTC	GCCAAGTAGG	CGTTCCTTAC	50
15	ATCATCGTAT	TCTTAAACAA	ATGCGACATG	GTGGATGATG	AAGAATTATT	100
	AGAATTAGTT	GAAATGGAAG	TGCGTGAAC	TCTTTCTCAA	TATGATTTC	150
	CAGGTGATGA	TACACCAATC	GTACGTGGTT	CAGCGTTACA	AGCGTTAAAC	200
	GGYGTAGCTG	AGTGGGAAGA	GAAAATTCTT	GAGTTAGCCA	ACCACTTAGA	250
	TACTTACATT	CCAGAGCCAC	AACGTGCAAT	CGACCAACCG	TTCCTTCTTC	300
20	CGATTGAAGA	CGTGTCTCA	ATTTCTGGTC	GTGGTACAGT	AGTAACAGGT	350
	CGTGTGAGC	GTGGTATCAT	CCGTACAGGT	GAAGAGGTTG	AAATTGTTGG	400
	TATTAAAGCG	ACAACGAAGA	CCACAGTAAC	AGGTGTTGAG	ATGTTCCGTA	450
	AATTATTAGA	CGAAGGTCGT	GCGGGTGAGA	ACGTTGGTGC	TTTATTACGT	500
	GGTACTAARC	GTGAAGAAAT	CGAACGTGGT	CAAGTGTTAG	CGAAACCGGG	550
25	TTCAATYACG	CCACACACTG	ATTTTGAATC	AGAAGTTTAC	GTGTTATCAA	600
	AAGAAGAAGG	TGGTCGTCAT	ACACCATTCT	TCAAAGGTTA	CCGTCCACAG	650
	TTCTACTTCC	GTACAACGGA	CGTAACAGGT	ACAATCGAAT	TACCGGAAGG	700
	TGTTGAGATG	GTGATGCCTG	GTGATAACAT	CAAGATGACT	GTAAGTTTGA	750
	TTCACCCAAT	CG				762

30

2) INFORMATION FOR SEQ ID NO: 137

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Peptostreptococcus anaerobius*
 (B) STRAIN: ATCC 27337

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137

	TGGAGCTATC	TTAGTTGTAT	CAGCAGCGGA	TGGACCAATG	CCACAAACAA	50
50	GAGAACACAT	CTTATTATCA	AGACAAGTAG	GAGTACCATA	TATCGTAGTA	100
	TATTTGAATA	AAGCAGATAT	GGTAGAAGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTAAGAGAAT	TACTATCTGA	ATATGGATTG	CCAGGAGATG	200
	AAATTCCAAT	CATAACAGGA	TCATCCTTAG	GAGCATTAAG	TGGAGAACAA	250
	AAATGGATAG	ATCAAATCAT	GGCATTGATG	AAAGCCGTAG	ATGAATATAT	300
55	TCCAACACCG	GAAAGAGCAG	TAGATCAACC	ATTCTTGATG	CCAATCGAAG	350
	ACGTATTTAC	AATTACAGGA	AGAGGAACTG	TAGTAACAGG	AAGAGTTGAA	400
	AGAGGAGTTG	TAAAAGTWGG	AGAAGAAGTT	GAAATCGTAG	GAATCAAAGC	450
	GACAACAAAG	ACAACCTGTA	CYGGAGTAGA	AATGTTCCGA	AAATTATTGG	500
	ATCAAGGACA	AGCAGGAGAT	AACATCGGAG	CTTTATTTRAG	AGGAACCAAG	550
60	AAAGAAGATG	TAGAAAGAGG	ACAAGTATTG	GCAAAACCAAG	GAACAATTCA	600

	TCCTCATACA	AACTTCAGTG	GAGAAGTATA	TGTATTGACA	AAAGAAGAAG	650
	GAGGAAGACA	TACTCCATTC	TTCTCAGGAT	ACAGACCACA	ATTTTACTTT	700
	AGAACCACAG	ATATTACAGG	AGCAGTAACA	TTACCAGAAG	GAGTAGAAAT	750
	GGTAATGCCR	GGAGATAATA	TCACAATGAC	AGTAGAATTG	ATTCACCCAA	800
5	TTGCAATGGA	AACAGGATTA	CGATTTGCAA	TT		832

10 2) INFORMATION FOR SEQ ID NO: 138

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 823 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Peptostreptococcus asaccharolyticus*
(B) STRAIN: LSPQ 2639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138

25	TAGTATGTTC	AGCAGCAGAY	GGTCCAATGC	CACAAACAAG	AGAACACATT	50
	CTACTAGCAA	GACAAGTTGG	TGTACCAAAG	ATAGTAGTAT	TCCTAAACAA	100
	AGAAGACCAA	GTAGACGATC	CAGAACTAAT	TGAATTAGTA	GAGATGGAAA	150
	TCAGAGACCT	ACTATCAGAA	TATGACTTCG	AYGGAGACAA	CACACCAATC	200
	GTAGTAGGAT	CAGCATTAAA	AGCCCTAGAC	GATCCAGACG	GAGAATGGGG	250
30	AGACAAAATC	GTAAAACTAA	TGGAAGMAGT	AGACGAATAC	ATCCCAACAC	300
	CAGTAAGAGA	TACAGAACAC	CCATTCTCTA	TGCCAATCGA	AGACRTATTC	350
	TCAATYACAG	GAAGAGGAAC	AGTAGCAACA	GGAAGAGTAG	AACAAGGTGT	400
	AGTAAAAGTA	GGMGACACAG	TAGAACTAGT	AGGCTTAACA	GACGAAAGCA	450
	GACAAGTAGT	AGTAACAGGT	GTAGAAATGT	TTAGAAAACA	ACTAGACCTA	500
35	GCAGAAGCMG	GAGACAACAT	TGGAGCCCTA	CTAAGAGGAG	TACAAAGAGA	550
	AGAAATCCAA	AGAGGACAAG	TACTAGCAGC	ACCAGGAACA	ATCAAACCAC	600
	ACACAAAATT	TGAAGCAGAA	GTATACGTAC	TAACAAAAGA	AGAAGGTGGA	650
	AGACACACAC	CATTCTTTAA	CGGATACAGA	CCACAATTCT	ACTTCAGAAC	700
	AACAGACGTA	ACAGGAGACA	TCCAAC TAGC	AGACGGAGTA	GAAATGGTAA	750
40	TGCCAGGAGA	CAACTCAACA	TTTACAGTAA	CACTAATCAC	ACCAATCGCA	800
	ATGGACGAAG	GACTAAGATT	CGC			823

45 2) INFORMATION FOR SEQ ID NO: 139

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 832 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Peptostreptococcus prevotii*
(B) STRAIN: ATCC 9321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139

60

	CTATCATCGT	AGTATCTGCA	GCAGACGGTC	CAATGCCCAA	ACAGAGAGAA	50
	CACATCCTAC	TAGCAAGACA	AGTAGGCGTT	CCAAAAATCG	CAGTATTCCT	100
	AAACAAAGAA	GACCAAGTAG	ACGATCCAGA	ACTAATCGAA	TTAGTAGAAA	150
	TGGAAATCAG	AGACCTACTT	TCAGAATACG	ACTTCGATGG	AGACAACGCT	200
5	CCAGTAGTAG	TAGGATCTGC	TCTTAAATCA	CTAGAAGAAG	GCGGAGAAGG	250
	CCCATGGTCA	GACAAAATCC	TTGACCTAAT	GGCACAAGTA	GACGAATACT	300
	TCGACATCCC	AGAAAGAGAC	AACGACCAAC	CATTCTTAAT	GCCAGTAGAA	350
	GACGTAATGA	CAATCTCAGG	ACGTGGAACA	GTCAGCAACAG	GAAGAGTTGA	400
	AAGAGGAACA	CTAAAAGTTG	GTGATACAGT	AGAAATCGTA	GGACTAACAG	450
10	AAGATACAAA	AGAAACAGTA	GTAACCTGGAG	TAGAAATGTT	CCACAAATCM	500
	CTAGACCAAG	CAGAATCTGG	AGATAACGTA	GGACTACTAC	TAAGAGGAGT	550
	AACAAGAGAT	CAAATCTCAA	GAGGACAAGT	ACTAGCAAAA	CCAGGWTCAG	600
	TAAACCCACA	CACAGAATTC	GAAGGTCAAG	TATACGTACT	AACAAAAGAA	650
	GAAGGTGGAC	GTCACACACC	ATTCTTCAGT	GGATATAGAC	CACAATTCTT	700
15	CTTTAGAACA	ACAGACGTAA	CAGGAGACAT	CGAACTAGAA	GAAGGCGTAG	750
	AAATGGTAAT	GCCAGGAGAC	AACGCAACAT	TCAAAATCAC	ACTCCAAAAA	800
	CCAATCGCTC	TAGAAGAAGG	ACTAAGATTC	GC		832

20

2) INFORMATION FOR SEQ ID NO: 140

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas asaccharolytica*
 (B) STRAIN: ATCC 25260

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140

	CGGTGCTATC	ATCGTAGTTG	CTGCAACTGA	TGGTCCTATG	CCTCAGACGC	50
	GTGAGCACAT	CCTACTAGCA	CGTCAGGTCA	ACGTACCTCG	TCTAGTTGTC	100
	TTTATGAACA	AGTGCGACCT	TGTTGATGAC	GAGGAGATGC	TCGAGCTCGT	150
40	AGAGATGGAT	ATGCGTGAGC	TACTAAGCTT	CTATGACTTT	GACGGCGACA	200
	ACACTCCTGT	CATCCGTGGT	TCTGCTCTTG	GTGCTCTCAA	TGGTGAGCCT	250
	AAGTGGGTAG	AGAAGGTTAT	GGAGCTCATG	GAGGCTGTAG	ACACTTGGAT	300
	CCCACTACCT	GAGCGCGACA	TCGACAAGCC	TTTCCTAATG	CCTGTAGAGG	350
	ACGTATTCTC	TATCACAGGT	CGTGGTACTG	TCGCTACTGG	TCGTATCGAG	400
45	ACTGGTGTCT	TTAAGGTCAA	CGATGAGGTT	CAGATCATCG	GTCTAGGTGC	450
	TGAGGGTAAG	AAGAGCGTCG	TAACTGGCGT	GGAAATGTTC	CGCAAGATCC	500
	TTGATGAGGG	TGAAGCTGGT	GATAACGTAG	GTCTCCTACT	CCGTGGTATC	550
	GACAAGGACG	AGATCAAGCG	CGGTATGGTC	CTAGCACACC	CAGGTCAGGT	600
	CAAGCCTCAC	GATCACTTCA	AGGCTGAGGT	CTATATCCTG	AAGAAGGAAG	650
50	AGGGTGGTCG	TCACACACCA	TTCCACAACA	AGTACCGTCC	TCAGTTCTAC	700
	ATCCGTACGC	TAGACGTAAC	GGGCGAGATC	ACACTCCCAG	AGGGTGTAGA	750
	GATGGTTATG	CCTGGTGATA	ACGTCACCAT	CGATGTCAAG	CTCATCTCTC	800
	CAGTAGCTTG	TAGCGTAGGT	CTACGCTTCG	C		831

55

2) INFORMATION FOR SEQ ID NO: 141

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases

85

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*
 (B) STRAIN: ATCC 33277

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141

	CGGTGCTATA	ATCGTTGTAG	CAGCTACAGA	CGGTCCTATG	CCTCAGACTC	50
	GCGAGCACAT	CCTTTTGGCT	CGCCAGGTAA	ACGTTCCCTCG	TCTGGTTGTT	100
15	TTCATGAACA	AATGTGACAT	GGTAGACGAT	GAAGAGATGC	TCGAGCTTGT	150
	TGAAATGGAC	ATGCGCGAAC	TCCTTTCTTT	CTACGATTTC	GATGGTGACA	200
	ATACCCCTAT	CATCCGTGGT	TCTGCTCTGG	GCGCTTTGAA	TGGAGAGCCT	250
	CAGTGGGAAG	ACAAGGTGAT	GGAGCTTATG	GAAGCTGTTG	ACAACTGGGT	300
	TCCCCTGCCT	GAGCGCGATA	TCGACAAACC	GTTCTTGATG	CCGGTTGAAG	350
20	ACGTGTTCTC	TATCACGGGT	CGTGGTACGG	TCGCTACAGG	ACGTATCGAA	400
	ACCGGTATTG	TGAAGACCGG	TGACGAAGTT	CAAATCATCG	GCCTCGGTGC	450
	AGAAGGAATG	AAGTCGGTTG	TTACGGGTGT	TGAAATGTTC	CGTAAGATTC	500
	TTGACGAAGG	TCAGGCTGGT	GACAACGTTG	GTCTCCTCCT	GCGTGGTATC	550
	GATAAGGATC	AGATCAAGCG	TGGTATGGTT	ATCTCTCACC	CGGGTAAGAT	600
25	TACTCCTCAC	AAGAGATTTA	AGGCCGAGGT	TTATATCTTG	AAGAAAGAAG	650
	AAGGTGGTCG	CCACACTCCT	TTCCACAACA	AATATCGTCC	GCAGTTCTAC	700
	ATCCGTACGC	TTGACGTGAC	CGGTGAAATC	ACTCTTCCCG	AAGGAACAGA	750
	AATGGTTATG	CCCGGTGACA	ACGTAACGAT	CACTGTAGAA	CTCATCTACC	800
30	CGGTTGCATG	TAATGTAG				818

2) INFORMATION FOR SEQ ID NO: 142

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pragia fontium*
 45 (B) STRAIN: ATCC 49100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142

	CGGCGCTATT	CTGGTTGTTG	CTGCAACTGA	TGGTCCTATG	CCTCAAACCTC	50
50	GTGAGCACAT	CCTGTTAGGY	CGCCAGGTTG	GCGTACCATA	CATCATTGTG	100
	TTCCTGAACA	AGTGTGACAT	GGTTGAYGAT	GAAGAGCTGT	TAGAACTGGT	150
	TGAAATGGAA	GTTTCGTGAGC	TTCTGTCTCA	GTACGATTTC	CCAGGTGATG	200
	ATACTCCAGT	TGTTTCGTGGT	TCTGCGCTGA	AAGCGTTRGA	AGGCGAAGCT	250
	GAGTGGGAAG	CTAAAATCAT	TGAATTGGCT	GACTCCCCTGG	AYAGCTACAT	300
55	TCCACAGCCA	GAGCGTGCAA	TTGATAAGCC	GTTCTTGCTG	CCAATCGAAG	350
	ACGTTTTTCTC	AATCTCTGGC	CGTGGTACAG	TAGTAACCGG	TCGTGTAGAG	400
	CGCGGTATCG	TTAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	TACTGTGAAA	ACAACTTGTA	CTGGCGTTGA	AATGTTCCGT	AARTTACTGG	500
	ATGAAGGCCG	TGCGGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTACTAAG	550
60	CGTGATGAAA	TCGAACGTGG	TCAAGTATTA	GCAAAACCAG	GTTCAATCAA	600

	CCCGCATACT	AACTTCGTAT	CAGAAGTTTA	TATCCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	TACTCCATTTC	TTCAAAGGCT	ACCGTCCACA	GTTYTACTTC	700
	CGTACAACCTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGTGATAACA	TTCAGATGAC	TGTAACCTCTG	ATTGCCCCAA	800
5	TCGCGATGGA	CGAAGGTTTA	CGCTTCGCTA			830

2) INFORMATION FOR SEQ ID NO: 143

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Prevotella melaninogenica*
 (B) STRAIN: ATCC 25845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143

25	TGGTGCTATC	TTGGTTGTAG	CTGCTACTGA	TGGTCCTATG	CCTCAGACTC	50
	GTGAGCACGT	ATTGCTCGCT	CGTCAGGTAA	ACGTACCTCG	CTTGGTTGTA	100
	TTCTTGAACA	AGTGTGATAT	GGTTGACGAT	GCTGAGATGC	TTGACCTCGT	150
	TGAGATGGAG	GTTCTGTGAG	TCCTCGAGCA	GTACGGTTAT	GAGGAGGATA	200
	CTCCTATTAT	TCGTGGTTCT	GCACTCGGTG	CTTTGAACGG	TGTTGAGAAG	250
30	TGGGTAGACT	CTGTAATGGA	GCTCATGGAT	ACTGTTGACA	CTTGATTGA	300
	AGAGCCAGAG	CGTGAGATTG	ACAAGCCATT	CTTGATGCCT	GTTGAGGACG	350
	TATTCTCTAT	CACAGGTCGT	GGTACTGTAG	CTACTGGTCG	TATCGAGACT	400
	GGTATCTGTA	AGGTAGGTGA	TGAGGTTTCA	TTGCTCGGTC	TCGGTGAGGA	450
	CAAGAAGTCT	GTTATCACTG	GTGTTGAGAT	GTTCCGTAAG	AACCTTCCAA	500
35	CAGGTCAGGC	TGGTGACAAC	GTAGGTTCTC	TCCTTCGTGG	TATCGATAAG	550
	GCTGAGGTTA	AGCGTGGTAT	GGTTGTTGTG	CACCCAGGTG	CTATTACTCC	600
	TCACGATCAC	TTCAAGGCAT	CTATCTATGT	ATTGAAGAAG	GAAGAGGGTG	650
	GTCGTCATAC	TCCATTCCGT	AACAAGTATC	GTCCACAGTT	CTACCTCCGT	700
	ACAATGGACT	GTACAGGTGA	AATCCACCTC	CCAGAGGGCG	TTGAGATGGT	750
40	TATGCCAGGT	GACAACGTAG	AGATTGAAGT	TGTATTGATC	TATAAGGTTG	800
	CTTTGAACGA	GGGTCTTCGT	T			821

45 2) INFORMATION FOR SEQ ID NO: 144

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Prevotella oralis*
 (B) STRAIN: ATCC 33269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144

60

	TGGTGCTATT	CTTGTAAGTAG	CTGCTACTGA	CGGTCCTATG	CCTCAAACCTC	50
	GTGAACACGT	GCTTCTTGCT	CGTCAGGTGA	ACGTACCTCG	TTTGGTCGTT	100
	TTCTTGAACA	AGTGCGATAT	GGTTGACGAT	GAAGAAATGC	TTGAGCTCGT	150
	AGAAATGGAG	CTTCATGAAC	TTCTCGAGCA	GTATGAATAT	GAGGAGGATA	200
5	CTCCTATTGT	TCGTGGTTCG	GCACTTGGCG	CTCTGAATGG	AGTAGAGAAG	250
	TGGGTTGACA	GCGTGATGAA	GTTGATGGAT	ACCGTTGATG	AATGGATACA	300
	GGAACCAACG	CGTGATCTTG	ATAAGCCTTT	CTTGATGCCG	GTAAGAGGATG	350
	TATTTTCTAT	TACTGGTCGT	GGAACGGTTG	TTACAGGCCG	TATTGAAACT	400
	GGTAAGGTTA	AGGTGGGCGA	TGAAGTTCAA	CTTCTTGGTC	TCGGTGAAGA	450
10	TAAGAAGTCC	GTTGTGACAG	GCGTTGAGAT	GTTCCGTAAG	ATTCTTGACG	500
	AAGGTGAAGC	TGGTGATAAT	GTAGGCTTGC	TGCTTCGTGG	TATCGATAAG	550
	ACGGAAGTAA	AGCGTGGTAT	GGTTGTCGTA	CATCCGGGGG	CTATTACTCC	600
	TCACGATCAT	TTCAAGGCTT	CAGTTTACGT	ATTGAAGAAA	GAAGAAGGCG	650
	GTCGCCATAC	TCCGTTTGGT	AMCAAGTATC	GTCCACAGTT	CTATCTTCGT	700
15	ACCATGGACT	GTACTGGTGA	AATTACTCTT	CCGGAAGGAG	TTGAGATGGT	750
	AATGCCGGGT	GATAACGTCG	AAATTGAAGT	TAAGTTGATC	TATCCGGTAG	800
	CTTTGAACGA	GGGACTTCGT	TTCGCTA			827

20

2) INFORMATION FOR SEQ ID NO: 145

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 833 bases
25	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Propionibacterium acnes</i>
(B)	STRAIN: ATCC 6919

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145

	CGGCGCCATC	CTCGTGGTTG	CTGCTACCGA	CGGCCCGATG	CCTCAGACTC	50
	GCGAGCACGT	TCTGCTCGCT	CGTCAGGTGG	GCGTGCCCGC	CATCGTCGTC	100
	GCCCTCAACA	AGTGCGACAT	GGTTGACGAT	GAGGAGCTCA	TTGAGCTCGT	150
40	CGAGATGGAG	GTCCGCGAGC	TGCTGACCTC	GCAGGAGTTC	GACGGCGACA	200
	ACTGCCCTGT	CGTTCGCATC	TCCGCCTTCC	AGGCCCTCCA	GGGTGATGAG	250
	AAGTGGACCC	AGTCGATCCT	CGACCTCATG	GACGCCGTGG	ACGAGTACAT	300
	CCCGCAGCCT	GAGCGCGATC	TCGACAAGCC	CTTCCTTATG	CCGATCGAGG	350
	ACGTCTTCAC	CATCACCAGC	CGTGGCACC	TTGTCACCGG	TCGTGTCGAG	400
45	CGCGGCGTCG	TCAAGACTGG	CGAAGAGGTC	GAGATCGTCG	GTATCCACGA	450
	GAAGACCCAG	AAGACCACCG	TTACCGGTGT	CGAGATGTTC	CGCAAGATCC	500
	TCGACGAGGG	CCGCGCTGGT	GAGAACGTCG	GCGTTCTGCT	CCGTGGCACC	550
	AAGAAGGAGG	ATGTCGTTTC	CGGCATGGTC	CTCTCCAAGC	CTGGTTCCAC	600
	CACCCCCAC	ACCGACTTCG	AGGGCCAGGT	CTACGTCCTC	AAGAAGGATG	650
50	AGGGTGGCCG	CCACAAGCCG	TTCTTCTCCC	ACTACAGCCC	CCAGTTCTAC	700
	TTCCGTACCA	CGGACGTGAC	TGGCACTGTT	GAGCTCCCCG	AGGGCACCGA	750
	GATGGTCATG	CCTGGCGACA	ACACCGACAT	GACTGTGCAC	CTGATTCACC	800
	CGGTTGCCAT	GGAGGATCAG	CTCAAGTTCC	CTA		833

55

2) INFORMATION FOR SEQ ID NO: 146

(i) SEQUENCE CHARACTERISTICS:

60	(A)	LENGTH: 745 bases
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(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*
 (B) STRAIN: ATCC 35659

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146

	CACAAACTCG	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	TGTTCCCTTAC	50
	ATCATCGTAT	TCCTGAACAA	ATGTGACATG	GTAGATGATG	AAGAGCTGTT	100
15	AGAATTAGTT	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAA	TACGATTTC	150
	CAGGTGATGA	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCACTGGAA	200
	GGCGAAGCAG	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	AAGCACTGGA	250
	TTCTTATATC	CCAGAGCCAG	AGCGTGCAAT	TGACAAACCA	TTCCTGTTAC	300
	CAATCGAAGA	TGTATTCTCA	ATCTCAGGCC	GTGGTACAGT	AGTTACTGGT	350
20	CGTGTAGAGC	GTGGTATCAT	CAAAGTAGGT	GATGAAGTTG	AGATTGTTGG	400
	TATCAAAGAA	ACCGCCAAAA	CAACTTGTA	TGGCGTTGAA	ATGTTCCGTA	450
	AATTACTTGA	CGAAGGTCGT	GCAGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	500
	GGTACAAAAC	GTGAAGAAAT	CGAACGTGGA	CAAGTACTGG	CRAAACCAGG	550
	CTCAATCAAC	CCACACAACA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	600
25	AAGATGAAGG	TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	650
	TTCTACTTCC	GTACAACCTGA	CGTAACTGGT	ACTATCGAAT	TACCAGAAGG	700
	CGTAGAAATG	GTAATGCCAG	GCGACAACGT	GAACATGATC	GTTGA	745

30

2) INFORMATION FOR SEQ ID NO: 147

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus penneri*
 (B) STRAIN: ATCC 33519

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147

	GGAGCTATCC	TGGTTGTTGC	TGCGACAGAT	GGCCCAATGC	CACAAACTCG	50
	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	TGTTCCCTTAC	ATCATCGTAT	100
	TCCTGAACAA	ATGTGACATG	GTAGATGATG	AAGAGTTACT	GGAATTAGTM	150
50	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTC	CAGGTGATGA	200
	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCACTGGAA	GGCGAAGCAG	250
	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	AAGCACTGGA	TTCATACATC	300
	CCAGARCCAG	AGCGTGCAAT	TGACAAACCA	TTCCTGTTAC	CAATTGAAGA	350
	CGTATTCTCA	ATTTCAGGCC	GTGGTACAGT	AGTAACAGGT	CGTGTGAGC	400
55	GTGGCGTAAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATTAAACCA	450
	ACAGCGAAAA	CAACTTGTA	TGGCGTTGAA	ATGTTCCGTA	AATTACTTGA	500
	CGAAGGTCGT	GCAGGTGAGA	ACGTAGGTGT	TCTTCTGCGT	GGTACTAAAC	550
	GTGAAGAAAT	CGAACGTGGA	CAAGTACTGG	CGAAACCAGG	TTCAATCAAC	600
	CCACACACTA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	650
60	TGGTCGTCAT	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700

GTACAACTGA	CGTAACTGGT	ACTATCGAAT	TACCAGAAGG	CGTAGAAATG	750
GTAATGCCAG	GTGACAACAT	CAACATGATC	GTTGAACTGA	TTCACCCAAT	800
CGCGATGGAC	GACGGTTTAC	GTTTCGCTA			829

5

2) INFORMATION FOR SEQ ID NO: 148

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus vulgaris*
 (B) STRAIN: ATCC 13315

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148

CGGAGCTATT	CTGGTTGTTG	CTGCGACTGA	TGGCCCAATG	CCACAAACTC	50
GTGAGCACAT	CCTGTTAGGT	CGCCAGGTTG	GTGTACCTTA	CATCATCGTA	100
25 TTCCTGAACA	AATGTGACAT	GGTTGATGAT	GAAGAACTGC	TGGAATTAGT	150
AGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCAGGTGATG	200
ACACTCCAGT	AATCCGTGGT	TCAGCGCTGA	AAGCACTGGA	AGGCGAAGCT	250
GAGTGGGAAG	CAAAAATTGT	TGAATTAGCA	GAAGCACTGG	ATTCTTACAT	300
CCCAGAACCA	GAGCGTGCAA	TTGACAAACC	ATTCCTGCTG	CCTATCGAAG	350
30 ACGTATTCTC	AATCTCTGGT	CGTGGTACAG	TAGTAACAGG	CCGTGTAGAG	400
CGTGGTGTG	TTAAAGTTGG	TGAAGAAGTT	GAGATTGTTG	GTATTAAAGA	450
CACAGTTAAA	ACAACCTTGT	CTGGCGTTGA	AATGTTCCGT	AAATTACTTG	500
ACGAAGGTCG	TGCAGGTGAG	AACGTAGGTG	TTCTTCTGCG	TGGTACTAAA	550
CGTGAAGAAA	TCGAACGTGG	ACAAGTACTG	GCTAAACCAG	GTTCAATCAA	600
35 GCCACACACT	AAATTCGAAT	CAGAAGTTTA	TATCCTGAGC	AAAGATGAAG	650
GTGGTCGTCA	CACTCCATT	TTCAAAGGTT	ACCGTCCACA	GTTCTACTTC	700
CGTACAACTG	ACGTAACCTG	TACTATCGAA	TTACCAGAAG	GCGTAGAAAT	750
GGTAATGCCA	GGTGACAACA	TCAACATGAT	CGTTGAACTG	ATTCACCCTA	800
TCGCGTAGGA	CGACGGTTTA	CGTT			824

40

2) INFORMATION FOR SEQ ID NO: 149

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 745 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia alcalifaciens*
 55 (B) STRAIN: ATCC 9886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149

CACAAACTCG	TGAGCACATC	CTGTTAGGTC	GCCAAGTAGG	TGTTTCCTTAC	50
60 ATCATCGTTT	TCCTGAACAA	ATGTGACATG	GTAGACGACG	AAGAACTGTT	100

90

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    AGAATTAGTT GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGATTTCC      150
    CAGGCGATGA CACTCCAGTT GTTCGCGGTT CAGCACTGAA AGCGCTGGAA      200
    GGCAACCCAG AGTGGGAAGC AAAAATTGTT GAATTAGCAG GTTACCTGGA      250
    TTCTTACATC CCAGAACCAG AGCGTGCAAT TGACAAGCCA TTCCTGCTGC      300
5   CAATCGAAGA CGTATTCTCA ATCTCTGGTC GTGGTACAGT AGTAACAGGC      350
    CGTGTTGAGC GTGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG      400
    TATTCAAGCG ACTGCGAAAA CAACTTGTAC TGGCGTTGAA ATGTTCCGTA      450
    AACTGCTGGA TGAAGGTCGT GCGGGTGAGA ACGTTGGTGT TCTGCTGCGT      500
    GGTACTAAAC GTGAAGAAAT TCAACGTGGT CAAGTACTGG CTAAACCAGG      550
10  TTCAATCAAG CCACACACTC AATTCTGAATC AGAAGTATAT ATTCTGAGCA      600
    AAGATGAAGG TGGTCGTCAT ACTCCATTCT TCAAAGGCTA CCGTCCACAG      650
    TTCTACTTCC GTACAACTGA CGTAACCGGT ACTATCGAAC TGCCAGAAGG      700
    CGTAGAGATG GTAATGCCAG GCGACAACAT CAACATGATC GTGAC          745

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15

2) INFORMATION FOR SEQ ID NO: 150

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    (i) SEQUENCE CHARACTERISTICS:
20   (A)   LENGTH: 830 bases
      (B)   TYPE: Nucleic acid
      (C)   STRANDEDNESS: Double
      (D)   TOPOLOGY: Linear

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25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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    (A)   ORGANISM: Providencia rettgeri
    (B)   STRAIN: ATCC 9250

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30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150

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    CGGTGCAATC CTGGTTGTTG CTGCGACTGA TGGCCCAATG CCACAAACTC      50
    GTGAGCACAT CCTGTTAGGY CGCCAAGTAG GTGTWCCTTA CATCATCGTT      100
35  TTCCTGAACA AATGTGACAT GGTAGACGAC GAAGAACTGT TAGAATTAGT      150
    TGAAATGGAA GTTCGTGAAC TTCTGTCTCA ATACGATTTC CCAGGCGACG      200
    AACTCCAGT TGTCCGTGGT TCAGCTCTGA AAGCGCTGGA AGGCAACCCA      250
    GAGTGGGAAG CGAAAATTGT TGAATTAGCA GGTCACCTGG ATTCTTACAT      300
    CCCAGAACCA GAGCGTGCAA TTGACAAACC ATTCCTGCTG CCAATCGAAG      350
40  ACGTATTCTC AATCTCTGGT CGTGGTACAG TAGTAACAGG CCGTGTTGAG      400
    CGTGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCCAAGA      450
    CACGGTTAAA ACAACTTGTA CTGGCGTTGA AATGTTCCGT AAAGTGTGCTGG      500
    ACGAAGGTCG TGCGGGTGAG AACGTTGGTG TTCTGCTGCG TGGTACTAAA      550
    CGTGAAGAAA TTCAACGTGG TCAAGTACTG GCAAAACCAG GTTCAATCAA      600
45  GCCACACACT AAATTCGAAT CAGAAGTCTA TATTCTGAGC AAAGATGAAG      650
    GTGGTCGTCA CACTCCATTC TTCAAAGGTT ACCGTCCACA GTTCTACTTC      700
    CGTACAACCTG ACGTAACAGG TACTATCGAA CTGCCAGAAG GCGTAGAGAT      750
    GGTAATGCCA GGTGATAACA TCAACATGAT CGTTACCCTG ATCCACCCAA      800
    TCGCGATGGA CGACGGTTTA CGTTTCGCAA          830

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50

2) INFORMATION FOR SEQ ID NO: 151

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55   (i) SEQUENCE CHARACTERISTICS:
      (A)   LENGTH: 826 bases
      (B)   TYPE: Nucleic acid
      (C)   STRANDEDNESS: Double
      (D)   TOPOLOGY: Linear

```

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rustigianii*
 5 (B) STRAIN: ATCC 33673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151

	CGGTGCAATC	CTGGTTGTTG	CTGCGACTGA	TGGCCCAATG	CCACAAACTC	50
10	GTGAGCACAT	CCTGTTAGGT	CGCCAAGTAG	GTGTTCCCTTA	CATCATCGTT	100
	TTCCTGAACA	AATGTGACAT	GGTTGACGAC	GAAGAACTGT	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCAGGCGACG	200
	ACACTCCAGT	TGTTTCGYGGT	TCAGCACTGA	AAGCGCTGGA	AGGTATCCCT	250
	GAGTGGGAAG	CGAAAATTGT	TGAATTAGCC	GGTTACCTGG	ACAGCTACAT	300
15	CCCAGAACCA	GAGCGCGCAA	TTGACCGTCC	ATTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	AATCTCTGGT	CGTGGTACAG	TAGTAACAGG	SCGTGTTGAG	400
	CGTGGTATCG	TTAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCCAAGA	450
	CACRGTTAAA	ACAACTTGTA	CTGGCGTTGA	AATGTTCCGT	AAACTGCTTG	500
	ACGAAGGTCG	TGCTGGTGAG	AACGTTGGTG	TTTTACTGCG	TGGTACTAAG	550
20	CGTGAAGAAA	TTCAACGTGG	TCAAGTACTG	GCTAAACCAG	GTTCAATCAA	600
	GCCACACACT	ACTTTTGAAT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	TACTCCATTC	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTAACCGG	TACTATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGCGACAACA	TCAACATGAT	CGTGACACTG	ATTCACCCAA	800
25	TCGCGATGGA	TGATGGTTTA	CGTTTC			826

2) INFORMATION FOR SEQ ID NO: 152

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia stuartii*
 40 (B) STRAIN: ATCC 33672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152

45	CGGTGCAATC	CTAGTTGTTG	CGGCAACAGA	TGGCCCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTGTTAGGT	CGTCAGGTTG	GCGTTCCTTA	CATCATCGTG	100
	TTCCTGAACA	AATGTGACAT	GGTAGACGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	ATACGATTTC	CCAGGTGATG	200
	ACACTCCAGT	TATCCGTGGT	TCAGCGCTGA	AAGCGTTGGA	AGGCAACCCA	250
50	GAGTGGGAAG	CGAAAATCGT	TGAACTAGCA	GAAGCACTGG	ACAGCTACAT	300
	CCCAGAGCCA	GAGCGTGCAA	TTGACAAGCC	ATTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	AATCTCAGGT	CGTGGTACAG	TAGTCACAGG	CCGTGTTGAG	400
	CGTGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTAG	GTATCAAAGA	450
	GACTGCGAAA	ACCACTTGTA	CTGGCGTTGA	AATGTTCCGT	AAACTGCTGG	500
55	ACGAAGGCCG	TGCGGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTACTAAG	550
	CGTGAAGAAA	TCGAACGTGG	TCAAGTTCTG	GCGAAACCAG	GTTCAATCAA	600
	GCCACACACA	ACTTTCGAAT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	CACGCCATTC	TTCAAAGGYT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTAACAGG	TACTATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
60	GGTAATGCCA	GGCGACAACG	TGAACATGAA	AGTAACTCTG	ATTCACCCAA	800

TCGCGATGGA CGATGGTTTG CGTTTCGCAA

5 2) INFORMATION FOR SEQ ID NO: 153

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
 (B) STRAIN: ATCC 35554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153

20 CCTGGTTTGC TCGGCTGCCG ACGGCCCAT GCCGCAGACC CGCGAGCACA 50
 TCCTGCTGTC CCGCCAGGTA GCGTTCCCT ACATCGTCGT GTTCCTGAAC 100
 AAAGCCGACA TGGTCGACGA CGCCGAGCTG CTGGAAGTGG TCGAGATGGA 150
 AGTTCGCGAT CTGCTGAACA CCTACGACTT CCCGGGCGAC GAACTCCGA 200
 25 TCATCATCGG TTCCGCGCTG ATGGCGCTGG AAGGCAAGGA TGACAACGGC 250
 ATCGGCGTAA GCGCCGTGCA GAAGCTGGTA GAGACCCTGG ACTCCTACAT 300
 TCCGGAGCCG GTTCGTGCCA TCGACCAGCC GTTCCTCATG CCGATCGAAG 350
 ACGTGTTCCTC GATCTCCGGT CGCGGTACCG TGGTAACCGG TCGTGTAAG 400
 CGCGGCATCA TCAAGGTCCA GGAAGAAGTG GAAATCGTCG GCATCAAGGC 450
 30 GACCACCAAG ACCACCTGCA CCGGCGTTGA AATGTTCCGC AAGCTGCTCG 500
 ACGAAGGTCG TGCTGGTGAG AACGTTGGTA TCCTGCTGCG TGGCACCAAG 550
 CGTGAAGACG TAGAGCGTGG CCAGGTACTG GCCAAGCCGG GCACCATCAA 600
 GCCGCACACC AAGTTCGAGT GCGAAGTGTA CGTGCTGTCC AAGGAAGAAG 650
 GTGGTCGTCA CACCCCGTTC TTCAAGGGCT ACCGTCCGCA GTTCTACTTC 700
 35 CGTACCACKG ACGTGACCGG TAMCTGCGAG CTGCCGGAAG GCGTAGAGAT 750
 GGTAATGCCG GGCGACAACA TCAAGATGGT TGTCAACCTG ATCGCTCCGA 800
 TCGCCATGGA AGATGGCTGC GTTCGCG 827

40

2) INFORMATION FOR SEQ ID NO: 154

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas fluorescens*
 (B) STRAIN: ATCC 13525

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154

CGGCGCAATC CTGGTTTGCT CGGCCGCTGA TGGTCCGATG CCACAAACCC 50
 GTGAACACAT CCTGCTGTCC CGTCAGGTTG GCGTTCCGTA CATCGTGGTT 100
 TACCTGAACA AGGCTGACCT GGTAGACGAC GCTGAGCTGC TGGAAGTGGT 150
 60 TGAGATGGAA GTGCGCGATC TGCTGAGCAC TTACGACTTC CCAGGCGACG 200

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    ACACTCCGAT CATCATCGGT TCTGCTCGTA TGGCTCTGGA AGGCAAAGAC 250
    GACAACGAAA TGGGCACCAC GTCCGTTCTG AACTGGTTG AACTCTGGA 300
    CAGCTACATC CCAGATCCAG TTCGTGTTAT CGACAAGCCG TTCCTGATGC 350
    CAATCGAAGA CGTGTTCTCG ATCTCCGGTC GCGGTACTGT TGTGACTGGT 400
5   CGTATCGAGC GCGGTATCGT TAAGGTTCAA GATCCACTGG AAATCGTTGG 450
    TCTGCGTGAC ACTACCGTCA CCACCTGCAC CCGTGTTGAA ATGTTCCGTA 500
    AGCTGCTCGA CGAAGGTCGT GCTGGCGAGA ACTGCGGCGT TCTGCTGCGT 550
    GGTACCAAGC GTGACGACGT TGAGCGTGGC CAGGTTCTGG TTAAGCCAGG 600
    TTCGGTTAAG CCGCACACCA AGTTCGAAGC TGAAGTCTAC GTACTGAGCA 650
10  AAGAAGAAGG CCGTCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCACAG 700
    TTCTACTTCC GTACTACTGA CGTGACTGGT AACTGCGAGC TGCCGGAAGG 750
    CGTTGAAATG GTTATGCCAG GCGACAACAT CAAAATGGTT GTTACCCTGA 800
    TCAAAACCAT CGCAATGGAA GACGGTCTGC GTTTCGCTAT T 841

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15

2) INFORMATION FOR SEQ ID NO: 155

(i) SEQUENCE CHARACTERISTICS:

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    (A) LENGTH: 841 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

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    (A) ORGANISM: Pseudomonas stutzeri
    (B) STRAIN: ATCC 17588

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155

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    CGGCGCGATC CTGGTCTGCT CGGCTGCTGA CGGCCCCATG CCGCAGACTC 50
    GCGAGCACAT CCTGCTGTCC CGTCAGGTTG GTGTTCCGTA CATCGTCGTG 100
    TTCCTGAACA AGGCCGACAT GGTGATGAC GCCGAGCTGC TCGAGCTGGT 150
35  CGAGATGGAA GTTCGYGACC TGCTGTCGAC CTACGACTTC CCGGGTGAYG 200
    ACACTCCGAT CATCATCGGC TCCGCGCTGA TGGCGCTGAA CGGCGAAGAC 250
    GACAACGAGC TCGGCACCAC TGCGGTGAAG AAGCTGGTCG AGACCCTGGA 300
    CAGCTACATT CCCGAGCCGG TTCGTGCCAT CGACAAGCCG TTCCTGATGC 350
    CGATCGAAGA CGTGTTCTCG ATCTCCGGTC GCGGCACSGT GGTAACCGGT 400
40  CGCGTAGAGC GCGGCATCGT CAAGGTTTCA GAAGAGATCG AGATCGTCGG 450
    TCTGCGTCCG ACCACCAAGA CTACCTGCAC CGGCGTTGAG ATGTTCCGCA 500
    AGCTGCTCGA YGARGGTCTG GCTGGCGAGA ACTGCGGYGT GCTGCTGCGT 550
    GGCACCAAGC GTGACGAAGT GGAGCGTGGT CAGGTTCTGG CCAAGCCGGG 600
    CACCATCAAG CCGCACACCA AGTTCGAAGC CGAAGTGTAC GTGCTGTCCA 650
45  AGGAAGAAGG TGGTCGTCAC ACCCCGTTCT TYAAGGGCTA CCGTCCKCAG 700
    TTCTACTTCC GTACCACTGA YGTGACYGGW TCGTGCGARC TGCCGGAAGG 750
    CGTCGAGATG GTAATGCCGG GCGACAACGT GAAGATGGTT GTCACCCTGA 800
    TCAAGCCGAT CGCCATGGAA GACGGCCTGC GCTTCGCGAT T 841

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50

2) INFORMATION FOR SEQ ID NO: 156

(i) SEQUENCE CHARACTERISTICS:

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    (A) LENGTH: 833 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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55

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Psychrobacter phenylpyruvicus*
 (B) STRAIN: ATCC 23333

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156

GCTATTCTAG TAGTATCAGC AACTGACGGT CCAATGCCAC AAACACGTGA 50
 GCACATTCTA TTATCACGTC AGGTTGGTGT ACCATACATC ATCGTATTCA 100
 10 TGAACAAATG TGACATGGTA GATGACGAAG AGTTACTAGA GCTAGTAGAA 150
 ATGGAAGTGC GTGAATTACT TTCAGACTAC GACTTCCCAG GTGATGACAC 200
 TCCAATCATC AAAGGTTTCAG CTTTAGAAGC GTTAAATGGT AACGACGGTA 250
 AGTACGGTGA GCCAGCAGTT ATCGAACTAC TAAACACTCT AGACACTTAC 300
 ATTCCAGAGC CAGAGCGTGA CATCGATAAG CCATTCCCTAA TGCCAATCGA 350
 15 AGACGTATTC TCAATCTCAG GTCGTGGTAC AGTAGTAACA GGCCGTGTTG 400
 AATCTGGTAT CATCAAAGTT GGTGACGAAA TCGAAATCGT TGGTATCAAA 450
 GACACAGTTA AAACAACCTG TACTGGTATC GAGATGTTCC GTAAGTTACT 500
 AGACGAAGGT CGTGCTGGTG AGAACTGTGG TGTACTATTA CGTGGTACTA 550
 AGCGTGAAGA CGTACAACGT GGTCAAGTAC TTGCTAAGCC AGGTTCAATC 600
 20 ACTCCACACA CCAACTTCGA CGCAGAAGTA TACGTACTAT CAAAAGAAGA 650
 AGGTGGTCGT CACACTCCAT TCTTAAATGG TTACCGTCCA CAGTTCTACT 700
 TCCGTACTAC TGACGTAACA GGTGCAATCA CGTTACAAGA AGGTACTGAA 750
 ATGGTAATGC CAGGCGATAA CGTTGAGATG AGCGTAGAGC TAATCCACCC 800
 AATCGCTAGG ACAAAGGTTT ACGTTTCGCA ATC 833
 25

2) INFORMATION FOR SEQ ID NO: 157

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rahnella aquatilis*
 40 (B) STRAIN: ATCC 33071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157

GCGCTATCC TGGTTGTTGC TGCAACTGAC GGCCCTATGC CTCAGACTCG 50
 45 TGAGCACATC CTGCTGGGTC GCCAGGTTGG CGTTCCATAC ATGATCGTGT 100
 TCATGAACAA ATGCGACATG GTAGATGACG AAGAGCTGCT GGAAGTGGTA 150
 GAAATGGAAG TTCGCGAACT TCTGTCTGCT TACGAATTCC CAGGCGACGA 200
 CATCCCGGTC ATCAAAGGTT CAGCGCTGAA AGCACTGGAA GGCGATGCTA 250
 CTTGGGAAGC GAAAATCATC GAACTGGCAG AAGCACTGGA CAGCTACATT 300
 50 CCATTGCCAG AGCGTGCTAT CGATAAGCCA TTCCTGCTGC CAATCGAAGA 350
 CGTATTCTCC ATCTCCGGTC GTGGTACAGT GGTACCAGG CGTGTAGAGC 400
 GCGGTATCGT TAAAGTGGGC GAAGAAGTTG AAATCGTCGG TATCAAGGAC 450
 ACTGTTAAGT CTACTTGTA TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
 CGAAGGCCGT GCGGGCGAGA ACGTGGGTGT TCTGCTGCGT GGTATCAAGC 550
 55 GTGAAGACAT CGAACGTGGT CAGGTTCTGG CTAAACCAGG TTCAATCAAA 600
 CCACACACCA AGTTTGATTC CGAAGTGTA ATCCTGAGCA AAGATGAAGG 650
 TGGTCGTCAC ACTCCATTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC 700
 GTACAACTGA CGTGACCGGT ACTATCGAAC TGCCAGAAGG CGTTGAGATG 750
 GTTATGCCTG GTGACAACGT GAACATGGTT GTTACCCTGA TCCACCCAAT 800
 60 CGCGATGGAT GACGGTCTGC GTTTC 825